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Number of sequences searched:
Number of scores above cutoff:
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19

2

Gaps Initial Score Residue Identity US-09-697-123B-24 (1-208) US-09-697-123B-2 Sequence 24, Application US/09697123B ٠., 90 100% Matches - 208 0 Conservative Substitutions 208 Optimized Score Matches 100 110 1 1 208 Significance 208 Mismatches 120 130 9 006

Gaps Initial Score Residue Identity 2. US-09-697-123B-24 (1-208) US-09-697-123B-1 Sequence 15, Application US/09697123B . . . 182 87% 0 Optimized Score Conservative Substitutions Matches 8 H 182 Significance 182 Mismatches

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Gaps
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Residue
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Residue
Gaps
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US-09-697-123B-2 Sequence
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US-09-697-123B-8 Sequence
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US-09-697-123B-1 Sequence 17,
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Conservative
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Conservative
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US-09-697-123B-24 (1-208) US-09-697-123B-1 Sequence

Application US/09697123B

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US-09-697-123B-1 Sequence
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US-09-697-123B-1 Sequence 11,
AGAATGCGCCAACCACCACGACCGTGACCGAAGAGGGCGTCGTCGCCACCATCGAATACCTGGTCGCCTTGC
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Conservative Substitutions
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US-09-697-123B-1 Sequence 10,
US-09-697-123B-24 (1-208)
US-09-697-123B-2 Sequence
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US-09-697-123B-24 (1-208)
US-09-697-123B-1 Sequence
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US-09-697-123B-2 Sequence
                                                                                                                                                                                                                                                        US-09-697-123B-24 (1-208)
US-09-697-123B-3 Sequence
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        US-09-697-123B-24 (1-208)
US-09-697-123B-2 Sequence
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US-09-697-123B-5
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ACGAGGGCACGCACGATGAAGGTCCCCGGTGGCGAGGTGCCGGTGGAGACCGACGACAT
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US-09-697-123B-6 Sequence
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US-09-697-123B-24 (1-208) US-09-697-123B-4 Sequence

Sequence

4

Application US/09697123B

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Initial
Residue
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Residue Identity
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ACGACAT
                      US-09-697-123B-24 (1-208)
US-09-697-123B-1 Sequence
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US-09-697-123B-1 9
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79%
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Matches
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ACGACAT
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US-09-697-123B-9
                                                                                          US-09-697-123B-24 (1-208)
US-09-697-123B-7 Sequence
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82%
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Gaps Residue

Initial Score

Identity

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111 80% 6

Optimized Sco Matches Conservative :

Score -

166 Significanc
173 Mismatches

Significance = Mismatches = =

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Substitutions

Sequence

21,

Application US/09697123B

Gaps

Residue Identity Initial Score

109 83**%** 6

Optimized Score = Matches Conservative Substi

Substitutions

171 Significance 178 Mismatches

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. 82 0

US-09-697-123B-24 (1-208)
US-09-697-123B-1 Sequence

Sequence 14,

Application US/09697123B

140

90

100

110

120

130

140

100

110

80

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23.
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                                                                                                                                      22.
                                          US-09-697-123B-24 (1-208)
US-09-697-123B-2 Sequence
                 US-09-697-123B-24 (1-208)
US-09-697-123B-1 Sequence
                                                                                                                       Score
                                                                                                                  Identity
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                                                                                                            119
79%
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167
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Similarity matrix
Mismatch penalty
Gap penalty
Gap size penalty
Cutoff score
Randomization group
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                                                The scores below are sorted by initial score. Significance is calculated based on initial score
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Number of sequences searched:
Number of scores above cutoff:
      Sequence Name
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Release
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US-09-697-123B-1 Sequence 15, Application US-09-697-123B-2 Sequence 2, Application US-09-697-123B-3 Sequence 16, Application US-09-697-123B-1 Sequence 16, Application US-09-697-123B-1 Sequence 5, Application US-09-697-123B-5 Sequence 2, Application US-09-697-123B-1 Sequence 1, Application US-09-697-123B-1 Sequence 1, Application US-09-697-123B-1 Sequence 11, Application US-09-697-123B-1 Sequence 11, Application US-09-697-123B-1 Sequence 12, Application US-09-697-123B-1 Sequence 14, Application US-09-697-123B-1 Sequence 17, Application US-09-697-123B-2 Sequence 17, Application US-09-697-123B-2 Sequence 17, Application US-09-697-123B-1 Sequence 20, Application US-09-697-123B-2 Sequence 21, Application US-09-697-123B-1 Sequence 21, Application US-09-697-123B-2 Sequence 23, Application US-09-697-123B-2 Sequence 24, Application US-09-697-123B-2 Sequence 25, Application US-09-697-123B-2 Sequence 27, Application US-09-697-123B-2 Sequence 28, Application US-09-697-123B-2 Sequence 29, Application US-09-697-123B-2 Sequence 21, Application US-09-697-123B-2 Sequence 21, Application US-09-697-123B-2 Sequence 21, Application US-09-697-123B-2 Sequence 23, Application US-09-697-123B-2 Sequence 25, Appli	1. US-09-697-123B-2 Sequence 23, Application The list of other best scores is: Sequence Name Description
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Initial Score - Residue Identity -US-09-697-123B-23 (1-208) US-09-697-123B-2 Sequence 23, Application US/09697123B 208 100% 0 Optimized Score - Matches -Matches = 208 Conservative Substitutions 208 Significance - 208 Mismatches - -1.16 0 0

. US-09-697-123B-23 (1-208)
US-09-697-123B-1 Sequence 15, Application US/09697123B

Initial Score Residue Identity Gaps . . . 188 Optimized Score 90% Matches 0 Conservative Sub Conservative Substitutions 0 .74 20 0

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US-09-697-123B-3
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US-09-697-123B-23 US-09-697-123B-2

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US-09-697-123B-1 Sequence 14, Application
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US-09-697-123B-1 Sequence 13,
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US-09-697-123B-7;
                                                                                                                                                US-09-697-123B-23 (1-208)
US-09-697-123B-2 Sequence 21,
                                                                                                                                                                                                                                                                                                                                        Score
Identity
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                                                         3 (1-208)
Sequence
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Sequence
                                   113
81%
3
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75%
6
                                                                                                                                                                                  Optimized Score = 155
Matches = 162
Conservative Substitutions
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Matches
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Matches
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Matches = 168
Conservative Substitutions
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                                      165 Significance
171 Mismatches
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Similarity matrix
Mismatch penalty
Gap penalty
Gap size penalty
Cutoff score
Randomization group
Sequence Name
                                                                                 Number
Number
Number
                                                                                                                                                                                                                                                                          SCORE
STDEV
                             A 100% identical sequence
                                             Significance
                                            The scores below are sorted by initial score. Significance is calculated based on initial score.
                                                                                                                             Times:
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                                                                                                                                                      Scores:
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Number of sequences searched:
Number of scores above cutoff:
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Release 5.
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                                                                              residues:
sequences searched:
scores above cutoff:
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155
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12
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Gaps

Initial Score Residue Identity

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207 99**%** 0

Optimized Score -Matches -Conservative Substitutions

207

Mismatches Significance

1.01 1

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    US-09-697-123B-22 (1-208)
    US-09-697-123B-1 Sequence 16, Application US/09697123B

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US-09-697-123B-2 Sequence 22, Application US/09697123B
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6. US-09-697-123B-1 Sequence 11, Application
7. US-09-697-123B-3 Sequence 3, Application
9. US-09-697-123B-3 Sequence 3, Application
9. US-09-697-123B-1 Sequence 15, Application
10. US-09-697-123B-1 Sequence 23, Application
11. US-09-697-123B-1 Sequence 19, Application
12. US-09-697-123B-1 Sequence 19, Application
11. US-09-697-123B-1 Sequence 24, Application
12. US-09-697-123B-2 Sequence 27, Application
13. US-09-697-123B-2 Sequence 24, Application
14. US-09-697-123B-1 Sequence 20, Application
15. US-09-697-123B-2 Sequence 20, Application
16. US-09-697-123B-1 Sequence 20, Application
17. US-09-697-123B-1 Sequence 20, Application
18. US-09-697-123B-1 Sequence 3, Application
19. US-09-697-123B-1 Sequence 3, Application
19. US-09-697-123B-1 Sequence 18, Application
24. US-09-697-123B-1 Sequence 18, Application
25. US-09-697-123B-2 Sequence 21, Application
26. US-09-697-123B-2 Sequence 21, Application
27. US-09-697-123B-2 Sequence 21, Application
28. US-09-697-123B-2 Sequence 21, Application
29. US-09-697-123B-2 Sequence 3, Application
29
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US-09-697-123B-6 Sequence
US-09-697-123B-5 Sequence
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Residue
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US-09-697-123B-1
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US-09-697-123B-6 sequence
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-09-697-123B-5 s
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Optimized Score = 185
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Initial
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US-09-697-123B-3
US-09-697-123B-22
US-09-697-123B-1 5
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Sequence 11,
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US-09-697-123B-22 (1-208)

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Residue
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Initial
Residue
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US-09-697-123B-22
US-09-697-123B-2 s
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US-09-697-123B-1
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US-09-697-123B-8 Sequence
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150 160 170 180 190 200 x
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181 Mismatches
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181 Mismatches
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Mismatches
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28
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Initial
Residue
                               Gaps
                                                                                                                                                           Initial Score
Residue Identity
Gaps
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Residue
                                                      16.
                                                                                                                                                                                   15.
                                                                                                                                                                                                                                                                                                               14.
US-09-697-123B-22
US-09-697-123B-2 s
                                                                   US-09-697-123B-22
US-09-697-123B-2
                                                                                                                                                                                               US-09-697-123B-22
US-09-697-123B-1
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                                  Identity
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                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                         2 (1-208)
Sequence 17,
                              160
84%
3
                                                      (1-208)
                                                                                                                                                           172
82%
0
                                                                                                                                                                                   (1-208)
                                                                                                                                                                                                                                                                                           177
85%
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                                       Optimized
                              Matches
Conservative
                                                                                                                                                                                                                                                                                           Optimized Matches
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                                                 Application
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                                       Score
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                             Substitutions
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                                                 US/09697123B
                                                                                                                                                                              US/09697123B
                                  170
176
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172 Mismatches
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177
                                  Significance
Mismatches
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Mismatches
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Initial Residue Gaps

Identity Score

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143 80% 15

Optimized Matches

Significance Mismatches

0 0 0

23 29

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Conservative Substitutions

19.

US-09-697-123B-22 US-09-697-123B-9

Sequence

9

Application

US/09697123B 169 179

(1-208)

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Initial
Residue
Gaps
                                                                                         Residue
                                                                                              Initial
                                                                                                                                                                                                                                 17.
                             US-09-697-123B-22 (1-208)
US-09-697-123B-4 Sequence
                                                                                                                      US-09-697-123B-22 (1-208)
US-09-697-123B-1 Sequence
                                                                                                                                                                                                              Score
Identity
                                                                                         Identity
                                                                                              Score
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                                                                                                                                                                                                                            Sequence 12,
                                                                                    153
87%
1
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868
1
                                                                                   Optimized Sco
Matches
Conservative
                                                                                                                                                                                                         Optimized Sco
Matches
Conservative
                                                                                                     4, Application US/09697123B
                                                                                                                                                                                                                           Application US/09697123B
                                                                                         Score -
                                                                                                                                                                                                                  Score
                                                                                   Substitutions
                                                                                                                                                                                                         Substitutions
                                                                                       178 Significance
183 Mismatches
                                                                                                                                                                                                             175
180
                                                                                                                                                                                                             Significance
Mismatches
                                                                                                                                                                                                          . . .
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Initial Score
Residue Identity
Gaps
                                                                                 21.
                                                                                                                                                                                                                                     Initial Score
Residue Identi
                                                                                                                                                                                                                                                           20.
                    US-09-697-123B-22
US-09-697-123B-7 S
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ACGACAT
ACGACAT
220 x
 GCGAGCC-----
                                                                                                                              US-09-697-123B-22 (1-208)
US-09-697-123B-1 Sequence 13, Application US/09697123B
                                                                                                                                                                                                                                                                                                                                         80
-CATCACGTCGTCGACGCTGACCGAAGAAGAAGACGTCGTGGCCACCATCGAATATCTGGTCC
                                                        0 0 0
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                                                                           Sequence 7, Application US/09697123B
                                                      120
778
6
                                                                                 (1-208)
                                                                                                                                                                                                                                136
78%
15
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                                                     Conservative Substitutions
                                                                Optimized
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165
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175
                                           50
                                                           Mismatches
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Mismatches
                                                                Significance
                                           60
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                                          70
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Residue

Score Identity

108 78% 6

Optimized Sco Matches Conservative

Substitutions

161 168

Significance Mismatches

0

40

21,

Application US/09697123B

Initial

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Initial
Residue
Gaps
        24.
                                                                                                                                            Gaps
                                                                                                                                                  Residue
                                                                                                                                                        Initial
                       US-09-697-123B-22 (1-208)
US-09-697-123B-2 Sequence
                                                             US-09-697-123B-22 (1-208)
US-09-697-123B-1 Sequence 14, Application US/09697123B
                                                                                                                                                                                                                                                                                                                                                            US-09-697-123B-22 (1-208)
US-09-697-123B-1 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                  CCAACCCGGCTCTGGTGACTGCCACCACGCTCACCGAGGAAGACGTCGTCGCCACCATCGGGTACCTGGTGC 80 90 100 110 120 130 140
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818
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Matches
Conservative
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                                                                                                                                                      Score
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174 Mismatches
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164
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Gap penalty
Gap size pena
Cutoff score
                                                                                              Number of
Number of
Number of
                                                                                                                                            Times:
     Sequence Name
                                       P
                                                        The scores below are sorted by initial score. Significance is calculated based on initial score.
                                                                                                                                                                                                                                                                                                              SCORE O
STDEV -
                                                                                                                                                                                                                                                    Similarity matrix Mismatch penalty
                                                                                                                                                                                                                                                                                                                                           SECZECOES
                                                                                                                                                                           Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                      7 O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 F F X C Z
                                                                                                                                                                                                            Randomization group
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery sequence being compared:US-09-697-123B-21 (1-214)
Number of sequences searched: 26
Number of scores above cutoff: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 × 0 × 0 × 0 × 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Results file us-09-697-123b-21.res made by shanley on Wed 13 Nov 102 14:11:41-PST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Release 5.4
                                       100%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FastDB - Fast Pairwise Comparison of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100-
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                                       identical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Results of the initial comparison of US-09-697-123B-21 (1-214) with: File : US09697123B.seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IntelliGenetics
                                                                                             f residues:
f sequences sean
f scores above (
                                                                                                                                                                                                                                 penalty
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12
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                                    query sequence was found:
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Joining penalty
Window size
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112
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143
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Length Score Score
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09-	-09-697	US-09-697	9-	9-	9	9	9	-60	ġ	US-09-697	115-09-697	05-09-697	05-09-697	769-60-50	12 00 697	9	769-60	3	.60	9	9	Name	of.	-09-
US-09-697-123B-2	US-09-697-123B-4 US-09-697-123B-1	697-	US-09-697-123B-2	US-09-697-123B-	US-09-697-123B-	US-09-697-123B-	US-09-697-123B-2	US-09-697-123B-	US-09-697-123B-	697-	707	7607	100	200	29	US-09-69/-123B-	- 69		US-09-69/-123B-	US-09-697-123B-7	\ }	Ō	other	US-09-697-123B-2
1231	-123B-4 -123B-1	-123B-9	123	123B-	123	123	123	123	123	-123B-2	-1238-3	123B-1	-123B-2	-123B-B	-123B-	2.2	123B-1	,	.T.2.3	123	,	; ,		-123
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Sequence	Sequence Sequence	Sequ	Seq	Seq	Seq	Seq	Seq	Seq	200	200	bas	Seq	Seq	Seq	Seq	Seq	Seq	*	Seq	Seq	*	Description	scores	Seq
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Initial Score Residue Identity - Gans US-09-697-123B-21 (1-214)
US-09-697-123B-2 Sequence 21, Application US/09697123B 214 Optimized Score = 214 100% Matches = 214 0 Conservative Substitutions 214 Significance 214 Mismatches . . .

. US-09-697-123B-21 (1-214) US-09-697-123B-7 Sequence 7, Application US/09697123B

Initial Score Residue Identity - Gans 197 92% 0 Optimized Score = 197
Matches = 197
Conservative Substitutions 197 Significance 197 Mismatches .99 17 0

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Initial Residue Gaps
                                                                                                                                     Residue
Gaps
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                                                                                                                                                                                                                                                                               Initial
                     US-09-697-123B-21
US-09-697-123B-1 $
                                                                                                                                                        US-09-697-123B-21 (1-214)
US-09-697-123B-1 Sequence
                                        US-09-697-123B-21 (1-214)
US-09-697-123B-1 Sequence 14,
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      Identity
             Score
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                     Sequence 11, Application
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                           (1-214)
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  138
82%
6
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82%
6
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798
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Matches
 Conservative Substitutions
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177
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171
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Mismatches
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32
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Residue
Gaps
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US-09-697-123B-21 (1-214)
US-09-697-123B-8 Sequence 8,
                                                                                                               US-09-697-123B-21
US-09-697-123B-1;
                                                                                                                                                                                                                                                            GCCTGCAGGAGGGCCAGACCACGATGACCGCCCCGGGCGGTCGAGGTGCGGTGGACGACAT | 190 | 200 | 210 | x | 190 | 200 | 210 | x | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 200 | 
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US-09-697-1238-21 (1-214)

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US-09-697-123B-21 (1-214)
US-09-697-123B-3 Sequence
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US-09-697-123B-1 S
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                                          US-09-697-123B-21 (1-214)
US-09-697-123B-2 Sequence
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US-09-697-123B-21 (1-214) US-09-697-123B-2 Sequence Score -Score Sequence Optimized Matches Conservative Substitutions 24, Application US/09697123B Score -166 173 Mismatches Significance ò

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US-09-697-123B-21 US-09-697-123B-1 TCAAGGAGAAGCGCTACGACCTCGCGCGGGTGGGCCGCTACAAGGTCAAGAAGAAGCTCGGCCTG-----X Score Identity Sequence 111 82**%** 6 (1-214)20 Conservative Optimized Matches 17, 30 Application Score Substitutions ø US/09697123B 169 176 Significance Mismatches ò

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Gaps
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Initial Residue Gaps

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Matches

Optimized

Application US/09697123B

Conservative Substitutions

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Significance Mismatches

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US-09-697-123B-21 (1-214) US-09-697-123B-1 Sequence 1,

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US-09-697-123B-21 (1-214)
US-09-697-123B-5 Sequence
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US-09-697-123B-6 Sequence
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US-09-697-123B-1
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US-09-697-123B-2 Sequence
                                                                                                                                                                                                                                                                                                                                 X 10 20 30 40 50 60 70 TCAAGGAGAAGCCTACGATCTGGCCCGCGTGGGTCGGTACAAGGTGAACAAGAAGCTGGGCCTGGGCGGCACAAGAAGCTGAACAAGAAGCTGAACAAGAAGCTGAGCCTTAGGCCGGCACA
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US-09-697-123B-21 (1-214) US-09-697-123B-9 sequence

Application

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US-09-697-123B-21 (1-214)
US-09-697-123B-1 Sequence
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US-09-697-123B-4 Sequence
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ATGTGGACGACAT
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Similarity matrix
Mismatch penalty
Gap penalty
Gap size penalty
Cutoff score
     Sequence Name Description
                                    A 100% identical sequence to the query sequence was found:
                                                         The scores below are sorted by initial score. Significance is calculated based on initial score.
                                                                                                Number of residues:
Number of sequences searched:
Number of scores above cutoff:
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Number of sequences searched:
Number of scores above cutoff:
25
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Init. Opt. Init. Opt. Init. Opt. 171 189 0.80 208 177 189 0.65 208 177 184 0.69 208 177 184 0.69 208 177 184 0.65 208 166 177 0.56 208 161 171 0.45 208 162 176 0.20 200 123 138 160 -0.07 200 130 159 -0.71 211 108 152 -0.74 211 108 152 -0.74 211 108 152 -0.74 211 108 152 -0.74 211 108 152 -0.74 211 108 152 -0.74 211 108 152 -0.74 211 108 152 -0.74 211 108 152 -0.74 211 108 152 -0.74 211 108 152 -0.74 211 108 152 -0.74 211 108 152 -0.74 211 108 152 -0.74 220	160 170 180 190 197-123B-20 (1-205) 197-123B-1 Sequence 15, Application US/096 197-123B-1 Sequence 15, Application US/096 10	30 40	tion US/096 re = 20 substitutio	ication U cation U Ca	1. US-09-697-123B-2 Sequence 20, Application
Init. Opt. Score Score Sig. Fr Score Score Sig. Fr 177 184 0.69 168 177 0.66 165 176 0.54 161 171 0.45 161 171 0.45 161 171 0.45 161 171 0.45 161 171 0.45 161 171 0.45 161 171 0.45 161 171 0.45 160 170 0.42 155 166 0.31 159 178 0.20 144 172 0.07 138 160 -0.07 138 160 -0.07 138 160 -0.07 139 159 -0.71 109 159 -0.71 108 152 -0.74 115 15 -2.81 160 170 0.42 170 170 0.42 170 170 0.42 170 170 0.42 170 170 0.42 171 0.13 171 0.13 172 0.07 173 163 -0.22 172 160 70 174 175 175 -2.81 175 175 -2.81 177 177 177 177 177 177 177 177 177 17	123 S1 S1 CAA CAA	SO CATO CATO CATO CATO CATO	97123 5 Si 5 Mi	208 208 208 208 208 208 208 208 208 208	õ
205 1.43 205 1.43 bore Sig. Fr 189 0.80 184 0.69 187 0.66 177 0.56 177 0.56 177 0.45 177 0.45 177 0.45 177 0.45 177 0.45 177 0.42 170 0.42 170 0.42 170 0.42 170 0.42 170 0.42 170 0.42 171 0.45 171 0.	200 nific match match	#I # # # # # # # # # # # # # # # # # #	n 1	177 177 177 177 178 166 166 166 163 161 161 161 161 161 161	0
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Initial
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Residue
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                               US-09-697-123B-20
US-09-697-123B-2 s
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US-09-697-123B-3 Sequence
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US-09-697-123B-1 Sequence 1,
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                                    (1-205)
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87%
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US-09-697-123B-1 s
US-09-697-123B-20 (1-205)
US-09-697-123B-1 Sequence
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US-09-697-123B-20 US-09-697-123B-8 g

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US-09-697-123B-1 Sequence 16, Application US/09697123B

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US-09-697-123B-20
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US-09-697-123B-4 S
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US-09-697-123B-2 Sequence
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US-09-697-123B-1 S
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Matches
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Conservative Substitutions
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183 Mismatches
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US-09-697-123B-20
US-09-697-123B-1 s
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US-09-697-123B-2 S
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Conservative Substitutions
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US-09-697-123B-1 Sequence 14, Application US/09697123B
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US-09-697-123B-9 Sequence 9,
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174
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183 Mismatches
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US-09-697-123B-7 Sequence
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US-09-697-123B-2 Sequence
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                                                                                                                                                 152 Significance
163 Mismatches
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170
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171
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Mismatch penalty
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Significance - Mismatches -

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Conservative Substitutions

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    US-09-697-123B-19 (1-208)
    US-09-697-123B-1 Sequence 15, Application US/09697123B

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4. US-09-697-123B-1 Sequence 11, Application 208
4. US-09-697-123B-1 Sequence 11, Application 208
5. US-09-697-123B-1 Sequence 12, Application 208
6. US-09-697-123B-1 Sequence 1, Application 208
7. US-09-697-123B-1 Sequence 17, Application 208
8. US-09-697-123B-1 Sequence 18, Application 208
19. US-09-697-123B-1 Sequence 16, Application 208
10. US-09-697-123B-1 Sequence 5, Application 208
11. US-09-697-123B-2 Sequence 22, Application 208
12. US-09-697-123B-3 Sequence 23, Application 208
13. US-09-697-123B-2 Sequence 24, Application 208
14. US-09-697-123B-2 Sequence 24, Application 208
15. US-09-697-123B-2 Sequence 27, Application 208
16. US-09-697-123B-3 Sequence 27, Application 207
18. US-09-697-123B-1 Sequence 29, Application 207
19. US-09-697-123B-1 Sequence 29, Application 207
19. US-09-697-123B-1 Sequence 21, Application 207
19. US-09-697-123B-1 Sequence 21, Application 211
22. US-09-697-123B-1 Sequence 21, Application 211
23. US-09-697-123B-1 Sequence 21, Application 211
24. US-09-697-123B-1 Sequence 21, Application 214
25. US-09-697-123B-2 Sequence 27, Application 214
26. US-09-697-123B-1 Sequence 27, Application 214
27. US-09-697-123B-1 Sequence 28, Application 214
28. US-09-697-123B-1 Sequence 29, Application 214
29. US-09-697-123B-2 Sequence 29, Application 214
29. US-09-697-123B-3 Sequence 29, Application 214
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US-09-697-123B-1 Sequence 19, Application US/09697123B
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Residue Identity
                                  US-09-697-123B-19
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US-09-697-123B-1 Sequence 10, Application US/09697123B
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US-09-697-123B-1 Sequence 11,
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           Conservative Substitutions
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                       Score
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 40
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184
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186
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187
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Mismatches
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US-09-697-123B-19 (1-208) US-09-697-123B-8 Sequence

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Application

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US-09-697-123B-1 Sequence 17,
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US-09-697-123B-1 Sequence 1, Application US/09697123B
150 160 170 180 190 200 X ACGAGGCCAGACCACGATGACCGCCCGGCCGGCGGCGTCGAGGTCGCGGTCGAGGTGGACGACAT
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Similarity matrix
Mismatch penalty
Gap penalty
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Cutoff score
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Number of sequences searched: 26
Number of scores above cutoff: 25
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Gaps Initial Score - Residue Identity - Cane US-09-697-123B-18 (1-211) US-09-697-123B-1 Sequence 18, Application US/09697123B 211 100% 0 Conservative Substitutions Optimized Score -Matches -211 Significance 211 Mismatches 2.90 0

Initial Score Residue Identity Gaps

ity -

125 Optimized Score = 170 83% Matches = 176 3 Conservative Substitutions

170 Significance 176 Mismatches

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US-09-697-123B-18 (1-211) US-09-697-123B-1 Sequence 19, Application US/09697123B

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US-09-697-123B-7 Sequence
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           D # E
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         36
36
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36
70
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US-09-697-123B-18 (1-211) US-09-697-123B-8 sequence

8

Application

US/09697123B

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Gaps
                                                                                           Residue
                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                      6.
                                                                                                Initial
                                                                                                                                                                                                                  Initial Score
Residue Identity
                                                                                                        US-09-697-123B-18 (1-211)
US-09-697-123B-1 Sequence
                                                                                                                                                    US-09-697-123B-18
US-09-697-123B-2 s
l Score = e Identity =
                                                                                               Score
                                                                                                        Sequence 15,
                                                                                                                                                                                                                                 8 (1-211)
Sequence
                                                                                                                                                                                                                                                                                90
                                                                                                                           160
                                                                                      117
79%
3
                                                                                                                                                                                                              119
79%
3
                                                                                    Conservative Substitutions
                                                                                          Optimized Score -
Matches -
                                                                                                                                                                                                             Conservative Substitutions
                                                                                                                                                                                                                  Optimized Score - Matches -
                                                                                                                                                                                                                                 24,
                                                                                                                           170
                                                                                                                                                                                                                                                                                100
                                                                                                      Application US/09697123B
                                                                                                                                                                                                                                Application US/09697123B
                                                                                                                          180
                                                                                                                                                                                                                                                   180
                                                                                         162
168
                                                                                                                                                                                                                  161
167
                                                                                                                          190
                                                                                                                                                                                                                                                   190
                                                                                         Significance - Mismatches -
                                                                                                                                                                                                                 Significance
Mismatches
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0
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41
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Initial
Residue
Gaps
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Residue Identity --
Gaos --
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US-09-697-123B-18 (1-211)
US-09-697-123B-2 Sequence
                                                                                                                                                   US-09-697-123B-18 (1-211)
US-09-697-123B-1 Sequence 13,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       150 160 170 180 190 200 210

TGCATCAGGGGGACAGAGGAGTGAGGTTCGAGGTTCGAGGTTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTTCGAGGTTCGAGGTTCGAGGTTCGAGGTTCGAGGTTCGAGGTTCGAGGTTCGAGGTTCGAGGTTCGAGGTTCGAGGTCGAGACGACGACAT

TGCACGAGGGCCAGGATGACCGTGCCGGGCGGGGGTGCAGACGACGACTAT

150 160 170 180 190 200 x
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Matches
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167
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170
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167 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Significance = Mismatches =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Significance
Mismatches
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Initial Score Residue Identity
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Residue
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TCGACGACAT
||||||||
CCGACGACAT
CCGACGACAT
220 X
                  US-09-697-123B-18
US-09-697-123B-2 S
                                                   US-09-697-123B-18 (1-211)
US-09-697-123B-1 Sequence 14, Application US/09697123B
                                                                                                                                                                                               TCGACGACAT
                                                                                                                                                                                                                                    US-09-697-123B-18 (1-211)
US-09-697-123B-9 Sequence 9, Application US/09697123B
                                                                                                                                                                                                                                                                                                               Score
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    (1-211)
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80%
3
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73%
18
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Matches
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172
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165
                                                                                                                             Significance
Mismatches
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43
0
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Residue Gaps

Identity Score

Conservative Substitutions

Sequence 22,

Application

US/09697123B

158 Significance 164 Mismatches

0.11 44 0

Optimized

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Initial
Residue
Gaps
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Gaps
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US-09-697-123B-18
US-09-697-123B-2 S
                                                                                                                                                            US-09-697-123B-18
US-09-697-123B-1
                                                                                                                                                                                                                                                                                                                                                                                         TGCACGAGGGTCAGACCACGATGATCGTTCCGGGCGGCGGCGAGGTGCGAGGTGGGAAACCGACGACAT
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TGCATCAGGGCGACAAGACGATGACCGTCCCGGGTGGAGTCGAGGTGCCCGTCGAGGTCGACGATGACAT
                                                                                                                     Identity
                                                                                                                           Score
                                                                                                                                                                                                                                                                             Identity
                                                                                                                                                                                                                                                                                   Score
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                                                                                                                                       Sequence 23,
                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                            (1-211)
                                                                                                                                                                                                                                                                      114
798
3
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                                                                                                              Matches
Conservative
                                                                                                                          Optimized Score
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Matches = 168
Conservative Substitutions
                                                                                                                                                                                                                                                                                              1,
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                                                                                                                                                                                                                                                                                             Application US/09697123B
                                                                                                                                      Application
                                                                                                               Substitutions
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                                                                                                                                      US/09697123B
                                                                                                                     165
171
                                                                                                                                                                                                                                                           50
                                                                                                                   Significance
Mismatches
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16.

US-09-697-123B-18 (1-211)
US-09-697-123B-1 Sequence

Sequence

17,

Application

us/09697123B

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Initial
Residue
Gaps
                                                                                                                                  18.
                                                                                                                                                                                                                                                                Initial
Residue
                                                                                                                                                                                                                                                                                     17.
                                                                                                          Residue Identity
                                                                                                                Initial
                              150 160 170 180 190 200 210
TGCATCAGGGCGACAAGACGATGACCGTCCCGGGTGGAGTCGAGGTCGCCGTCGAGGTCGACGACAT
                                                                                                                          US-09-697-123B-18 (1-211)
US-09-697-123B-6 Sequence
TGCACGAGGTCAGACCACGATGACCGTTCCGGGCGGCGTCGAGGTGCCGGTGGAAACCGACGACAT
                                                                                                                                                US-09-697-123B-18
US-09-697-123B-1 5
                                                                                                                                                                                                                                                                                                     Score Identity
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Sequence
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78%
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78%
3
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82%
3
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Matches
Conservative
                                                                                                    Conservative
                                                                                                               Optimized
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Matches -
                                                                                                        Matches
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                                                                                                                          6,
                                                                                                                                                                                                                                                                               16,
                                                                                                                          Application US/09697123B
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                                                                                                               Score
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                                                                                                        159
165
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165
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175
                                                                                                                                                                                                                                                             Significance
Mismatches
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Mismatches
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Mismatches
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Initial Score Residue Identity Gaps

113 78% 3

Optimized Matches Conservative

Score

90

40

-0.06 42 0

100

19.

US-09-697-123B-18 US-09-697-123B-5 §

Sequence

5,

Application

(1-211)

50

160

180

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Optimized Score - 160
Matches - 166
Conservative Substitutions
                                                                                                                                                                                                    3, Application US/09697123B
                                                         core 170
176
Substitutions
                                                                                                                                                                                                                                                                                                           Substitutions
                                                                            US/09697123B
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                                                                                                                                                                                                                                                                                                                159
165
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                                                              Mismatches
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Mismatches
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Residue Identity *
Gaps
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Residue
Gaps
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                                                                                                                                                                   Initial Score
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 US-09-697-123B-18 (1-211)
US-09-697-123B-1 Sequence
                                                                                                                          US-09-697-123B-18 (1-211)
US-09-697-123B-4 Sequence 4,
                                                                                                                                                                                           US-09-697-123B-18 (1-211)
US-09-697-123B-2 Sequence
                                                                                                                                                           Identity -
                                                                                                                                                                                                                                                                                   Identity =
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78%
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788
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778
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                                  Optimized
Matches
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Matches
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Matches
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                                                 12,
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                                       Score
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                                                US/09697123B
                                 155 Significance = 166 Mismatches =
                                                                                                                                                            154
165
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163 Mismatches
                                                                                                                                                           Significance
Mismatches
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.11 42 0

Initial Residue Gaps

Identity

9 D E

112 78% 3

Optimized Matches

20.

US-09-697-123B-18 US-09-697-123B-3

8 (1-211) Sequence

Gaps

Residue Initial

Identity Score

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111 82% 3

Optimized Score Matches Conservative (

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04.34

Score

US-09-697-123B-18 US-09-697-123B-2

8 (1-211) Sequence

21,

Application

us-09-697-123b-17.res

Frame

Init. Score

Length

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1.15

208

208

FastDB

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0 4

8 E O D E S O E S

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Optimized Score - 187 Significance
Matches - 187 Mismatches
Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-697-123B-17 (1-208)
US-09-697-123B-1 Sequence 17, Application US/09697123B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-697-123B-17 (1-208)
US-09-697-123B-8 Sequence 8, Application US/09697123B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Optimized Score = 208
Matches = 208
Conservative Substitutions
                                                                                          8 Sequence 8, Application U
1 Sequence 19, Application
1 Sequence 17, Application
2 Sequence 11, Application
1 Sequence 11, Application
1 Sequence 11, Application
2 Sequence 12, Application
3 Sequence 16, Application
1 Sequence 16, Application
2 Sequence 5, Application
2 Sequence 21, Application
2 Sequence 22, Application
2 Sequence 23, Application
2 Sequence 24, Application
3 Sequence 12, Application
1 Sequence 12, Application
1 Sequence 13, Application
1 Sequence 13, Application
2 Sequence 14, Application
3 Sequence 17, Application
5 Sequence 17, Application
6 Sequence 18, Application
7 Sequence 11, Application
8 Sequence 11, Application
1 Sequence 11, Application
2 Sequence 21, Application
3 Sequence 21, Application
3 Sequence 21, Application
4 Sequence 21, Application
5 Sequence 25, Application
  US-09-697-123B-1 Sequence 17, Application
                               18:
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100%
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                              The list of other best
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Identity
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Identity
                                                                   Name
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                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Initial Residue
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Residue 1
Gaps
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                                                                                          Wed 13 Nov 102 14:09:30-PST.
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Length Score Score Sig. Frame
                                                                                                                                                                                 of US-09-697-123B-17 (1-208) with:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30
207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Total Elapsed 00:00:00.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  162
                                                                                                                         compared:US-09-697-123B-17 (1-208)
searched:
pe cutoff: 25
                                                                                             ou
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             K-tuple
Joining penalty
Window size
                                                                                          shanley
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| 139
| 0
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    Fast Pairwise Comparison of Sequences

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEARCH STATISTICS
                                                                                          ρλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        116
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177
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26
25
                                                                                                                                                                                 Results of the initial comparison File: US09697123B.seq
                                                                                          made
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PARAMETERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        - 6
                                                                                        Results file us-09-697-123b-17.res
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A 100% identical sequence to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CPU
00:00:00.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unitary
1
5.00
0.33
12
0
                                                                                                                             Query sequence being compared: 
Number of sequences searched: 
Number of scores above cutoff:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequences searched:
scores above cutoff:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mean
152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -69
             IntelliGenetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        <del>-</del> 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity matrix
Mismatch penalty
Gap penalty
Gap size penalty
Cutoff score
Randomization group
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              residues:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                53
                                                                Release 5.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Number of
Number of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -0
> 0 ^
0 = 0
                                                                                                                                                                                                                                                                                                                                                          10-
                                                                                                                                                                                                                                                               50-
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SCORE

1.15

Significance = Mismatches =

below

140

130

120

110

0.72

.

Description

Sequence Name

Scores:

Times:

```
| 80 | 90 | 140 | 120 | 130 | 140 | 120 | 130 | 140 | 120 | 130 | 140 | 120 | 130 | 140 | 120 | 130 | 130 | 140 | 120 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 |
```

(1-208) Sequence 19, Application US/09697123B US-09-697-123B-17 US-09-697-123B-1

64 25 0 0 Optimized Score = 183 Significance Matches = 183 Mismatches Conservative Substitutions Optimized Score Matches 183 878 0 Score Identity Residue] Gaps Initial

ACGAGGCCACACACATGACCGTCCGGGCGGAGTCGAGGTGCGGTGCGGTGCAAACCGACGACT 190 170

4. US-09-697-123B-17 (1-208) US-09-697-123B-1 Sequence 15, Application

0.64 Significance = Mismatches = US/09697123B Optimized Score = 183
Matches = 183
Conservative Substitutions Optimized Score Matches 183 878 0 . . . Initial Score Residue Identity Gaps

(1-208) Sequence 1, Application US-09-697-123B-17 US-09-697-123B-1 'n.

US/09697123B

62 26 0 0 Significance Mismatches ore = 182 | Substitutions Optimized Score Matches Conservative Subs 30 182 878 0 0 0 0 Score Identity 10 Initial S Residue 1 Gaps ×

9

20

40

| 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140

180 170 160

US/09697123B 7 (1-208) Sequence 24, Application US-09-697-123B-17 US-09-697-123B-2

0.60 27 0 . . Significance Mismatches ore = 181 s 181 h Substitutions Optimized Score Matches Conservative Subs 181 878 0 . . Score Identity Initial Residue Gaps

US-09-697-123B-17 (1-208) US-09-697-123B-1 Sequence 11, Application US/09697123B

0.60 . . . Optimized Score - 181 Significance Matches - 181 Mismatches Conservative Substitutions 181 878 0 . . . Score Identity Initial S Residue I Gaps

US-09-697-123B-17 (1-208) US-09-697-123B-1 Sequence 10, . 80

Application US/09697123B

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| 80 | 90 | 100 | 110 | 120 | 130 | 140 | 120 | 130 | 140 | 120 | 130 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 |

9. US-09-697-123B-17 (1-208) US-09-697-123B-3 Sequence 3, Application US/09697123B Initial Score = 179 Optimized Score = 179 Significance = 0.56
Residue Identity = 86% Matches = 179 Mismatches = 29
Gaps = 0 Conservative Substitutions = 0

10. US-09-697-123B-17 (1-208)
US-09-697-123B-1 Sequence 16, Application US/09697123B

Initial Score = 178 Optimized Score = 178 Significance = 0.53
Residue Identity = 85% Marches = 178 Mismatches = 30
Gaps = 0 Conservative Substitutions = 0

12. US-09-697-123B-17 (1-208) US-09-697-123B-5 Sequence 5, Application US/09697123B Initial Score = 178 Optimized Score = 178 Significance = 0.53
Residue Identity = 85% Matches = 178 Mismatches = 30
Gaps = 0 Conservative Substitutions = 0

13. US-09-697-123B-17 (1-208) US-09-697-123B-2 Sequence 22, Application

US/09697123B

Initial Score = 177 Optimized Score = 177 Significance = 0.51
Residue Identity = 85% Matches = 177 Mismatches = 31
Gaps = 0 Conservative Substitutions = 0

4. US-09-697-123B-17 (1-208) US-09-697-123B-2 Sequence 23, Application US/09697123B Initial Score 176 Optimized Score 176 Significance 0.49
Residue Identity 84% Matches 176 Mismatches 32
Gaps 0 Conservative Substitutions 0

15. US-09-697-123B-17 (1-208) US-09-697-123B-2 Sequence 2, Application

US/09697123B

Initial Score = 176 Optimized Score = 176 Significance = 0.49
Residue Identity = 84% Matches = 176 Mismatches = 32
Gaps = 0 Conservative Substitutions = 0

| 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140

16. US-09-697-123B-17 (1-208)
US-09-697-123B-2 Sequence 20, Application US/09697123B

Initial Score = 160 Optimized Score = 170 Significance = 0.16
Residue Identity = 84% Matches = 176 Mismatches = 29
Gaps = 3 Conservative Substitutions = 0

130

120

90

. US-09-697-123B-17 (1-208) US-09-697-123B-1 Sequence 12, Application Initial Score - 150 Optimized Score - 172 Significance - -0.04
Residue Identity - 85% Matches - 177 Mismatches - 30
Gaps - 1 Conservative Substitutions - 0

US/09697123B

i. US-09-697-123B-17 (1-208) US-09-697-123B-4 Sequence 4, Application Initial Score = 144 Optimized Score = 171 Significance = -0.16
Residue Identity = 84% Matches = 176 Mismatches = 31
Gaps = 1 Conservative Substitutions = 0

US/09697123B

. US-09-697-123B-17 (1-208) US-09-697-123B-1 Sequence 13, Application

US/09697123B

Initial Score = 144 Optimized Score = 170 Significance = -0.16
Residue Identity = 80% Matches = 180 Mismatches = 28
Gaps = 15 Conservative Substitutions = 0

20. US-09-697-123B-17 (1-208) US-09-697-123B-7 Sequence 7, Application US/09697123B Initial Score = 137 Optimized Score = 165 Significance = -0.31
Residue Identity = 80% Matches = 172 Mismatches = 36
Gaps = 6 Conservative Substitutions = 0

x 10 50 60 60 For transpared corrected control of the control of t

21. US-09-697-123B-17 (1-208) US-09-697-123B-9 Sequence 9, Application US/09697123B Initial Score = 137 Optimized Score = 164 Significance = -0.31
Residue Identity = 78% Matches = 174 Mismatches = 34
Gaps = 15 Conservative Substitutions = 0

| 80 | 90 | 100 | 110 | 120 | 140 | 140 | 120 | 130 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 |

X ACGACAT 111111 ACGACAT 220 X 22. US-09-697-123B-17 (1-208) US-09-697-123B-1 Sequence 18, Application US/09697123B Initial Score = 113 Optimized Score = 169 Significance = -0.80
Residue Identity = 82% Matches = 175 Mismatches = 33
Gaps = 3 Conservative Substitutions = 0

| 100 | 130 | 140 | 140 | 150 | 130 | 140 | 140 | 150 | 130 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140

. US-09-697-123B-17 (1-208) US-09-697-123B-2 Sequence 21, Application US/09697123B Initial Score = 111 Optimized Score = 169 Significance = -0.84
Residue Identity = 82% Matches = 176 Mismatches = 32
Gaps = 6 Conservative Substitutions = 0

4. US-09-697-123B-17 (1-208) US-09-697-123B-1 Sequence 14, Application US/09697123B Initial Score = 109 Optimized Score = 169 Significance = -0.88
Residue Identity = 82% Matches = 176 Mismatches = 32
Gaps 6 Conservative Substitutions = 0

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| 80 | 90 | 110 | 120 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 |
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25. US-09-697-123B-17 (1-208) US-09-697-123B-2 Sequence 25, Application US/09697123B

Initial Score = 19 Optimized Score = 19 Significance = -2.73

Residue Identity = 100% Matches = 19 Mismatches = 0

Gaps = 0 Conservative Substitutions = 0

0

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Similarity matrix
Mismatch penalty
Gap penalty
Gap size penalty
Cutoff score
Randomization group
 Sequence Name
                                                                            Number
Number
Number
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0 0 v
                                                                                                                                        Scores:
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                               100% identical
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                                                                         residues:
sequences searched:
scores above cutoff:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fast
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                                             v are sorted to calculated t
                              sequences to
       Description
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155
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0.33
12
0
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                                            d by initial score. based on initial s
                                                                                                                                                        SEARCH
                                                                                                                                                                                                                             PARAMETERS
                              the
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                             query sequence were
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US-09-697-123B-1 Sequence
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US-09-697-123B-5
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US-09-697-123B-16

US-09-697-123B-1

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Application US/09697123B

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                                                                                                                                                                           Residue
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                                                                                                                                                                                                                                                                                                 Initial
Score
                                                       Identity
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Gaps

1 1 0

181 87**%** 0

Optimized Matches Conservative

Score

core = 181 181 e Substitutions

Significance Mismatches

0

. 50 27

10.

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US-09-697-123B-16
US-09-697-123B-8
                                                                                     ACGAGGGCCAGACGATGACCGTCCCCGGCGGCGTCGAGGTCGACGTCGACGATAT 150 160 170 180 190 200 x
    Score -
Identity -
                                           6 (1-208)
Sequence
  182
87%
0
                      Optimized Score -
Conservative Substitutions
            Matches
                                            8
                                           Application
                                          US/09697123B
            182
                      182
         Significance
Mismatches
                   8
                   0
```

26

US-09-697-123B-16 US-09-697-123B-2 S US-09-697-123B-16 US-09-697-123B-1 S Score -Sequence Sequence (1-208) 182 87% 0 (1-208)Conservative Optimized Matches 2 1, Application 30 Application US/09697123B Score Substitutions 6 US/09697123B 182 182 50 Significance Mismatches 60 0 26

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Gaps
                                     Initial
Residue
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Residue
                                                                                                                                                                  Gaps
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Residue
Gaps
                                                         16.
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US-09-697-123B-16
US-09-697-123B-2 s
                                                                     US-09-697-123B-16 (1-208)
US-09-697-123B-2 Sequence
                                                                                                    US-09-697-123B-16
US-09-697-123B-1 S
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85%
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Sequence 17,
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82%
0
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85%
0
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Matches = 172
Conservative Substitutions
                                         Optimized
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Matches
                               Conservative
                                     Matches
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                                                   Application US/09697123B
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                              Substitutions
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                                    171
177
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178
                                   Significance
Mismatches
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Mismatches
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Mismatches
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28
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30
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0
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Initial Residue

Score Identity

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144 80% 15

Optimized Matches

170 180

Significance Mismatches

ò

.21 28 0

Conservative Substitutions

19.

US-09-697-123B-16 US-09-697-123B-9

Sequence

9, Application

US/09697123B

(1-208)

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Initial
Residue
                                                                                   Gaps
                                                                                                                                                                                                      Residue Identity Gaps
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                          US-09-697-123B-16 (1-208)
US-09-697-123B-4 Sequence
                                                                                                                                                 US-09-697-123B-16 (1-208)
US-09-697-123B-1 Sequence 12,
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                                                                                  147
878
1
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87%
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Matches
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183
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181
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Mismatches
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US-09-697-123B-7 Sequence
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US-09-697-123B-1 Sequence
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ACGACAT
ACGACAT
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78%
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Matches = 166
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176
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Mismatches
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Gaps
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Residue
Gaps
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                                                                     US-09-697-123B-16 (1-208)
US-09-697-123B-2 Sequence
GCGAGCC-----CATCACGTCGTCGACGCTGACCGAAGAAGACGTCGTGGCCACCATCGAATATCTGGTCC
                                                                                                                                                                                                                                                US-09-697-123B-16
US-09-697-123B-1
                                                                                                                                                                                                                    US-09-697-123B-16
US-09-697-123B-1 S
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Sequence
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78%
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81%
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78%
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                            Conservative Substitutions
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Conservative Substitutions
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169
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Mismatches
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X 10 X Y TCAAGGAGAGGCTACGA 11 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Initial Score ** Residue Identity ** Gaps **	25. US-09-697-123B-16 (1-208) US-09-697-123B-2 Sequence 25, Application US/09697123B	140 150 160 170 180 190 200 X GCTTGCACGAGGGTCAGACCACGATGACCGTTCCGGGCGGCGTCGAGGTGGCGGTGGAACCGACGACAT	100 120 130	x 10
TACGA X	19 100% 0	-16 (1-20 -2 Sequen	160 ;TCAGACCACG CCAGACCACG	90 ATCACGTCGTU GTGACCACCAU	20
	Optimized Score Matches Conservative Sul	8) ce 25, Appl	170 ATGACCGTTCC ATGACCGCCCC 170	0 100 TCGACGCTGAC ACCACCCTCAC	30
	Optimized Score = 19 Matches = 19 Conservative Substitutions	ication US/	180 CGGGCGCGTCGAC CCGGCGGCGTCGAC 180 190	90 100 120 120 130 TCACGTCGTCGACGCTGACCGAAGAAGAACGTCGTGGCCACCGACGATGTCTGGTC	40
		′09697123в	190 ;AGGTGCCGG ;AGGTGCCGG	120 FICGIGGCCA FICGICGCCA	50
	Significance = Mismatches =		200 GTGGAAACCGA GTGGATGTGGA 200	130 CCATCGAATA CCATCGAGTA	60
	-2.62 0 0		ACGACAT	ATCTGGTCC CCTGGTGC	70

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Similarity matrix
Mismatch penalty
Gap penalty
Gap size penalty
Cutoff score
Randomization group
    Sequence Name
                                               The scores below are sorted by initial score. Significance is calculated based on initial score.
                                                                                Number
Number
Number
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Number of sequences searched:
Number of scores above cutoff:
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                               100% identical sequence to the
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r of scores above (
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File : US09697123B.seq
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Sig. Frame
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2. US-09-697-123B-1 Sequence 1, Application U 208
3. US-09-697-123B-3 Sequence 2, Application U 208
4. US-09-697-123B-2 Sequence 11, Application U 208
5. US-09-697-123B-1 Sequence 11, Application 208
6. US-09-697-123B-1 Sequence 19, Application 208
8. US-09-697-123B-1 Sequence 10, Application 208
10. US-09-697-123B-1 Sequence 10, Application 208
11. US-09-697-123B-1 Sequence 6, Application U 208
12. US-09-697-123B-1 Sequence 6, Application U 208
13. US-09-697-123B-2 Sequence 7, Application 208
14. US-09-697-123B-2 Sequence 22, Application 208
15. US-09-697-123B-2 Sequence 7, Application 208
16. US-09-697-123B-2 Sequence 20, Application 208
17. US-09-697-123B-2 Sequence 20, Application 207
18. US-09-697-123B-1 Sequence 20, Application 207
19. US-09-697-123B-1 Sequence 21, Application 207
19. US-09-697-123B-1 Sequence 3, Application 223
20. US-09-697-123B-1 Sequence 7, Application 223
21. US-09-697-123B-2 Sequence 7, Application 214
22. US-09-697-123B-1 Sequence 18, Application 214
23. US-09-697-123B-1 Sequence 14, Application 214
24. US-09-697-123B-2 Sequence 27, Application 214
25. US-09-697-123B-2 Sequence 27, Application 214
26. US-09-697-123B-1 Sequence 27, Application 214
27. US-09-697-123B-1 Sequence 28, Application 214
28. US-09-697-123B-1 Sequence 29, Application 214
29. US-09-697-123B-2 Sequence 29, Application 214
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Initial Score Residue Identity - Gaps US-09-697-123B-15 (1-208) US-09-697-123B-1 Sequence 15, Application US/09697123B X 10 20 30 40 50 TCAAGGAGGCTACGACCTGGCCCGGGTGGGCCGCTTACAAGGTCAACAAGGTCAACAAGGTCACGACGCGGCTGCACGCCGGCTGCACGCCGGCTGCACGAGGTCAACAAGGTCACAAAGGTCACAAGATGTCAACGCCGGCTGCACGCCGGCTGCACGCCGGCTGCACGCCGGCTACGAAGAGAAGATCCTCGGCCTGCACGCCGX 10 20 30 40 50 60 70 208 Optimized Score 100% Matches 0 Conservative Sub Conservative Substitutions . . 208 208 Mismatches Significance 0 . 98 0

US-09-697-123B-15 (1-208) US-09-697-123B-1 Sequence 1, Application US/09697123B

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US-09-697-123B-15 US-09-697-123B-1 9

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US/09697123B

(1-208)

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US-09-697-123B-15
US-09-697-123B-1
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US-09-697-123B-1 S
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Initial
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Residue
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US-09-697-123B-9 g
                                                     X 10 20 70 FCAAGGAGAGCTACGACCTGGCCCGGTTGGGCCGCTACAAGGTCAACAAGAAGCTCGGCCTGCACGCCG
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US-09-697-123B-4
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US-09-697-123B-1
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                                    5 (1-208)
Sequence
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Matches
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Conservative
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Matches
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190
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188
                    Significance
Mismatches
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Initial Score
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ACGACAT
                                                                               US-09-697-123B-15 (1-208)
US-09-697-123B-7 Sequence
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US-09-697-123B-1 Sequence 13, Application US/09697123B
                                                                                                                                                                                                                                                                                                                    Score
Identity
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82%
6
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818
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Conservative Substitutions
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177 Mismatches
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Initial Score
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US-09-697-123B-1 8
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Number of
                                           The scores below are sorted by initial score. Significance is calculated based on initial score.
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Gap size penalty
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Number of sequences searched:
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Release
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sequences searched:
scores above cutoff:
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4. US-09-697-123B-1 Sequence 1, Application user in the control of the control of
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US-09-697-123B-7 Sequence
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US-09-697-123B-1 Sequence 14, Application US/09697123B
<u>ω</u> Ν
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Matches -
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                       US-09-697-123B-14 (1-214)
US-09-697-123B-2 Sequence
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US-09-697-123B-1 Sequence 1, Application US/09697123B
                                            US-09-697-123B-14 (1-214)
US-09-697-123B-2 Sequence
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                       Application US/09697123B
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US-09-697-123B-1 Sequence
US-09-697-123B-14 (1-214)
US-09-697-123B-1 Sequence
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Mismatches
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US-09-697-123B-14 (1-214)

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Initial
Residue
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Residue
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Residue
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US-09-697-123B-1;
US-09-697-123B-14 (1-214)
US-09-697-123B-8 Sequence
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818
9
                                                                                                              Optimized Score 
Matches
                                                                                                       Conservative Substitutions
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Matches
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                                                                                                                                Application US/09697123B
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175
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179
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174
                                                                                                            Significance
Mismatches
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Mismatches
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10.

Gaps

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Initial
Residue
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US-09-697-123B-1 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                   Residue Identity Gaps
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US-09-697-123B-14 (1-214)
US-09-697-123B-1 Sequence
                                                                                                                   GCCTGCACGAGGGCCAGGCCACGi.TGACCGTGCCGGGGGGGGGGGTGCGAGGTGGCAGACCGACGACAT 150 150 170 180 190 200 x
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US-09-697-123B-1 Sequence
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84%
6
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80%
3
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818
911
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                                                                                 Optimized
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Matches - 172
Conservative Substitutions
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180
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Mismatches
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Initial
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US-09-697-123B-1 Sequence
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US-09-697-123B-2 Sequence
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US-09-697-123B-3 Sequence 3,
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31
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Initial Residue

Score

109 83% 6

Optimized Matches

171 178

Significance Mismatches

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Conservative Substitutions

19.

US-09-697-123B-14 US-09-697-123B-2

Sequence

24,

Application US/09697123B

(1-214)

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Gaps
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                                                                                              Residue
                                                                                                           18. US-09-697-123B-14 (1-214)
US-09-697-123B-5 Sequence 5,
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US-09-697-123B-6 sequence
                                                                                                    Initial
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l Score = e Identity =
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818
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818
6
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Conservative Substitutions
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Matches • 175
Conservative Substitutions
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175
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Mismatches
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Initial
Residue
Gaps
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200 200 x
US-09-697-123B-14 (1-214)
US-09-697-123B-4 Sequence
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US-09-697-123B-1 Sequence
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US-09-697-123B-2 Sequence
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828
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818
6
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Conservative
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176
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174 Mismatches
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Mismatches
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34
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Application US/09697123B

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Gaps
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Residue
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Residue
Gaps
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AAACCGACGACAT
AAACCGACGACAT
220 x
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US-09-697-123B-14 (1-214)
US-09-697-123B-9 Sequence
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US-09-697-123B-1 S
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758
21
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21
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808
7
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Conservative
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172
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173
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Mismatches =
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35
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Similarity matrix
Mismatch penalty
Gap penalty
Gap size penalty
Cutoff score
                                                                                  Number of
Number of
Number of
Sequence Name
                                               The scores below are sorted by initial score. Significance is calculated based on initial score.
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                               A 100% identical
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sequences searched:
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                                                                                                                                                                                                                                                                                            74
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13
                              the
                                                                                                                                                                        SEARCH STATISTICS
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                             query
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Joining penalty
Window size
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                                                                                 5077
26
25
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                                                                                                                                                                                                                                                                                           124
                              sequence was
                                                                                                                                                                                                                                                                                    149|
1
                                                                                                                    Total Elapsed 00:00:00:00.00
                                                                                                                                               Standard Deviation 44.18
Init. Opt.
Length Score Score Sig. Frame
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               on Wed
                             found:
                                                                                                                                                                                                                                                                                           173
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                                                                                                                                                                                                                                                                                 198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nov 102
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208
                                                                                                                                                                                                                                                                                         223
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25.

US-09-697-123B-13 (1-223) US-09-697-123B-1 Sequence 13, Application US/09697123B

19

-2.44

0

2.17

00

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2. US-09-697-123B-9 Sequence 9, Application US-09-697-123B-1 Sequence 17, Application US-09-697-123B-1 Sequence 18, Application US-09-697-123B-1 Sequence 17, Application US-09-697-123B-1 Sequence 18, Application US-09-697-123B-1 Sequence 19, Application US-09-697-123B-1 Sequence 19, Application US-09-697-123B-1 Sequence 11, Application US-09-697-123B-1 Sequence 11, Application US-09-697-123B-1 Sequence 11, Application US-09-697-123B-1 Sequence 12, Application US-09-697-123B-1 Sequence 24, Application US-09-697-123B-1 Sequence 27, Application US-09-697-123B-1 Sequence 29, Application US-09-697-123B-1 Sequence 29, Application US-09-697-123B-1 Sequence 19, Application US-09-697-123B-1 Sequence 19, Application US-09-697-123B-1 Sequence 19, Application US-09-697-123B-1 Sequence 29, Application US-09-697-123B-1 Sequence 18, Application US-09-697-123B-1 Sequence 19, Application US-09-697-123B-1 Sequence 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                list of
US-09-697-123B-2 Sequence 21, Application 2:

**** 2 standard deviations below
US-09-697-123B-2 Sequence 25, Application
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-697-123B-1 Sequence 13,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            other best scores is:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Application
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length Sc
    w mean '
214
ow mean
19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Opt.
Score
                                                                                       223
                                           -1.04
                                                                                0.61
0.36
0.36
0.36
0.34
0.34
0.32
0.29
0.29
0.29
0.29
0.23
0.23
0.23
0.23
0.23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sig. Frame
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       . 17
```

000000000000000000

Gaps Initial Score - Residue Identity - Gaps - -220 X ACGACAT !!!!!! ACGACAT 220 X 223 Optimized Score = 100% Matches = 0 Conservative Substi Conservative Substitutions 223 223 Significance - Mismatches -

US-09-697-123B-13 (1-223) US-09-697-123B-9 Sequence Sequence 9, Application US/09697123B

Initial Score 195 Optimized Score . 195 Significance 1.54

```
Initial Score
Residue Identity Gaps
                                  Gaps
                                        Initial
Residue
                                                                                                                                                                                                                                                                                                                                                                                     Residue
Gaps
                                                     US-09-697-123B-13 (1-223)
US-09-697-123B-1 Sequence 17, Application US/09697123B
                                                                                                                                                                                                                             US-09-697-123B-13 (1-223)
US-09-697-123B-8 Sequence 8, Application US/09697123B
220 X
ACGACAT
                                                                                                          220 X
ACGACAT
||||||
ACGACAT
220 X
                                                                             ACGACAT
X
                                                                                                                                                                                                                                                                                  Score
                                                                                                                                                                                                                                                                                                                                                                                         Identity
                                                                                                                                                                                                            e e o
                                                                                                                                 160
                                                                                                                                                                                                                                                                                                                                                                                     0 0
                                  144
80%
15
                                                                                                                                                                                                          154 Optimized Score
87% Matches
15 Conservative Sub
                                                                                                                                                                                                                                                                                                                                                                                    87%
0
                                             Optimized
                                                                                                                                                                                                          Conservative Substitutions
                                 Conservative Substitutions
                                        Matches
                                                                                                                                 170
                                                                                                                                                                                                                                                                                                                                                                                   Matches
Conservative
                                                                                                                                                                                                                                                                                                                                                                                   Substituti
                                        B 8
                                     170
180
                                                                                                                                                                                                              181 Significance
195 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                        195 Mismatches
                                      Significance
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                    . .
                                           0
                                                                                                                                                                                                                    0
                                .38
28
                                                                                                                                                                                                        .61
13
0
                                                                                                                                                                                                                                                                                                                                                                                  28
0
```

```
Gaps
                                                                                                 Initial Score = Residue Identity = Gaps
                                                                                                                              6.
                                                                                                                                                                                                                                                                                       Initial Score Residue Identity - Gaps
                                                                                                           Initial Score
                                                                                                                                                                                                                                                                                                   Initial Score
                                                                                                                   US-09-697-123B-13 (1-223)
US-09-697-123B-1 Sequence 15, Application US/09697123B
                       US-09-697-123B-13 (1-223)
US-09-697-123B-1 Sequence 19, Application US/09697123B
                                                          220 X
ACGACAT
ACCACGCCTCTCAGGGTGGCCAGGCCCCCGTTATGACTGTCCCCGGGGGGTCGAGGTGCCGGTGGAAACCG
                                                                                                                                                                                                               220 X
ACGACAT
                                                                                                                                                                                                                                                                                                                                                                     ACGACAT
               160
                                                                                                     143
81%
                                                                                                                                                                                                                                                                                       143
82%
15
                                                                                                    Optimized 
Matches
                                                                                             Conservative Substitutions
                                                                                                                                                                                                                                                                                                 Optimized Score
                                                                                                                                                                                                                                                                                     Conservative Substitutions
                                                                                                                                                                                                                                                                                             Matches
                                                                                                    Score -
              180
                                                                                                                                                                                                                                                                                              . .
              190
                                                                                                    172
182
                                                                                                                                                                                                                                                                                            169
183
                                                                                                   Significance
Mismatches
                                                                                                                                                                                                                                                                                           Significance
Mismatches
             200
                                                                                                                                                                                                                                                                                                 B
                                                                                             0.36
26
0
                                                                                                                                                                                                                                                                                                 0
                                                                                                                                                                                                                                                                                     36
25
```

```
Initial Score Residue Identity - Cans
                                                                                                                                                                   8. US-09-697-123B-13 (1-223)
US-09-697-123B-1 Sequence 1, Application US/09697123B
                                                                                                                                                                                                                                                                                                                                                Residue
Gaps
                                                                                                                                                                                                                                                                                                                                                            Initial
                                                                                                                                                                                                                                                                                                                                                                     US-09-697-123B-13 (1-223)
US-09-697-123B-3 Sequence 3, Application US/09697123B
220 X
ACGACAT
||||||
ACGACAT
                                                               220 X
ACGACAT
||||||
ACGACAT
                                                                                                                                                                                                                                                                                                        220 X
ACGACAT
IIIIII
ACGACAT
                                                                                                                                                                                                                                                                                                                                                                                                                                          ACGAGG-
                                                                                                                                                                                                                                                                                                                                                    Score
Identity
                                                                                                                                                                                                                                                                                                                                                0 B 0
                                                        160
                                                                                                                                             142
798
15
                                                                                                                                                                                                                                                                                                                                                142
798
15
                                                                                                                                                                                                                                                                                                                                                                                                                                   -GTCAGCCCACGATGACCGTCCCCGGCGGCATCGAGGTGCCGGTGGAGACCG
                                                                                                                                                                                                                                                                                                                                                    Optimized Score
Matches
                                                                                                                                            Conservative Substitutions
                                                                                                                                                         Optimized Score
                                                       170
                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                               Conservative Substitutions
                                                       180
                                                                                                                                                    . .
                                                       190
                                                                                                                                                 168 Significance
178 Mismatches
                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                          Significance
                                                       200
                                                                                                                                                                                                                                                                                                                                                9 N 9
                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                                                         0.
                                                                                                                                          .34
30
0
```

Residue Gaps

10

20

30

6

60

70

11.

US-09-697-123B-13

3 (1-223) Sequence

10,

Application

US/09697123B

Score Identity

. . .

140 78% 15

Optimized Sco Matches Conservative

Substitutions

Significance Mismatches

4 0

32

```
Initial Score
Residue Identity •
Gaps
                                                                                                                                                                                                                                                                                                                                              Initial Score - Residue Identity - Gaps
                                                                                                                                                                          10.
                                                                                                                                                                                                                                                                                                                                                                 US-09-697-123B-13 (1-223)
US-09-697-123B-1 Sequence 11, Application US/09697123B
220 X
ACGACAT
||||||
ACGACAT
                            \begin{array}{lll} US-09-697-123B-13 & (1-223) \\ US-09-697-123B-2 & Sequence & 24 \,, & Application \end{array}
                                                                                                                                                                                            ACGACAT
X
                                                                                                                                                                                                        220 X
ACGACAT
[[[]]]]
                                                                                                                                                                                                                                                                 140
79%
15
                                                                                                                                                                                                                                                                                                                                             141
798
15
                                                                                                                                                 Optimized Matches
                                                                                                                                                                                                                                                                                                                                           Optimized Sco
Matches
Conservative
                                                                                                                                          Conservative Substitutions
                                                                                                                                                     Score
                                                                                                                                                                                                                                                                                                                                            Substitutions
                                                                                                                                                                                                                                                                                                                                                  . .
                                                                                                                                                                  US/09697123B
                                                                                                                                               168
178
                                                                                                                                                                                                                                                                                                                                                167 Significance
177 Mismatches
                                                                                                                                               Significance
Mismatches
                                                                                                                                                                                                                                                                                                                                             . . .
                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                          30
```

```
Initial Score Residue Identity = Gaps
                                                                                                                                                                                                                                                                               Initial Score
Residue Identity =
Gaps
                                                                                                                                                                                                                                                                                                               12.
                                                                                             US-09-697-123B-13 (1-223)
US-09-697-123B-2 Sequence 20, Application US/09697123B
220 X
ACGACAT
|||||||
ACGACAT
                                                                                                                                                           220 X
ACGACAT
                                                                                                                                                                                                                                        US-09-697-123B-13 (1-223)
US-09-697-123B-2 Sequence
                                                                                                                                                                                                                                                                                                                                                                   ACGACAT
                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/09697123B
                                                                      138 Optimized Score = 78% Matches = 18 Conservative Substi
                                                                                                                                                                                                                                                                               140 Optimized Score = 78% Matches = 15 Conservative Substi
                                                                     Conservative Substitutions
                                                                                                                                                                                                                                                                              Conservative Substitutions
                                                                          160 Significance
175 Mismatches
                                                                                                                                                                                                                                                                                   166 Significance
176 Mismatches
                                                                   0.25
30
0
                                                                                                                                                                                                                                                                           0.29
32
0
```

150 160 170 180 200 200 210 ACCACGCCTCTCAGGGTGGCCAGGCCCCCGTTATGACTGTCCCCGCGCGGGGTCGAAGCCCGTGGAAACCC	ာ ဂိ 🗎	X 10 20 70 TCAAGGACAAGCGCTACGACCTGGCCCGCGTCGGCCGCTACAAGGTCAACAAGAAGCTCGGCCTGAACACCG	Initial Score = 137 Optimized Score = 162 Significance = 0.23 Residue Identity = 78% Matches = 176 Mismatches = 32 Gaps = 15 Conservative Substitutions = 0	15. US-09-697-123B-13 (1-223) US-09-697-123B-6 Sequence 6, Application US/09697123B	220 X ACGACAT - - - - ACGACAT ACGACAT X	150 160 170 180 190 200 210 ACCACGCCTCTCAGGGTGGCACAGCCCCCGTTATGACTGTCCCGGCGGGGGTGGAGAGCCGGTGGAAACCC		10 GAAGCGCTA GAAGCGCTA 10	Initial Score = 137 Optimized Score = 162 Significance = 0.23 Residue Identity = 78% Matches = 176 Mismatches = 32 Gaps = 15 Conservative Substitutions = 0	14. US-09-697-123B-13 (1-223) US-09-697-123B-1 Sequence 16, Application US/09697123B	220 X ACGACAT	150 160 170 180 190 200 ACCACGCCTCTCAGGGTGGCAGGCCCCGGTTATGACTGTCCCCGGCGGGGGCGAGGTGCCGGGTGGAAACCG	80 90 100 110 120 130 140
AACCG AACCG 200	O CCTGC CTTGC	70 CACCG 11 TGTCG 70	32 0			AAACCG 11111 AAACCG 200	AO GCCTGC H HH GCTTGC	70 ACACCG ATGTCG 70	0.23 32 0			AAACCG AGACCG	

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Gaps
                                                                                                                                                                             Initial
Residue
                                                                                                                                                                                                                                                                                                                                                                             Initial
Residue
     18.
                                                                                                                                                                                                                                                                                                                                                                                                     16.
                        220 X
ACGACAT
|||||||
|ACGACAT
X
US-09-697-123B-13 (1-223)
US-09-697-123B-2 Sequence
                                                                                                                               US-09-697-123B-13 (1-223)
US-09-697-123B-2 Sequence 23, Application US/09697123B
                                                                                                                                                                                                                            220 X
ACGACAT
||||||
ACGACAT
                                                                                                                                                                                                                                                                                            US-09-697-123B-13 (1-223)
US-09-697-123B-5 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                            ACGACAT
                                                                                                                                                                                                                                                                                                                                  Score Identity
                                                                                                                                                                                                                                                                                                                                                                            Score
Identity
                                                                                                                                                                                                                                                                                                                                                                         . . .
                                                                                                                                                                                                                                                                                                                                                                                              Sequence 5, Application US/09697123B
                                                                                                                                                                       136
75%
15
                                                                                                                                                                                                                                                                                                                                                                        137
78%
15
                                                                                                                                                                       Optimized Score
Matches
Conservative Sub
                                                                                                                                                                                                                                                                                                                                                                       Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                   Optimized Score
                                                                                                                                                                                                                                                                                                                                                                              Matches
22,
Application US/09697123B
                                                                                                                                                                       Substitutions
                                                                                                                                                                             159
169
                                                                                                                                                                                                                                                                                                                                                                            162
176
                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                            Significance
Mismatches
                                                                                                                                                                                   Significance -
                                                                                                                                                                         . .
                                                                                                                                                                                                                                                                                                                                                                              8 0
                                                                                                                                                                       0.20
39
0
                                                                                                                                                                                                                                                                                                                                                                                   0
```

```
Initial
Residue
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                    Residue Identity Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Initial Score
Residue Identity
                                                                             20.
                                                                                                                                                                                                                                                                                  Initial
                                                                                                                                                                                                                                                                                                      19.
220 X
ACGACAT
                                                                                                                                                                                ACGACAT
                                                                                                                                                                                                                                                                                                                                        220 X
ACGACAT
                                                                                                                                                                                                                                                                                           US-09-697-123B-13 (1-223)
US-09-697-123B-4 Sequence 4, Application US/09697123B
                                                                                                                                                                                                                                                                                                                                                                                                                US-09-697-123B-13 (1-223)
US-09-697-123B-1 Sequence
                                                                                                                                                      150 160 170 180 190 200 210 ACCACGCCTCTCAGGGCCAGGCCCCCGTTATGACTGTCCCCGGGGGGGTCGAGGTGCCGGTGGAAACCG
                                                                                                                                                                                                                                                                                                                                                                  ACGACAT
                                                 Score Identity
                                                                                                                                                                                                                                                                                  Score
                                                                                                                                                                                                                                                                                                                                                                                                             80
                                                                                                                                                                                                                                                                      . . .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              . . .
                                                                                                                                         -GAGGGTCAGCACACGATGA----CGTTCCGGGCGGGACCGAGGTTCCGGTGGAGACCG 150 150 200
                                                                                                                                                                                                                                                                                                                                                                                                            90
                                                                    Sequence 18, Application US/09697123B
                                          116
73%
18
                                                                                                                                                                                                                                                                    131
79%
16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            136
78%
15
                                          Optimized Score
Matches
Conservative Sub
                                                                                                                                                                                                                                                                  Conservative Substitutions
                                                                                                                                                                                                                                                                         Optimized Score - Matches -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Optimized 
Matches
                                                                                                                                                                                                                                                                                                                                                                                                           100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score
                                                                                                                                                                                                                                                                                                                                                                                                           110
                                          Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Substitutions
                                           161
175
                                                                                                                                                                                                                                                                         163 Significance
178 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                           120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Significance
Mismatches
                                                                                                                                                                                                                                                                     . .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  . .
                                                                                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
```

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Initial Score
Residue Identity *
Gaps
                                                                                                                    Initial Score
Residue Identity
Gaps
                                                                                                                                                    22. US-09-697-123B-13 (1-223)
US-09-697-123B-7 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                            21. US-09-697-123B-13 (1-223)
US-09-697-123B-1 Sequence 12, Application US/09697123B
140 150 160 170 180 190 200 210 GCCTGCACGCCCCTCTCAGGGTGGCCAGGCCCCCGTTATGACTGTCCCCGGGGGGTCGAGGTGCCGGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                             220 X
CCGACGACAT
||||||||
TCGACGACAT
710
                                                                                                                                                                                                  220 X
ACGACAT
                                                                                                                                                                                                                                                                                  ACGACAT
X
                                                                                                                                                                                                                                  150
                                                                                                                                                    Sequence 7, Application US/09697123B
                                                                                                                     92 Optimized Score - 150
74% Matches - 171
21 Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                              112 Optimized Score - 160
80% Matches - 179
16 Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             170
                                                                                                                                                                                                                                                                                                                                                                                      160 Significance
179 Mismatches
                                                                                                                             150 Significance
171 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                               ı
                                                                                                                                                                                                                                                                                                                                                                              -0.34
28
0
                                                                                                                                      0
                                                                                                                      .79
37
```

220 X AAACCGACGACAT	140 150 160 170 180 190 200 210 GCCTGCACGCCTCTCAGGGTGGCCAGGCCCCGGTTATGACTGTCCCCGGCGGGGTCGAGGTGCCGGTGG HILLIH	80 90 100 120 130 ATCATCCGATCACCACCACCACGACGCTGGCGCGACGAGAAGAAGAAGAAGACGTCGGTCG	X 10 20 30 70 TCAAGGAGAAGACTACGACCTGGCCCGCGCTGGCCGCTCAAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAA	Initial Score = 81 Optimized Score = 155 Significance = -1.04 Residue Identity = 76% Matches = 176 Mismatches = 32 Gaps = 21 Conservative Substitutions = 0	24. US-09-697-123B-13 (1-223) US-09-697-123B-2 Sequence 21, Application US/09697123B	AAACCGACAT AGACCGACAT AGACCGACACAT 210 x	140 150 160 170 180 190 200 210 GCCTGCACGACGCCTCCAGGGTGGCCAGGCCCGTTAGGACTGTCCCGGCGGGGGTCGAGGTGCCGTGG	80 130 120 130 ATCATCGCATCACCACCACGACGCGCTGCGCGACGACGACGACGACGACGACGACGACGACGACGAC	X 10 20 30 40 50 50 70 TCAAGGAGAAGGCTAAGAACCTGGCCCGCTGGCCGCTGAAAGGTCAACAAGAAGCTGGGCCTGAACACCG	Initial Score = 83 Optimized Score = 152 Significance = -1.00 Residue Identity = 75% Matches = 173 Mismatches = 35 Gaps = 21 Conservative Substitutions = 0	23. US-09-697-123B-13 (1-223) US-09-697-123B-1 Sequence 14, Application US/09697123B	220 X AAACCGACAT AGGTCGACGACAT AGGTCGACGACAT 210 X	
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ATGTGGACGACAT 210 X

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25. US-09-697-1238-13 (1-923)

Initial Score 19 Optimized Score 19 Significance - 2.44
Residue Identity 100% Matches 19 Mismatches 0 0

X NORTH OF THE OCCUPACY OF THE OCCUPACY OF THE OCCUPACY OF THE OCCUPACY OC
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Similarity matrix
Mismatch penalty
Gap penalty
Gap size penalty
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , 0 v
0 0 v
0 0 v
                                                                                           Number
Number
Number
                                                                                                                                                                                                                                                                                                                                      0 E O Z E C O E 0
                                                                                                                                                                                                                                                                                                                                                                                                                                чО
                                                     The scores below are sorted by initial score. Significance is calculated based on initial score.
                                                                                                                                                                                                                                                                                                         SCORE
STDEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FastDB - F
Release 5.
 Sequence Name
                                                                                                                                           Times:
                                                                                                                                                                                                        Cutoff score
Randomization group
                                                                                                                                                                                                                                                                                                                                                                                                                                                         z \cap v \subseteq z \subseteq z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query sequence being compared:US-09-697-123B-12 (1-207) Number of sequences searched: 26 Number of scores above cutoff: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Results file us-09-697-123b-12.res made by shanley on Wed 13 Nov 102 14:07:14-PST
                                                                                                                                                                       Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100-
                                                                                                                                                                                                                                                                                                                                                                                                                                  10-
                                                                                                                                                                                                                                                                                                                                                                                                      5.
                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Results of the initial comparison of US-09-697-123B-12 (1-207) with: File : US09697123B.seq
                                                                                         of residues:
of sequences searched:
of scores above cutoff:
                                   identical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IntelliGenetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fast Pairwise Comparison of Sequences 5.4
                                  sequence
 Description
                                                                                                                                                                                                                                                                                                                   46-
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Joining penalty
Window size
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207
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2 US-09-697- 3 US-09-697- 4 US-09-697- 5 US-09-697- 6 US-09-697- 7 US-09-697- 10 US-09-697- 11 US-09-697- 11 US-09-697- 12 US-09-697- 13 US-09-697- 14 US-09-697- 15 US-09-697- 17 US-09-697- 18 US-09-697- 19 US-09-697- 21 US-09-697- 22 US-09-697- 23 US-09-697- 24 US-09-697- 25 US-09-697-	The list of o	1. US-09-6
238-3 Seque 238-1 Seque 238-1 Seque 238-1 Seque 238-1 Seque 238-1 Seque 238-2 Seque 238-2 Seque 238-2 Seque 238-3 Seque 238-2 Seque 238-1 Seque 238-1 Seque 238-2 Seque 238-1 Seque 238-1 Seque 238-1 Seque 238-2 Seque 238-3 Seque 238-2 Seque 238-3 Seque 238-2 Seque	other best scores	US-09-697-123B-1 Sequence
nce 3, Application Unnce 15, Application Unnce 10, Application Unnce 10, Application Unnce 11, Application Unnce 16, Application Unnce 16, Application Unce 27, Application Unce 27, Application Unce 28, Application Unce 27, Application Unce 28, Application Unce 29, Application Unce 11, Application Unce 12, Application Unce 13, Application Unce 21, Application Unce 18, Application Unce 18, Application Unce 28, Application Unce 28, Application Unce 28, Application Unce 29, Application Unce 27, Application Unce 28, Application Unce 29, Application Unce 27, Application Unce 28, Application Unce 29, Application Unce 29, Application Unce 29, Application Unce 21, Application Unce 21, Application Unce 25, Application Unce 26, Application Unce 27, Application Unce 27, Application Unce 28, Application Unce 29, Application Unce	is:	ce 12, Application
U 208 1 U 2	Init. Length Score	207 207
63 184 61 184 62 183 60 183 60 183 60 187 77 176 77	Opt. Score)7 207
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Gaps Initial Score Residue Identity -1. US-09-697-123B-12 (1-207) US-09-697-123B-1 Sequence 12, Application US/09697123B 100% 207 Optimized Score - 207
Matches - 207
Conservative Substitutions 207 Significance 207 Mismatches 1.68 0 0

	2.
US-09-697-123B-3	US-09-697-123B-12
Sequence	2 (1-207)
ω	
Application	
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X TCAA TCAA X	Initial Score Residue Identi Gaps
10 .GGAGAAGCK 	Initial Score Residue Identity Gaps
11.00	
20 CGACCTO CGACCTO CGACCTO	163 90% 1
30 3G-TCGCGTCGC 	Optimized Score - 184 Matches - 189 Conservative Substitutions
40 3CCGTTACAAG 	Score - /e Substitu
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X 10 20 70 TCAAGGAGAACGCTACGACCTGG-TCGGCTCGGCCGTTACAAGGTCAACAAAAAGCTCGGTCTGAACGTCG	184 Significance - 189 Mismatches - ions
70 SAACGTCG GCACGTCG	0.67 18 0

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Initial
Residue
Gaps
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Residue
Gaps
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Residue Identity
Gaps
                                 US-09-697-123B-12
US-09-697-123B-1:
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US-09-697-123B-1 Sequence
                                                                                                                                                                                                                                                                                                                            US-09-697-123B-12
US-09-697-123B-2
                                                                                                                    TCAAGGAGAAGCGCTACGACCTGGCCCGGGTGGGCCGCTCAACAAGGTCAACAAGAAGCTCGGTCTGAACGTCGX
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                                2 (1-207)
Sequence
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88%
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1
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90%
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20
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Conservative
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6
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              179 Significance
184 Mismatches
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Mismatches
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18
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70
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US-09-697-123B-12 (1-207) US-09-697-123B-1 Sequence

Sequence 16,

Application

US/09697123B

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Initial
Residue
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Residue
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US-09-697-123B-1 Sequence
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US-09-697-123B-1
Score Identity
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Identity
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878
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898
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187
Substitutions
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181 Mismatches
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187
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Initial
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US-09-697-123B-6 Sequence
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US-09-697-123B-5 Sequence 5, Application US/09697123B
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GCGAGCCGATCACCACTCGACGCTGACCGAAGAGAGACGTCGTGCCCACCACTACTGGTCGGCTTCGCCTTGC
GCGAGCCCATCACGTCGACGCTGACCGAAGAAGAGGATGTCGTGGCCACCATCGAATATCTGGTCCGCTTGC
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Matches
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181
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Mismatches
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Mismatches
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                                                                               Residue
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US-09-697-123B-1 Sequence 11,
                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-697-123B-12
US-09-697-123B-2 S
                                  US-09-697-123B-12
US-09-697-123B-8 s
                                                                                                                                                             Score -
                                                                                                                                                                                                                                                                                                                        90
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Sequence 22, Application US/09697123B
                                                                                                 Sequence
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868
1
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87%
1
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86%
1
                                                                                                        (1-207)
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183
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180
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179 Mismatches
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Mismatches
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Mismatches
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Initial
Residue
Gaps
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Gaps
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US-09-697-123B-1 Sequence
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                                   US-09-697-123B-12
US-09-697-123B-2 S
                                                                                                                                                                                                                                                                                                                                   | 100 | 120 | 130 | 140 | 120 | 130 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 
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US-09-697-123B-2 Sequence
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e Identity =
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                                                                                                                                                                                                                                                    2 (1-207)
Sequence 20,
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878
4
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85%
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87%
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Conservative Substitutions
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Matches
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Conservative
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                                                                                                                                                                             172 Significance = 183 Mismatches =
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177 Mismatches
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  120
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130
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21
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25
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Residue
Gaps
        Residue
              Initial
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                                                                                                                                                                                                                                                                                                                            17. US-09-697-123B-12 (1-207)
US-09-697-123B-2 Sequence 24,
                                                                                                                                                                                                                                                                                                                    Initial Score
                      US-09-697-123B-12 (1-207)
US-09-697-123B-1 Sequence 14,
                                           US-09-697-123B-12 (1-207)
US-09-697-123B-4 Sequence 4, Application US/09697123B
                                                                                                               Score Identity
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 120
83%
7
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89%
2
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82%
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      Optimized
Matches
 Conservative
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                      Application US/09697123B
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Substitutions
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179
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186
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172
     Mismatches
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TCAAGGAGAAGCGCTACGACCTGGTC-GCGTCGGCCGTTACAAGGTCAACAAAAAGCTCGGTCTGAACGTCG

30

40

50

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Residue Identity
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Residue Identity
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                                                                                                                                               ACGACAT
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US-09-697-123B-9 Sequence
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US-09-697-123B-1 Sequence 13, Application US/09697123B
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US-09-697-123B-7 Sequence
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US-09-697-123B-12 (1-207) US-09-697-123B-1 Sequence 18, Application US/09697123B

Initial Score = Residue Identity = Gaps 98 78% 4 Optimized Conservative Substitutions Matches Score 155 166 Significance Mismatches .83 41

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3. US-09-697-123B-2 Sequence 2, Application U
5. US-09-697-123B-1 Sequence 2, Application U
5. US-09-697-123B-1 Sequence 1, Application U
6. US-09-697-123B-1 Sequence 16, Application U
10. US-09-697-123B-1 Sequence 6, Application U
11. US-09-697-123B-3 Sequence 5, Application U
11. US-09-697-123B-3 Sequence 22, Application U
11. US-09-697-123B-3 Sequence 22, Application U
11. US-09-697-123B-1 Sequence 27, Application U
12. US-09-697-123B-1 Sequence 27, Application U
13. US-09-697-123B-1 Sequence 27, Application U
14. US-09-697-123B-2 Sequence 27, Application U
15. US-09-697-123B-1 Sequence 17, Application U
18. US-09-697-123B-1 Sequence 18, Application U
19. US-09-697-123B-1 Sequence 21, Application U
19. US-09-697-123B-1 Sequence 21, Application U
21. US-09-697-123B-1 Sequence 21, Application U
22. US-09-697-123B-1 Sequence 21, Application U
23. US-09-697-123B-1 Sequence 24, Application U
24. US-09-697-123B-1 Sequence 27, Application U
25. US-09-697-123B-1 Sequence 28, Application U
26. US-09-697-123B-1 Sequence 29, Application U
27. US-09-697-123B-1 Sequence 29, Application U
28. US-09-697-123B-1 Sequence 29, Application U
29. US-09-697-123B-2 Sequence 29, Application U
29. US-09-697-123B-3 Sequence 3, Application U
29. US-09-6
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US-09-697-123B-1 Sequence 10, Application
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US-09-697-123B-1 Sequence 11, Application US/09697123B
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US-09-697-123B-11 US-09-697-123B-6

Sequence

6,

Application US/09697123B

(1-208)

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US-09-697-123B-1 Sequence
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US-09-697-123B-1 Sequence
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Residue
Gaps
                                                                                                             0.
US-09-697-123B-11 (1-208)
US-09-697-123B-5 Sequence
                                                       US-09-697-123B-11
US-09-697-123B-3
                                                                                                                        l Score = e Identity =
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888
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88%
0
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888
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Conservative Substitutions
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Matches = 185
Conservative Substitutions
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185
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Residue
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US-09-697-123B-11
US-09-697-123B-1
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US-09-697-123B-8 Sequence
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US-09-697-123B-2 s
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Identity
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111
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Sequence 17,
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Sequence
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Residue
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         US-09-697-123B-11 (1-208)
US-09-697-123B-2 Sequence
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US-09-697-123B-2 Sequence
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US-09-697-123B-2
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Conservative Substitutions
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 110
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177 Mismatches
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Residue
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                                         US-09-697-123B-11 (1-208)
US-09-697-123B-1 Sequence
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US-09-697-123B-4 Sequence 4, Application US/09697123B
                                                                                                                                                                                                                 US-09-697-123B-11 (1-208)
US-09-697-123B-1 Sequence 12,
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      Identity
             Score
                     Sequence 13, Application
 141
79%
15
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87%
1
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87%
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 Optimized Sco
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183
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Initial Score
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                                      ACGACAT
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US-09-697-123B-2 Sequence
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US-09-697-123B-9 Sequence
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150 160 170 180 190 200 210
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                                                                                                         Sequence 21, Application
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82%
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79%
15
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176
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178 Mismatches
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Mismatches
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Residue
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US-09-697-123B-7 Sequence
                                                                                       US-09-697-123B-11 (1-208)
US-09-697-123B-1 Sequence 18, Application US/09697123B
                                                                                                                                                                                                                                                                                                 80 90 100 120 130
GCCAGCC ----- 10 120 130 130 130 120 130 140
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US-09-697-123B-1 :
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81%
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80%
6
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                                      Optimized Score - 168
Matches - 175
Conservative Substitutions
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                                                                 7,
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                                                                Application US/09697123B
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                                             168 Significance
175 Mismatches
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172
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173
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Mismatches
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33
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36
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Similarity matrix
Mismatch penalty
Gap penalty
Gap size penalty
Cutoff score
                                                                                                 Number of residues:
Number of sequences searched:
Number of scores above cutoff:
                                                                                                                                                                                                                                                                                                                                   SCORE 0
    Sequence Name
                                       A 100% identical sequence to the
                                                           The scores below are sorted by initial score. Significance is calculated based on initial score.
                                                                                                                                                                                                                                                                                                                                                                   ν ω Ο Σ ω ⊂ Ο ω ν
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0 0 v
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Results file us-09-697-123b-10.res made by shanley on Wed 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Release 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FastDB -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Results of the initial comparison of US-09-697-123B-10 (1-208) with: File : US09697123B.seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IntelliGenetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fast Pairwise Comparison of Sequences 5.4
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         Description
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                                       query sequence was
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Joining penalty
Window size
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Init. Opt.
Length Score Score Sig. Frame
                                       found:
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1
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30
207
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Gaps

Initial Score Residue Identity = Gaps

205 Optimized Score - 205 98% Matches - 205 0 Conservative Substitutions

205 Significance - 205 Mismatches -

0.98 3

2. US-09-697-123B-10 (1-208) US-09-697-123B-1 Sequence 11, Application US/09697123B

80 90 100 120 130 140 GCCAGCCCATCACCAGCTCGACCGAGGAAGACGTCGTCGCCACCATCGCATCGCACCTGGCCTTGC	10 20 70 TCAAAGGACACCTACCACCTGGCTCGGTGGGTCGGTAAAAAGGTCAACAAGAAGCTCGGCCTGAACGCCG	Initial Score = 208 Optimized Score = 208 Significanc Residue Identity = 100% Matches = 208 Mismatches Gaps = 0 Conservative Substitutions	 US-09-697-123B-10 (1-208) US-09-697-123B-1 Sequence 10, Application US/09697123B 	Sequence 25, Application 19 1	. US-09-697-123B-7 Sequence 7, Application U 214	. US-09-697-123B-1 Sequence 14, Application 214 . US-09-697-123B-1 Sequence 18, Application 211	US-09-697-123B-9 Sequence 21, Application U 223	09-697-123B-1 Sequence 13, Application 223	. US-09-697-123B-1 Sequence 12, Application 207	US-09-697-123B-2 Sequence 20, Application 208	US-09-697-123B-1 Sequence 17, Application 208	. US-09-697-123B-2 Sequence 8, Application U 208	US-09-697-123B-3 Sequence 3, Application U 208	. US-09-697-123B-1 Sequence 1, Application U 208	. US-09-697-123B-2 Sequence 2, Application U 208	. US-09-697-123B-6 Sequence 6, Application U 208	. US-09-697-123B-1 Sequence 16, Application 208	. US-09-697-123B-1 Sequence 15, Application 208	US-09-697-123B-1 Sequence 11, Application 208	Length S	The list of other best scores is:	1. US-09-697-123B-1 Sequence 10, Application 208 20	
130 AATA 130	AGC! AGC!	ific late			107	126 122	139 139	140	160	174 165	179	182 179	183	186	186	186	186	981	205	. 4 4		208	
CCTGGTC	60 CGGCCTG	eance -		19				166												Opt. Scor		208	
140 CGCTTGC CGCTTGC	70 AACGCCG [111111 AACGCCG	1.04 0		-2.75	-0.98	9		-0.32	0							-				Sig. Fr		1.04	
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Initial
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Residue
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Residue
Gaps
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US-09-697-123B-1 S
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US-09-697-123B-1 Sequence
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US-09-697-123B-1 Sequence
                                                                X 10 20 30 40 50 FOR TCAAGGAGGCCTACGACCTGGCCTGGCTGGGTCGGTACAAGGTCAACAAGAAGCTCGGCTGAACGCCGCTGAACGCCGTACAAGAAGCTCAACAAGAAGCTCGGCCTGAACGCCGCTGAACGCCGCTGAACGCCGCTGAACGCCGCTGAAGGAGAGCTCAACAAGAAGCTCAACAAGAAGCTCAACGACGAAGCTCAACGACGAAGCTCAACGACGAAGCTCAACGCCCG X 10 20 30 40 50 60 70
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Identity
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Sequence
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898
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898
0
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881
              Matches
Conservative
                            Optimized
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Conservative Sub
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                                         16,
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  30
                                        Application US/09697123B
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186
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188
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Mismatches
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Mismatches
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Initial
Residue
Gaps
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US-09-697-123B-5 s
US-09-697-123B-10
US-09-697-123B-6 S
                                              Score Identity
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898
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898
0
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Matches = 186
Conservative Substitutions
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186
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Mismatches
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22
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US-09-697-123B-10 US-09-697-123B-2 S

Sequence

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Application

US/09697123B

(1-208)

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Initial
Residue
Gaps
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Residue
Gaps
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Residue
Gaps
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US-09-697-123B-10
US-09-697-123B-1 S
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US-09-697-123B-2 s
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Sequence 1,
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Sequence
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US-09-697-123B-2 :
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US-09-697-123B-8 5
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US-09-697-123B-3 S
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        US-09-697-123B-10 (1-208)
US-09-697-123B-2 Sequence
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US-09-697-123B-2 S
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US-09-697-123B-1 S
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US-09-697-123B-4 Sequence
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US-09-697-123B-1 5
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US-09-697-123B-1 s
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10

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Initial Score
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US-09-697-123B-9 s
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US-09-697-123B-2 Sequence 21, Application US/09697123B
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177
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177 Mismatches
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Initial Score
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US-09-697-123B-7 &
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US-09-697-123B-1 Sequence
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e Identity
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Sequence 14,
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                                                                                                                                                                167 Significance - 174 Mismatches -
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173 Mismatches
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Similarity matrix
Mismatch penalty
Gap penalty
Gap size penalty
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Number
Number
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Initial Score

US-09-697-123B-9 US-09-697-123B-1

(1-223) Sequence 13, Application US/09697123B

195 Optimized Score

195 Significance

1.54

220 X ACGACAT |||||| ACGACAT 220 X

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Initial Score Residue Identity Gaps
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4. US-09-697-123B-1 Sequence 19, Application 208
5. US-09-697-123B-1 Sequence 1, Application 208
6. US-09-697-123B-1 Sequence 1, Application 208
7. US-09-697-123B-1 Sequence 6, Application 208
8. US-09-697-123B-1 Sequence 5, Application 208
9. US-09-697-123B-2 Sequence 2, Application 208
10. US-09-697-123B-2 Sequence 2, Application 208
11. US-09-697-123B-2 Sequence 21, Application 208
12. US-09-697-123B-1 Sequence 21, Application 208
13. US-09-697-123B-1 Sequence 23, Application 208
14. US-09-697-123B-1 Sequence 27, Application 208
15. US-09-697-123B-2 Sequence 27, Application 208
16. US-09-697-123B-3 Sequence 27, Application 208
17. US-09-697-123B-3 Sequence 27, Application 208
18. US-09-697-123B-3 Sequence 27, Application 208
19. US-09-697-123B-1 Sequence 27, Application 207
20. US-09-697-123B-1 Sequence 27, Application 207
21. US-09-697-123B-1 Sequence 18, Application 207
22. US-09-697-123B-2 Sequence 19, Application 207
23. US-09-697-123B-3 Sequence 27, Application 214
24. US-09-697-123B-2 Sequence 27, Application 214
25. US-09-697-123B-2 Sequence 27, Application 214
26. US-09-697-123B-2 Sequence 27, Application 214
27. US-09-697-123B-3 Sequence 27, Application 214
28. US-09-697-123B-2 Sequence 27, Application 214
29. US-09-697-123B-2 Sequence 28, Application 29, US-09-697-123B-3 Sequence 29, Application 214
29. US-09-697-123B-2 Sequence 29, Application 214
29. US-09-697-123B-3 Sequence 29, Application 214
29. US-09-697
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US-09-697-123B-9 Sequence
                                                                                                                                                       US-09-697-123B-9 Sequence 9, Application
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of other best scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        **** 1 standard deviation above
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         223 Optimized Score = 100% Matches = 100%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence 13, Application
** 0 standard deviation from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9, Application US/09697123B
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223
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ow mean
19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mean
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Score
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0.433
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Initial
Residue
                                                                                                                                                                                                                                                                                                      Initial Score
Residue Identity
Gaps
                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Residue
Gaps
                                                                              US-09-697-123B-9
US-09-697-123B-1
                                                                                                              220 X
ACGACAT
||||||
ACGACAT
X
                                                                                                                                                                                                                                                                                                                                    US-09-697-123B-9
US-09-697-123B-1
80 90 100 120 130 130 GCGAGCGATCACGTCGCCACGCTGACCAGGAAGACGTCGTCGCGACGAATACCTGGTCCGCGCCGACGAGGAAGACGTCGTCGCGACGAATACCTGGTCCGCGCCGCTGCGACGAGGAAGACGTCGTCGCACCATCGAATACCTGGTCCGCCGCCTGCGTCGCCGACGATCACCAGCTCGACGACGACGAGAAGACGTCGTCGCCACCATCCAGTACCTGGTCGCCCTGC 110 110 120 130 140
                                                                                                                                                                                                                                                      220 X
ACGACAT
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ACGACAT
220 X
                                                                                                                                                            Score Identity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0 0
                                                                            (1-223)
Sequence 19, Application US/09697123B
                                                                                                                                                                                                                                                                                                                                   (1-223)
Sequence 15, Application US/09697123B
                                                 146
82%
15
                                                                                                                                                                                                                                                                                                      148
84%
15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            878
0
                                                        Optimized Score -
Matches -
                                                                                                                                                                                                                                                                                                             Optimized Score - Matches -
                                                       Matches
                                                 Conservative
                                                                                                                                                                                                                                                                                                  Matches - 189
Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
Conservative
                                                Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Substitutions
                                                      173 Significance
183 Mismatches
                                                                                                                                                                                                                                                                                                           175 Significance
189 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                 . . .
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25
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19
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Initial Score Residue Identity - Gaps
                                                                                                                                                                           6
                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                        Residue
                                                                                                                                                                                                                                                                                                                                                                                                               Initial
                                                                                                                                                              US-09-697-123B-9 (1-223)
US-09-697-123B-1 Sequence 16, Application US/09697123B
                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-697-123B-9
US-09-697-123B-1
                                                                                                                                                                                                                  220 X
ACGACAT
ACCACGCCCGTACGGATGGCCAGCCCGCCGTCATGÀCTGTCCCCGGCGGGGGATCGAGGTGCCGGTGGAGACCG
                               80 90 100 120 130 140 GCGAGCCGATCGACGTCGACGCTGACCGAGGAAGACGTCGTCGACGATCGACTGGACGATCGAATACCTGGTCCGGCTGCGACGAGGAAGACGTCGTCGCGACCATCGAATACCTGGTCCGGCTGCGACGACGACGACGACGACGACGACGACGACGATCACGTCGTCGACGCTGACCGAAGAAGACGTCGTGGCCACCATCGAATACTCTGGTCCGCTTGC 80 90 100 110 120 130 140
                                                                              220 X
ACGACAT
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X
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                                                                                                                                                                                                                                                                                                                                                                                                                          (1-223)
Sequence 1, Application US/09697123B
                                                                                                                                  144
80%
15
                                                                                                                                                                                                                                                                                                                                                                                              146
83%
15
                                                                                                                               Optimized Score - 170
Matches - 180
Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                            Matches = 187
Conservative Substitutions
                    170
                                                                                                                                                                                                                                                                                                                                                                                                             Optimized
                                                                                                                                         Score
                   180
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                 190
                                                                                                                                                                                                                                                                                                                                                                                                     173
187
                                                                                                                                       Significance
Mismatches
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Mismatches
                 200
                 210
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28
0
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21
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Initial Score
Residue Identity :
Gaps
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Residue Identity
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US-09-697-123B-5
220 X
ACGACAT
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ACGACAT
X
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US-09-697-123B-6 Sequence 6, Application US/09697123B
                                                                                                                                             X 10 20 30 40 50 FOR TRANSPORTED TO THE TRANSPORT TO THE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              220 X
ACGACAT
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ACGACAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80 90 100 120 130 130 GGGAGCGATCACGTCGACGCTGACCGAGGAGGAGAGACGTGGTCGGGCTGCGGGCTGCGGACGATCACTGGTCCGGCTGCCGGCTGCGACGAGGAATACCTGGTCCGGCTGCGACGACGATCACGTCGACGTGACGACGATCACGTCGACGCTGACGAGAGAAGACGTCGTGGCCACCATCGACTATCTGGTCCGCTTGC 80 90 100 110 120 130 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        X 10 20 30 40 50 60 70 TCHARGAGAGAGCTGCACGACTGGCCCGCTCGGCCCGCTACAAGGTCAACAAGAAGCTGGGTCTGCACGCCGCTCGGCCCGCTACAAGGTCAACAAGAAGCTTGGGTCTGCACGCCCGCTCGACGACGACAGAAGACTTCGGGTCGCTTCGGCCTCGGTCGCTATAAAGCAAGAAAAGATCAGGACTGCATGTCG X 10 20 30 40 50 60 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      220 X
ACGACAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (1-223)
Sequence 5, Application US/09697123B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        144
80%
15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Optimized Score 
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Optimized Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches - 180
Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -CCACGATGACCGTTCCGGGCGGCGTCGAGGTGCCGGTGGAAACCG 160 170 180 190 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                180
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180
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180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Significance
Mismatches
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Mismatches
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Initial Score
Residue Identity
Gaps
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                                                                                                                                                                                                                                                           Initial Score - Residue Identity - Gaps
                                                                                                                                                                                                                                                                                                  10.
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Residue Identity
                                 US-09-697-123B-9
US-09-697-123B-1
                                                                         220 X
ACGACAT
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ACGACAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-697-123B-9
US-09-697-123B-2
                                                                                                          80 90 100 120 130 140 GGGAGCGATCACGTCGTCGACGAGGAAGAAGGTCGTCGCGACCATCGAATACCTGGTCCGGGTGCGCTGCCGAGGAAGACGTCGTCGCGACCATCGAATACCTGGTCCGGCTGCGCTGCGCTGCGCTGCCGACGACATCACGTCGTCGACGCTGACCGAAGAAGACCGTCGTGGCCACCATCGAATATCTGGTCCGCTTGC 80 90 100 110 120 130 140
                                                                                                                                                                                                       US-09-697-123B-9
US-09-697-123B-2
                                                                                                                                                                                                                                                                                                                                         220 X
ACGACAT
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                             (1-223)
Sequence 11, Application US/09697123B
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Sequence 2, Application
                                                                                                                                                                                                                                                                                      (1-223)
Sequence 22, Application US/09697123B
   140
798
15
                                                                                                                                                                                                                                                          143
80%
15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  144
80%
15
  Conservative
          Matches
                 Optimized
                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                        Optimized
                                                                                                                                                                                                                                                        Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Optimized Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                Score
                                                                                                                                                                                                                                                                        Score
Substitutions
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        168
178
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179
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180
                                                                                                                                                                                                                                                                                                                                                                                                                    120
                                                                                                                                                                                                                                                              Significance
Mismatches
        Mismatches
               Significance
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Mismatches
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30
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29
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28
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30

40

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Initial Score
Residue Identity Gaps
                                                                                                                                                                                                                                                                Initial Score
Residue Identity =
Gaps
                                                                                      13. US-09-697-123B-9 (1-223)
US-09-697-123B-2 Sequence 23, Application US/09697123B
                                                                                                                                                                                                                                                                                               12.
                                                                                                                       220 X
ACGACAT
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ACGACAT
US-09-697-123B-9 (1-223)
US-09-697-123B-1 Sequence 10, Application US/09697123B
                                                                                                                                                   220 X
ACGACAT
                                                                                                                                                                                                                                                                                                                                                                                    ACGACAT
                                                                    ity =
                                                                   138 Optimized Score = 77% Matches = 15 Conservative Substi
                                                                                                                                                                                                                                                              139 Optimized Score = 167
798 Matches = 177
15 Conservative Substitutions
                                                                  Conservative Substitutions
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173 Mismatches
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US-09-697-123B-3
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ACGACAT
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US-09-697-123B-2 Sequence
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Sequence 3, Application US/09697123B
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185
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US-09-697-123B-9 (1-223) US-09-697-123B-2 Sequence

20,

Application

US/09697123B

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Initial
Residue
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Residue
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US-09-697-123B-4 Sequence 4, Application US/09697123B
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Residue Identity
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ACGACAT
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ACGACAT
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US-09-697-123B-1 Sequence 18, Application US/09697123B
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US-09-697-123B-1 Sequence 12, Application US/09697123B
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Sequence 7, Application US/09697123B
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Sequence 14, Application US/09697123B
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2. US-09-697-123B-1 Sequence 17, Application
3. US-09-697-123B-1 Sequence 15, Application
4. US-09-697-123B-1 Sequence 11, Application
5. US-09-697-123B-1 Sequence 19, Application
6. US-09-697-123B-1 Sequence 19, Application
7. US-09-697-123B-1 Sequence 16, Application
8. US-09-697-123B-1 Sequence 16, Application
9. US-09-697-123B-1 Sequence 10, Application
10. US-09-697-123B-2 Sequence 5, Application
11. US-09-697-123B-2 Sequence 2, Application
12. US-09-697-123B-2 Sequence 2, Application
13. US-09-697-123B-2 Sequence 2, Application
14. US-09-697-123B-2 Sequence 2, Application
15. US-09-697-123B-2 Sequence 2, Application
16. US-09-697-123B-3 Sequence 13, Application
17. US-09-697-123B-1 Sequence 17, Application
18. US-09-697-123B-1 Sequence 17, Application
19. US-09-697-123B-3 Sequence 17, Application
20. US-09-697-123B-3 Sequence 17, Application
21. US-09-697-123B-3 Sequence 17, Application
22. US-09-697-123B-3 Sequence 17, Application
23. US-09-697-123B-1 Sequence 18, Application
24. US-09-697-123B-1 Sequence 18, Application
25. US-09-697-123B-1 Sequence 18, Application
26. US-09-697-123B-1 Sequence 18, Application
27. US-09-697-123B-1 Sequence 18, Application
28. US-09-697-123B-1 Sequence 18, Application
29. US-09-697-123B-1 Sequence 19, Application
29. US-09-697-123B-2 Sequence 19, Application
29. US-09-697-123B-3 Sequence 29, Ap
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Initial Score Residue Identity Gaps . US-09-697-123B-8 US-09-697-123B-8 (1-208) Sequence 8, Application US/09697123B 208 Optimized Score - 208
100% Matches - 208
0 Conservative Substitutions 208 Significance 208 Mismatches . . . 1.11 0 0

19

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2. US-09-697-123B-8 (1-208) US-09-697-123B-1 Sequence 17, Application US/09697123B

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Gaps Initial Score Residue Identity . . . 187 89**8** 0 Optimized Score = 187
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US-09-697-123B-1
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US-09-697-123B-8 US-09-697-123B-1

(1-208) Sequence

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Application

US/09697123B

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Initial Residue Gaps

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Substitutions

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US-09-697-123B-8 US-09-697-123B-2

(1-208) Sequence

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Application US/09697123B

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ACGAGGGCCACGATGACCGTGCCGGGCGGGGTCGAGGTGCCGGTGGAAACCGACGACAT
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-09-697-123B-2
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US-09-697-123B-8 US-09-697-123B-4

(1-208)

Sequence

Application

US/09697123B

Substitutions

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US-09-697-123B-1
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US-09-697-123B-7
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US-09-697-123B-9
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Sequence 7, Application US/09697123B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9,
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171
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175 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      179 Significance
184 Mismatches
                                                                                                                                                                                                                                                       Significance
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Significance
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37
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Initial
Residue
                                Gaps
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Residue
Gaps
                                                                                                                                                                                                                                                                                  Initial Score Residue Identity - Gaps
                                                                                                                                                                                                                                                                                                         22.
                                                                 US-09-697-123B-8
US-09-697-123B-1
                                                                                            US-09-697-123B-8
US-09-697-123B-1
                                                                                                                                                                                                                                                                                                    US-
                                                                                                                                                                                                                                                                                                                    Score Identity
                                                                                                                                                            Score
Identity
                                                                                                                                                                                                                                                                                                    -09-697-123B-8
-09-697-123B-2
                                . . .
                                                 (1-208)
Sequence
                                                                                                                                                                        (1-208)
Sequence 14, Application US/09697123B
                                                                                                                                                                                                                                                                                                   (1-208)
Sequence
                               117
80%
3
                                                                                                                                                             118
81%
                                                                                                                                                                                                                                                                                 122
828
6
                                                                                                                                                         6
                                                                                                                                                            Optimized
Matches
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Matches
Conservative
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                                                 18,
                                                                                                                                                                                                                                                                                                 21, Application
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                                       Score
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                              Substitutions
                                                                                                                                                       Substitutions
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                                                US/09697123B
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                                  164
170
                                                                                                                                                                                                                                                                                     170
177
                                 Significance
Mismatches
                                                                                                                                                           Significance
Mismatches
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Mismatches
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38
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33
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Mismatch penalty
Gap penalty
Gap size penalty
Cutoff score
                                                                                                                                                                                                                                                                                                                                                                    SCORE 0
Sequence Name
                                          A 100% identical sequence to the
                                                               The scores below are sorted by initial score. Significance is calculated based on initial score.
                                                                                                           Number of residues:
Number of sequences searched:
Number of scores above cutoff:
                                                                                                                                                                                                                                                                                                  Similarity matrix Mismatch penalty
                                                                                                                                                                                                                                                                                                                                                                                                       ω ΕΙ Ω ΕΙ ΕΙ Ο ΕΙ Ν
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0 0 \
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Number of sequences searched: 26
Number of scores above cutoff: 25
                                                                                                                                                                                                       Scores:
                                                                                                                                                                                                                                                   Randomization group
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Results file us-09-697-123b-7.res made by shanley on Wed 13 Nov 102 13:57:41-PST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FastDB - Fast Pairwise Comparison of Sequences Release 5.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        - 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Results of the initial comparison of US-09-697-123B-7 (1-214) with: File : US09697123B.seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IntelliGenetics
                                                                                                                                                                                                                                                                                                                                                                                24
       Description
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- - -
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00:00:00.00
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5.00
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117
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                                                                                                                                                                                                                             SEARCH STATISTICS
                                                                                                                                                                                                                                                                                                                                   PARAMETERS
                                        query sequence was found:
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                                                                                                                                                                                                                                                                                    K-tuple
Joining penalty
Window size
                                                                                                                                                                                             Median
122
                                                                                                              5077
26
25
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                                                                                                                                                          Total Elapsed 00:00:00:00.00
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    Init. Opt.
Length Score Score Sig. Frame
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208
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US-09		l. US-09-697-123B-7
US-09-697-123B-2 US-09-697-123B-1 US-09-697-123B-1 US-09-697-123B-1 US-09-697-123B-1 US-09-697-123B-3 US-09-697-123B-4 US-09-697-123B-4 US-09-697-123B-4 US-09-697-123B-4 US-09-697-123B-4 US-09-697-123B-3		-09-69
7-1238-1 7-1238-1 7-1238-1 7-1238-1 7-1238-1 7-1238-1 7-1238-3 7-1238-3 7-1238-3 7-1238-3 7-1238-1 7-1238-1 7-1238-1 7-1238-1 7-1238-2 7-1238-2 7-1238-2	1	.697-12:
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devil		pplic
l standard deviation a puence 21, Application () standard deviation for the property of the pr		Application
	_	n U
above mean * 214 from mean * 208 208 208 208 208 208 208 208 208 208	Length	214
mean ** 214		-
1197 1197 1137 1137 1139 1129 1129 1129 1129 1121 1121 1121	(n) ·	214
197 172 172 172 165 166 168 164 164 161 161 161 161 161 161 161 161	Opt. Score	214
1.90 0.33 0.288 0.194 0.194 0.194 0.099 0.099 0.099 0.099 0.099 0.099 0.099 0.099	Sig	2.30
31 39 39 39 39 39 39 39 39 39 39 39 39 39	•	30
0 0000000000000000000000000000000000000	Frame	0

150 160 170 180 190 200 210 x GCCTGCACGACGGCCACGACCACGATGACCGCCCCCGGGGCCTCGAGGTCCGAGGTCGACGACAT [80 100 120 130 140 CCAACCCGGCTCTGGTGACCTACCCACCACCACCACCACCCAC	X	Initial Score = 214 Optimized Score = 214 Significance = 2.30 Residue Identity = 100% Matches = 0 Gaps = 0 Conservative Substitutions = 0	1. US-09-697-123B-7 (1-214) US-09-697-123B-7 Sequence 7, Application US/09697123B
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Initial Score Residue Identity - Gans

197 92**%** 0

Optimized Score = 197 Matches = 197 Conservative Substitutions

197 Significance - 197 Mismatches - tions -

2. US-09-697-123B-7 (1-214) US-09-697-123B-2 Sequence 21, Application US/09697123B

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Initial
Residue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Initial Score
Residue Identity
Gaps
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Residue Identity
                                                                                   US-09-697-123B-7
US-09-697-123B-1
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US-09-697-123B-1
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US-09-697-123B-1 Sequence 14,
                                                                                                                                                            150 170 180 210 x
GCCTGCAGGAGGGCAGCAGCAGCAGCAGCGCCGGGGGGCCTGAGGGTCGAGGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGAAACCGACGACGACTAGAGCGACGAGGAGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTGGAAAACCGACGACGACTAGAGCGACGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCAGAGTCAGAGTCAGAGTCAGAGTCAGGTCAGGTCAGGTCAGGTCAGGTCAGGTCAGGTCAGGTCAGGTCAGGTCAGGTCAGGTCAGGTCAGGTCAGGTCAGGTCAGGTCAGGTCAGGTCAGGTCAGGTCAGGTCAGGTCAGGTCAGGTCAGGTCAGGTCAGGTCAGGTCAGGTCAGGTCAGGTCAGGTCAGGTCAGGTCAGGTCAGGTCAGGTCAGGTCAGGTCAGGTCAGGTCAGGTCAGGTCAGGTCAGGTCAGAGGTCAGGTCAGGTCAGGTCAGGTCAGGTCAGGTCAGGTCAGGTCAGGTCAGGTCAGGTCAGGTCAGGTCAGGTCAGGTCAGGTCAGGTCAG
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                                                                               Sequence 15,
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Sequence 17, Application
                                                                                                       (1-214)
                                                                                                                                                                                                                                                                                                                                                                           90
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  131
82%
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80%
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80%
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  Conservative Substitutions
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Matches
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                       170
177
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172
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172
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                     Mismatches
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Mismatches
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Mismatches
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US-09-697-123B-7 (1-214)

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Initial
Residue
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                                                                                                                                                                                      Initial
US-09-697-123B-7
US-09-697-123B-1
                                                                                                     US-09-697-123B-7
US-09-697-123B-2
                       l Score
e Identity
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                                                                         ity =
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                                                                                                                                                                                                                             160
                                                                                      (1-214)
Sequence 1, Application US/09697123B
                                                                                                                                                                                            (1-214)
Sequence
                                                                        129
81%
6
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80%
6
                                                                                                                                                                                 Optimized
Matches
                                                                             Optimized Score
                                                                                                                                                                                                                                    90
                                                                       Conservative Substitutions
                                                                           Matches
                                                                                                                                                                             Conservative
                                                                                                                                                                                                                            170
                                                                                                                                                                                            Application
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175
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Mismatches
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US-09-697-123B-8

Sequence

8, Application US/09697123B

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Residue
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US-09-697-123B-3
GCCTGCACGACGCACGACCACGATGACCACCACCACCCCCCGGCCCTCGAGGTCCGAGGTCGACGTCGACGACAT
                     US-09-697-123B-7
US-09-697-123B-2
                                                                                                                                                                      Identity
                                                                                                                                                                                                                                          Score -
                                                                                                     Score
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                                             80
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                                                                                                                                                                                                                                                              (1-214)
Sequence
                                             90
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Sequence 24,
                                                                                          123
788
6
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798
6
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                                                                                                    Optimized Score
                                                                                        Conservative Substitutions
                                                                                              Matches
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    Application

                                                                                                               Application US/09697123B
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                                                                                                                                                                                                                                                              US/09697123B
                                                                                              161
168
                                                                                                                                                                                                                                           164 Significand
171 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                            164
171
                                                        50
                                                                                              Mismatches
                                                                                                   Significance
                                                                                                                                                                                                                                                                                                                                                                                           Significance
Mismatches
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                                            140
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                                                                                                                                                                                                                                       . 19
37
0
                                                           Gaps
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Residue
                                                                                                  Initial
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US-09-697-123B-7
US-09-697-123B-6
                                                                                                                                     TCAAGGAGAAGCGCTACGACCTGGCCCGCGTCGCTCATAAGGTCAACAAGAAGCTCGGGCTGCATGTCG

x 10 20 30 40 50 60 70
                                                TCAAGGAGAAGCGCTACGACCTGGCCCGCGTGGGCCGGTACAAGGTGAACAAGAAGCTGGGTTGGCGGTG
                                                                                                                                                                                 US-09-697-123B-7
US-09-697-123B-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCTTGCACGAGGGGCACGCCACGATGAAGGTCCCCGGTGGGCGTCGAGGTGCCGGTGGACGACGACAT 150 160 170 180 190 200 x
                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-697-123B-7
US-09-697-123B-1
                                                                                                Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Identity -
                                                                                        Identity
                                                                                                                                                                                                                                                                                         Score
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                                                                    10
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                                                                                                             (1-214)
Sequence
                                                                                                                                                                                                                                                                                                       Sequence 16,
                                                                                                                                                                                                                                                                                                              (1-214)
                                                                                 121
778
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US-09-697-123B-5 Sequence 5, Application US/09697123B
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US-09-697-123B-1
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US-09-697-123B-1
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US-09-697-123B-7 US-09-697-123B-4

(1-214) Sequence

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Application US/09697123B

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Page 6

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Similarity matrix
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Initial Score
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US-09-697-123B-6
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US-09-697-123B-1 Sequence 16, Application US/09697123B
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Sequence 6, Application US/09697123B
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US-09-697-123B-5
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US-09-697-123B-1
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US-09-697-123B-2
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US-09-697-123B-3
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US-09-697-123B-1
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US-09-697-123B-2
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US-09-697-123B-1
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US-09-697-123B-2 Sequence
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US-09-697-123B-1 Sequence
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US-09-697-123B-8
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US-09-697-123B-6
US-09-697-123B-2
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US-09-697-123B-2
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US-09-697-123B-1
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Sequence 17,
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Initial Residue

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US-09-697-123B-6 US-09-697-123B-9

(1-208) Sequence

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Application

US/09697123B - 170 Sig - 180 Misi

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US-09-697-123B-4
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US-09-697-123B-1
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Sequence 4,
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Sequence 12, Application US/09697123B
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US-09-697-123B-7
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US-09-697-123B-1
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ACGACAT
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(1-208)
Sequence 7, Application US/09697123B
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Sequence 13, Application US/09697123B
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US-09-697-123B-2
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US-09-697-123B-1 Sequence 14, Application US/09697123B
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US-09-697-123B-1
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80 90 100 110 120 130 140
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Sequence 18,
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Similarity matrix
Mismatch penalty
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Conservative Substitutions Optimized Score - Matches -

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US-09-697-123B-5 (1-208) US-09-697-123B-6 Sequence 6, Application

US/09697123B

208 208

Significance Mismatches

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5. US-09-697-123B-1 Sequence 10, Application from 6. US-09-697-123B-1 Sequence 11, Application 7. US-09-697-123B-3 Sequence 11, Application 9. US-09-697-123B-3 Sequence 15, Application 9. US-09-697-123B-3 Sequence 15, Application 10. US-09-697-123B-1 Sequence 15, Application 11. US-09-697-123B-1 Sequence 19, Application 11. US-09-697-123B-1 Sequence 19, Application 11. US-09-697-123B-1 Sequence 1, Application 11. US-09-697-123B-2 Sequence 2, Application 11. US-09-697-123B-2 Sequence 27, Application 11. US-09-697-123B-2 Sequence 27, Application 11. US-09-697-123B-2 Sequence 27, Application 11. US-09-697-123B-3 Sequence 27, Application 11. US-09-697-123B-3 Sequence 29, Application 11. US-09-697-123B-3 Sequence 31, Application 12. US-09-697-123B-3 Sequence 14, Application 12. US-09-697-123B-1 Sequence 14, Application 12. US-09-697-123B-1 Sequence 14, Application 12. US-09-697-123B-3 Sequence 11, Application 12. US-09-697-123B-3 Sequence 27, Application 12. US-09-697-123B-3 Sequence 27, Application 12. US-09-697-123B-3 Sequence 27, Application 13. US-09-697-123B-3 Sequence 28, Application 14. US-09-697-123B-3 Sequence 19, Application 15. US-09-697-123B-3 Sequence 27, Application 17. US-09-697-123B-3 Sequence 19, Application 18. US-09-697-123B-3 Sequence 28, Application 19, US-09-697-123B-3 Sequence 29, Application 19, US-09-697-123B-3 Sequence 30, Application 19, US-09-697-123B-3 Seq
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US-09-697-123B-1 Sequence 16, Application US/09697123B
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US-09-697-123B-5 (1-208)

-09-697-123B-1

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US-09-697-123B-8
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Initial
Residue
Gaps
                                                           16.
                                                                                                                                                                      Gaps
                                                                                                                                                                          Initial Score
Residue Identity
                                                                                                                                                                                                                                                                                                             Initial Score
Residue Identity
                                                                                                                                                                                               15.
                                                                                                                                                                                                                                                                                                                                   14.
US-09-697-123B-5
US-09-697-123B-2
                                                                       US-09-697-123B-5
US-09-697-123B-2
                                                                                                                                                                                                           US-09-697-123B-5
US-09-697-123B-1
                                      Identity
                                                                                                                                                                                                                                                                                                                                                                                 80
                                  a e e
                                                                                                                                                                                                                                                                                                          D 0 0
                                                     (1-208)
Sequence 20,
                                                                                                                                                                                                                                                                                                                                                                                 90
                                                                                                                                                                                         (1-208)
Sequence 24,
                                                                                                                                                                                                                                                                                                                             (1-208)
Sequence 17,
                                                                                                                                                                     172
82%
0
                                                                                                                                                                                                                                                                                                         178
85%
0
                                     Optimized
Matches
                                 Conservative Substitutions
                                                                                                                                                                          Optimized 
Matches
                                                                                                                                                                    Conservative Substitutions
                                                                                                                                                                                                                                                                                                                   Optimized
                                                                                                                                                                                                                                                                                                        Conservative Substitutions
                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                 100
                                                    Application
                                                                                                                                                                                         Application US/09697123B
                                                                                                                                                                                                                                                                                                                             Application
                                                                                                                                                                               Score
                                      p #
                                                    US/09697123B
                                                                                                                                                                                                                                                                                                                            US/09697123B
                                      171
177
                                                                                                                                                                         172
172
                                                                                                                                                                                                                                                                                                                                                                                120
                                     Significance = Mismatches =
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Mismatches
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Mismatches
                                                                                                                                                                                                                                                                                                                                                                                130
                              0.12
28
0
                                                                                                                                                                                                                                                                                                                                                                               140
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                                                                                                                                                                   36
                                                                                                                                                                                                                                                                                                       . 4.4
30
0
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Initial Residue

Score Identity

144 80% 15

Optimized Score = 170
Matches = 180
Conservative Substitutions

Significance Mismatches

- -0.21 - 28 - 0 19.

US-09-697-123B-5 US-09-697-123B-9

(1-208) Sequence

9, Application

US/09697123B

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Gaps
                                                                                    Residue
                                                                                                                                                                                               Gaps
                                                                                                                                                                                                  Initial
Residue
                                                                                                     18.
                                                                                        Initial
US-09-697-123B-5 (1-208)
US-09-697-123B-4 Sequence 4, Application
                                                                                                              US-09-697-123B-5
US-09-697-123B-1
                                                                                                                                                                                                                              Score Identity
                                                                                                                                                                                               . . .
                                                                                                                                                                                                               (1-208)
Sequence 12,
                                                                                   147
878
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87%
1
                                                                                   Optimized 
Matches
                                                                                                                                                                                                  Optimized 
Matches
                                                                             Conservative Substitutions
                                                                                                                                                                                             Conservative Substitutions
                                                                                                                                                                                                              Application US/09697123B
                                                                                                                                                                                                      Score
                                                                                               US/09697123B
                                                                                 178 Significance
183 Mismatches
                                                                                                                                                                                                  176
181
                                                                                                                                                                                                 Significance
Mismatches
                                                                             .15
24
0
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26
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Residue
Gaps
                                                                                                                                                                                                                                                                                                               Initial
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                                                                                                  X 20 30 40 50 FOR TRANSCRAFT TO THE PROPERTY OF THE PROPERTY O
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACGACAT
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US-09-697-123B-7 Sequence 7, Application US/09697123B
               GCGAGCC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-697-123B-5
US-09-697-123B-1
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Identity
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Sequence 13, Application US/09697123B
                                                                                                                                                                                                                                                          121
778
6
                                                                                                                                                                                                                                                                                 Optimized Matches
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166
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176
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Mismatches
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0
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Residue
                                                                                                                                                                                                                                                                                                                                                                                                           Initial
Residue
                                                                                                                                                                                                                             Residue
                                                                                                                                                                                                                                                 23. US-09-697-123B-5
US-09-697-123B-1
                                                                                                                                                                                                                                   Initial
                                                                                                                            US-09-697-123B-5
US-09-697-123B-2
                                                                                        X 10 20 30 40 50 60 70 TCAAGGAGAAGCGCTACGACCTGGCCCCGCGTCGGCTCGGTCACAAGAAGCTCGGGCTGGCATGTCG
                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-697-123B-5
US-09-697-123B-1
                                                                                                                                                                                                                                                                                                                                                         TCAAGGAGAAGGGCTACGACCTGGCCCGCGTGGGTCGGTACAAGGTCAAGAAGAAGGTGGGCATCACCGAGA
X 10 50 60 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCAACCCGGCTCTGGTGACTGCCACCACGCTCACCGAAGAAGACGTCGTCGCCACCACCATCGGGTACCTGGTGC 80 90 100 110 120 130 140
                                            Score
Identity
                                                                                                                                                                                                                          Score Identity
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                                                                (1-208)
Sequence
                                                                                                                                                                                                                                             (1-208)
Sequence 14, Application US/09697123B
                                                                                                                                                                                                                                                                                                                                                                                                                             (1-208)
Sequence
                                     78%
6
                                                   109
                                                                                                                                                                                                                     110
81%
6
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78%
3
                                          Optimized
Matches
                                                                                                                                                                                                                           Optimized Score
Matches
                                   Conservative Substitutions
                                                                                                                                                                                                                   Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                  Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                         Optimized Score
Matches
                                                                21,
                                                                                                                                                                                                                                                                                                                                                                                                                            18, Application
                                                              Application US/09697123B
                                                  Score
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                                                                                                                                                                                                                                                                                                                                                                                                                             US/09697123B
                                          162
169
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175
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165
                                         Significance
Mismatches
                                                                                                                                                                                                                         Significance
Mismatches
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0
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33
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43
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25. US-05-697-123B-5 (1-208) 25. US-05-697-123B-5 (2-208) 25. US-05-697-123B-5 (2-208) 25. US-05-697-123B-7 (2-208) 26. US-05-697-123B-7 (2-208) 27. US-05-697-123B-7 (2-208) 28. US-05-697-123B-7 (2-208) 29. US-05-697-123B-7 (2-208) 29. US-05-697-123B-7 (2-208) 29. US-05-697-123B-7 (2-208) 20. US-05-697-123B-7 (2-208) 20. US-05-697-123B-7 (2-208) 21. US-05-697-123B-7 (2-208) 21. US-05-697-123B-7 (2-208) 21. US-05-697-123B-7 (2-208) 21. US-05-697-123B-7 (2-208) 22. US-05-697-123B-7 (2-208) 23. US-05-697-123B-7 (2-208) 23. US-05-697-123B-7 (2-208) 24. US-05-697-123B-7 (2-208) 25. US-05-697-12	10 120 130 140 150	x 10 20 30 40 50 60 70
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Mismatch penalty
Gap penalty
Gap size penalty
Cutoff score
                                                                                           Number of
Number of
Number of
                                                                                                                                                                                                                                                                                                       SCORE
STDEV
  Sequence Name
                                                    The scores below are sorted by initial score. Significance is calculated based on initial score.
                                                                                                                                                                                                                                                                                                                                  SECSECOES
                                                                                                                                                                                                                                                                                                                                                                                                                       7 O
                                                                                                                                                                                                                                                                                                                                                                                                                                                    z \in z \in z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FastDB - F
Release 5.
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0 0 \
0 0 \
                                    A 100% identical
                                                                                                                                           Times:
                                                                                                                                                                      Scores
                                                                                                                                                                                                        Randomization group
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query sequence being compared: US-09-697-123B-4 (1-207) Number of sequences searched: 26 Number of scores above cutoff: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Results file us-09-697-123b-4.res made by shanley on Wed 13
                                                                                                                                                                                                                                                                                                                                                                        10-
5-
-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Results of the initial comparison File : USO9697123B.seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IntelliGenetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fast Pairwise Comparison of Sequences 5.4
                                                                                         residues:
sequences searched:
scores above cutoff:
                                  sequence to the
       Description
                                                                                                                                                                                                                                                                                                                46
                                                                                                                                CPU
00:00:00.00
                                                                                                                                                                                                                                                Unitary
1
                                                                                                                                                            Mean
130
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0.33
12
                                                                                                                                                                                                                                                                                                        -1
69
                                                                                                                                                                                       SEARCH STATISTICS
                                                                                                                                                                                                                                                                          PARAMETERS
                                  query sequence was found:
                                                                                                                                                                                                                                                                                                                92
                                                                                                                                                                                                                                   K-tuple
Joining penalty
Window size
                                                                                          5077
26
25
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                                                                                                                                                                                                                                                                                                                                            * * *
                                                                                                                                                           Standard Deviation 42.91
                                                                                                                               Total Elapsed 00:00:00:00.00
Init. Opt.
Length Score Score Sig. Frame
                                                                                                                                                                                                                                                                                                       161
                                                                                                                                                                                                                                                                                                                184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nov 102 14:02:31-PST
                                                                                                                                                                                                                                   30
207
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|207
|2
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2. 3. 3. 3. 5. 6. 6. 6. 7. 7. 7. 112. 112. 113. 113. 114. 115. 115. 115. 115. 115. 115. 115	Sequence	1. The 1
US-09		. US-0
US-09-697-123B-1 US-09-697-123B-3 US-09-697-123B-3 US-09-697-123B-1	Name	US-09-697-123B-4 lst of other best
7-1238-J 7-1238-J	.	7-123 her b
eque eque eque eque eque eque eque eque	Description	Sequence
		nce 4,
13, Ap. 10, Ap. 110,) (!	
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1, Application U 3, Application U 2, Application U 2, Application U 2, Application U 1, Application U 1, Application U 2, Application U 2, Application U 2, Application U 3, Application U 3, Application U 6, Application U 7, Application U 7, Application U 17, Application U 17, Application U 18, Application U 19, Application U 17, Application U 18, Application U 19, Application U 110, Application U 111, Application U 112, Application U 113, Application U 114, Application U 115, Application U 116, Application U 117, Application U 118, Application U 119, Application U 119, Application U 119, Application U 110, Application U 110, Application U 110, Application U 1110, Application U 1121, Application U 1212, Application D 1213, Application D 1214, Application D 1215, Application D 1255, Application S) 	Application
	! !	ğ
U 208 U 208 U 208 208 208 208 208 208 208 208 208 208	Length	2
208 208 208 208 208 208 208 208 208 208	1	207
* 115562 115562 115562 11552 1	Init. Score	207
189 195 197 178 178 178 179 179 179 178 178 179 179 179 179 179 179 179 179 179 179	Opt. Score	207
	6.	07
0.75 0.75 0.75 0.54 0.49 0.44 0.44 0.44 0.44 0.44 0.44 0.40	Sig.	1.7
	Frame	٠
0 0 00000000000000000000000000000000000	ne e	0

Initial Score - Residue Identity - Gaos -1. US-09-697-123B-4 (1-207) US-09-697-123B-4 Sequence 4, Application US/09697123B 207 100% 0 Optimized Score = 207
Matches = 207
Conservative Substitutions 207 Significance = 207 Mismatches =

Initial Score = Residue Identity = Gaps

162 93% 1

Optimized Score - 189
Matches - 194
Conservative Substitutions

189 Significance = 194 Mismatches =

0.75 13 0

2. US-09-697-123B-4 (1-207) US-09-697-123B-1 Sequence 1, Application US/09697123B

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Initial Score
Residue Identity
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                   Initial
Residue
Caps
                                                                                                                                                                                                           Residue
Gaps
                                                                                                                                                                                                                           Initial
                                 US-09-697-123B-4
US-09-697-123B-2
                                                                                                                                                                                                                                          US-09-697-123B-4
US-09-697-123B-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-697-123B-4
US-09-697-123B-3
                                                             TCAAGGAGAAGCGCTACGACCTGGCCCGTGTCGGCCCGTACAAGGTCAACAAGAAGCTGGGCCTGCATGTCGGCCTACAAGGTCAACAAGAAGCTGGGCCTGCATGTCGGCCTGCATGTCGGCCTGCAAGAAGCTGGGCCTGCAAGAAGCTGGGCCTGCAAGAAGCTGGGCCTGCAAGAAGAAGCTCGGCCTGCAACGAAGAAGCTCGGCCTGCAACGAAGAAGCTCGGCCTGCAACGAAGAAGCTCGGCCTGCAACGAAGAAGCTCGGCCTGCAACGAAGAAGCTCGGCCTGCAACGAAGAAGCTCGGCCTGCAACGTCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Identity
                                                                                                                                                                                                                                                                                                                                                                                                                          Identity
                                                                                                                                                                                                                                                                                                                                                                                                                                    Score
                                                                                                                                                                                           10
   0 0 0
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                                (1-207)
Sequence
                                                                                                                                                                                                                                         (1-207)
Sequence 15,
                                                                                                                                                                                                                                                                                                                                                                                                                                                (1-207)
Sequence 3,
                                                                                                                                                                                                           156
918
1
  153
87%
1
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96%
1
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                                                                                                                                                                                                          Optimized Sco
Matches
Conservative
 Matches
Conservative
                Optimized
                                                                                                                                                                                                                                                                                                                                                                                                                Optimized Score • 195
Matches • 200
Conservative Substitutions
                                22,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Application US/09697123B
                                Application
                                                                                                                                                                                                                                         Application US/09697123B
                                                                                                                                                                                                                          Score
core = 178
= 183
e Substitutions
                                                                                                                                                                                                          Substitutions
                                                                                                                                                                                           40
                                                                                                                                                                                                                   . .
                                US/09697123B
                                                                                                                                                                                                                185 Significance
190 Mismatches
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200 Mismatches
                                                                                                                                                                                           50
       Significance
Mismatches
                                                                                                                                                            60
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               c
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7
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.54
0
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17
0
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Residue
Gaps
                                                                            Residue Identity
Gaps
                                                                                     Initial
                                                                                                                                                                                                            6.
                                                                                                                                                                                               Initial Score
                                                                                            US-09-697-123B-4
US-09-697-123B-1
US-09-697-123B-4
US-09-697-123B-8
                          Score
                                                                                                                                                                                          Identity
                                                                             . . .
                                                                                          (1-207)
Sequence 11, Application US/09697123B
                                                                                                                                                                                                      (1-207)
Sequence 8,
                                                                                                                                                                                                                                                 90
                                                                                151
87%
                                                                                                                                                                                      152
88%
1
                                                                                Optimized 
Matches
                                                                           Conservative Substitutions
                                                                                                                                                                                     Conservative Substitutions
                                                                                                                                                                                              Optimized
                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                100
                                                                                                                                                                                                      Application
                                                                                   Score
                                                                                                                                                                                              Score
                                                                                                                                                                                                                                               110
                                                                                                                                                                                                      US/09697123B
                                                                                182
                                                                                                                                                                                         179
184
                                                                                                                                                                                                                                               120
                                                                               Significance
Mismatches
                                                                                                                                                                                         Significance
Mismatches
                                                                               a
                                                                                   0
                                                                                                                                                                                                                                               140
                                                                                                                                                                                             0
                                                                          .49
25
                                                                                                                                                                                     .51
23
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US-09-697-123B-4 (1-207) US-09-697-123B-2 Sequence 20,

Application US/09697123B

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Initial
Residue
Gaps
                                                                                                                                                                                              Initial
Residue
Gaps
                                                                                                                                                                                                                                                                                                               Initial
Residue
Gaps
                                                                                                 10.
                     US-09-697-123B-4
US-09-697-123B-1
US-09-697-123B-4
US-09-697-123B-2
                                                                                                            Score
Identity
                                                                                                                                                                                                  Identity
                                                                                                                                                                                                                                                                                                                    Identity
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                                                                                                                                                                                               0 0 0
                                                                                                                                                                                                                                                                                                                0 0 0
                                                                                                                                                                                                              (1-207)
Sequence
                                                                                             (1-207)
Sequence
                                                                           149
88%
1
                                                 20
                                                                                                                                                                                             149
868
1
                                                                                                                                                                                                                                                                                     20
                                                                                                                                                                                                                                                                                                                150
88%
2
                                                                           Conservative
                                                                               Matches
                                                                                    Optimized
                                                                                                                                                                                                                                                                                                                   Optimized Matches
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                                                                                                                                                                                                     Optimized
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                                                                                                                                                                                                               10,
                                                                                            2
                                                                                            Application US/09697123B
                                                                                                                                                                                                                                                                                     30
                                                                                                                                                                                                              Application US/09697123B
                                                                                    Score
                                                                                                                                                                                                      Score
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                                                                           Substitutions
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                                                                               180
185
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180
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183
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                                                                              Significance
Mismatches
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Mismatches
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Mismatches
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22
0
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27
                                                   Gaps
                                                       Initial
Residue
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Residue
Gaps
                                                                        13.
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Residue
Gaps
                                                                                                                                                                                          12.
                                                                                                                                                                                                                                                                                                             11.
                                                           Score
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x 10 20 30 40 50 FOR TRANSPARENT TO THE PROPERTY OF THE PROPER
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US-09-697-123B-1
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US-09-697-123B-1
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US-09-697-123B-2
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US-09-697-123B-4 (1-207)
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US-09-697-123B-1
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US-09-697-123B-2
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^{19.} US-09-697-123B-4 (1-207)
 US-09-697-123B-9 Sequence 9, Application US/09697123B

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US-09-697-123B-4
US-09-697-123B-1
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US-09-697-123B-1 Sequence 12,
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165 Mismatches
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Number of sequences searched:
Number of scores above cutoff:
                                           The scores below are sorted by initial score. Significance is calculated based on initial score.
Sequence
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US-09-697-123B-2

Sequence

Application

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4. US-09-697-123B-1 S
5. US-09-697-123B-1 S
6. US-09-697-123B-2 S
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12. US-09-697-123B-1 S
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  -1 Sequence 1, Application U
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-1 Sequence 2, Application U
-1 Sequence 16, Application U
-1 Sequence 6, Application U
-1 Sequence 6, Application U
-2 Sequence 7, Application U
-2 Sequence 8, Application U
-2 Sequence 10, Application U
-2 Sequence 11, Application U
-2 Sequence 12, Application U
-2 Sequence 13, Application U
-2 Sequence 14, Application U
-2 Sequence 17, Application U
-2 Sequence 18, Application U
-3 Sequence 9, Application U
-4 Sequence 9, Application U
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Initial Residue Gaps US-09-697-123B-3 US-09-697-123B-3 l Score -(1-208)
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Conservative Substitutions Mismatches Significance . . 1.05 0

Gaps

Initial Score Residue Identity

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Optimized Score Matches

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Conservative Substitutions

US-09-697-123B-3 (1-208) US-09-697-123B-1 Sequence 1, Application US/09697123B

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US-09-697-123B-3 (1-208) US-09-697-123B-5 Sequence

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Application US/09697123B

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US-09-697-123B-1
                                                                                                                                                  TCAAGGAGAAGCGCTACGACCTGGCCCGTTCGGCCGCTACAAGGTCAACAAGAAGCTTCGGCCTGCACGTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-697-123B-3
US-09-697-123B-4
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US-09-697-123B-1
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Sequence 4,
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Sequence 12,
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96%
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Matches
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Mismatches
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Initial
Residue
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Gaps
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US-09-697-123B-9
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                                                                                                                       US-09-697-123B-3
US-09-697-123B-7
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Identity
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Sequence 7, Application US/09697123B
                                                                                                                                                                                                                                                                                                                                                                  (1-208)
Sequence 9, Application
                                                                                          125
79%
6
                                                                                         Optimized Score = 164
Matches = 171
Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                       Matches - 185
Conservative Substitutions
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185 Mismatches
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Mismatches
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23
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37
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Gaps
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Residue Identity =
Gaps =
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US-09-697-123B-1
US-09-697-123B-3
US-09-697-123B-1
                                                                            US-09-697-123B-3
US-09-697-123B-2
                                                                                                                                                                                                                                                         Score -
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                                                                                                                                                                                                   (1-208)
Sequence
                                                       (1-208)
Sequence 14,
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Sequence 18,
                                                                                                                                                                              112
80%
6
                                 112
81%
6
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Matches
                                      Optimized
Matches
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                                 Conservative Substitutions
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175
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173 Mismatches
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166 Mismatches
                                      Significance
Mismatches
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33
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42
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Similarity matrix
Mismatch penalty
Gap penalty
Gap size penalty
Cutoff score
                                                                                  Number of
Number of
Number of
                                                                                                                                                                                                                                                                                                OF NEGDEROES
  Sequence Name
                                                The scores below are sorted by initial score. Significance is calculated based on initial score.
                                                                                                                                                                                                                                                                        SCORE
STDEV
                                                                                                                           Times:
                                                                                                                                                                                    Randomization group
                                                                                                                                                                                                                                                                                                                                                                                                     ಸಣಹತ್ವಾ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery sequence being compared:US-09-697-123B-2 (1-208)
Number of sequences searched: 26
Number of scores above cutoff: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Results file us-09-697-123b-2.res
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                                100% identical sequence to the
                                                                                                                                                                                                                                                                                                                                                                                  10-
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5.4
                                                                                residues:
sequences searched:
scores above cutoff:
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       Description
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155
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Joining penalty
Window size
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                                query sequence was
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179
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                                                                                                                                                                                                                                                                       139
0
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                                                                                                                   Total Elapsed 00:00:00:00.00
     Init. Opt.
Length Score Score
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                                 found:
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208
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      sig.
Frame
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Gaps Initial Score Residue Identity Gaps US-09-697-123B-2 US-09-697-123B-1 US-09-697-123B-2 80 90 100 120 130 130 GCAAGCCGATCACCAGCTGAGCGTGACCGAGGAACGTCGAGGACCGAGCATCACCAGCTGAGGTGCGAGGAGACGTCGAGGAGCACCATCGAGTACCCAGCAGCAGGAGGAGGAGGAGGAGGAGGAGGAGAGACGTCGTAGCCAACCATCGAGTACCTGGTGCGGCTGCGCTGCGCTGCGACGAGGAACACGTCGTAGCCAACACCATCGAGTACCTGGTGCGGCTGC 80 90 100 110 120 130 (1-208) Sequence 15, 208 100**%** 0 (1-208) Sequence 2, Application US/09697123B Optimized Score = 208
Matches = 208
Conservative Substitutions 208 Significance - 208 Mismatches -1.07 0 0

Initial Score Residue Identity Gaps

194 93% 0

Optimized Score = 194
Matches = 194
Conservative Substitutions

194 Significance = 194 Mismatches =

0.78 14 0

Application us/09697123B

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Initial :
Residue
Gaps
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Residue
Gaps
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Residue
Gaps
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US-09-697-123B-1
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US-09-697-123B-3
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US-09-697-123B-1 Sequence
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                    Score
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Sequence
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Sequence
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681
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90%
0
 20
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908
0
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Matches
Conservative Sub
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Conservative
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 40
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              189
189
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50
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Mismatches
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Mismatches
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Mismatches
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60
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19
70
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US-09-697-123B-2 US-09-697-123B-1

(1-208) Sequence

19,

Application

US/09697123B

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Initial
Residue
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Residue
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US-09-697-123B-2
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US-09-697-123B-1
Score
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Sequence
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Sequence
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88%
0
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89%
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Matches
Conservative
                                                                         Optimized Score - 185
Matches - 185
Conservative Substitutions
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186
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Mismatches
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Initial
Residue
Gaps
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Residue
Gaps
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Residue
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US-09-697-123B-2
US-09-697-123B-1
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US-09-697-123B-6
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Sequence 16, Application
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Sequence
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87%
0
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87%
0
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888
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Matches
Conservative:
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181 Mismatches
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184
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Mismatches
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27
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24
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Gaps
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US-09-697-123B-2
US-09-697-123B-2
                                                                                                                        80 90 100 120 130 140 GCAAGCCGATCACCACCACCACCACCATCGACGCTGACGCTGACGAGGAGAACGTCGTAGCCACCATCGATGACGTGACGCTGACGAGGAGAGACGTCGTAGCCACCATCGATTACCTGGTCGACGATGAGACGTCGTGGCACCATCGATTACTGGTCCGTTGC 100 110 120 130 140
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US-09-697-123B-2
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US-09-697-123B-5
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                                                                                                  (1-208)
Sequence
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Sequence
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Sequence
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86%
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868
081
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878
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                                                                          Optimized Sco
Matches
Conservative
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179
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181
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Mismatches
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Mismatches
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Initial
Residue
Gaps
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Residue
Gaps
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Gaps
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                            US-09-697-123B-2
US-09-697-123B-2
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US-09-697-123B-1
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US-09-697-123B-8
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90
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Sequence
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Sequence
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87%
3
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84%
0
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858
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Matches
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Conservative
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183
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176 Mismatches
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178
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Mismatches
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Mismatches
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22
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Initial
Residue
                            19.
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Residue
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Residue
Gaps
                                                                                                                                                                18.
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                      US-09-697-123B-2
US-09-697-123B-9
                                       US-09-697-123B-2
US-09-697-123B-4
                                                                                                                                                                           US-09-697-123B-2
US-09-697-123B-1
                                                                                                                                                                                                                                                                                                                                                 Score Identity
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Identity
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                                                                                                                                                                                                                                                                           0 0 0
                    (1-208)
Sequence
                                                                                                                                                         (1-208)
Sequence 4,
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Sequence
                                                                                                                                      149
88%
1
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90%
1
Matches
Conservative
                                                                                                                                    Optimized Score = 180
Matches = 185
Conservative Substitutions
           Optimized
                                                                                                                                                                                                                                                                      Optimized Score 184
Matches 189
Conservative Substitutions
                     9,
                                                                                                                                                                                                             100
                                                                                                                                                                                                                                                                                             12,
                    Application
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Substitutions
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                    US/09697123B
     170
180
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    Significance
Mismatches
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Mismatches
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Mismatches
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Initial Score
Residue Identity (
Gaps
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Residue Identi
Gaps
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| 100 | 120 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 
                                                                                                                                                   ACGACAT
                                                                                                                                                                                                                                                                                                                                                                                                     US-09-697-123B-2 (1-208)
US-09-697-123B-7 Sequence 7, Application US/09697123B
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|||||||
ACGACAT
ACGACAT
220 X
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US-09-697-123B-1 Sequence 13, Application US/09697123B
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80%
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78%
15
                                                                                                                                                                                                                                                                                                                                                   Optimized Score
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Matches
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173 Mismatches
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176 Mismatches
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35
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Gaps
                                                                                                                                                                                        Initial
Residue
                                         Initial Score
Residue Identity
                                                                24.
                                                                                                                                                                                                               23.
                                                                                                                                                                                                                                                                                                                                 Initial Score = Residue Identity = Gaps
                                                                                                                                                                                                                                                                                                                                                            22.
                                                                            US-09-697-123B-2
US-09-697-123B-1
                                                                                                            US-09-697-123B-2 (1-208)
US-09-697-123B-2 Sequence
                                                                                                                                                                                                                           US-09-697-123B-2
US-09-697-123B-1
                                                                                                                                                                                       Score Identity
                                      ity -
                                                                                                                                                                                    lty -
                                                                                                                                                                                                                                                    160
                                                         (1-208)
Sequence 14,
                                    112
82%
6
                                                                                                                                                                                                                                                                                                                                                    (1-208)
Sequence 18, Application US/09697123B
                                                                                                                                                                                  112 Optimized Score
81% Matches
6 Conservative Sub
                                                                                                                                                                                                                                                                                                                                 117
798
3
                                 Optimized Score = 170
Matches = 177
Conservative Substitutions
                                                                                                                                                                                 Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                     Optimized Matches
                                                                                                                                                                                                                                                                                                                               Conservative Substitutions
                                                                                                                                                                                                                                                   170
                                                                                                                                                                                                     21, Application US/09697123B
                                                         Application
                                                                                                                                                                                                                                                                                                                                          Score
                                                                                                                                                                                                                                                   180
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                                                         US/09697123B
                                                                                                                                                                                     167 Significance = 174 Mismatches =
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                                       Significance
Mismatches
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                                 . 86
31
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4.86
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41
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Similarity matrix
Mismatch penalty
Gap penalty
Gap size penalty
Cutoff score
    Sequence Name
                                      A 100% identical sequence to the query sequence was found:
                                                            The scores below are sorted by initial score. Significance is calculated based on initial score.
                                                                                                                                                                                                                                                                                                                                     SCORE 0
                                                                                                   Number of residues:
Number of sequences searched:
Number of scores above cutoff:
                                                                                                                                                                                                                                                                                                                                                                    0 H O 2 H C O H 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        O F
                                                                                                                                                         Times:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  z n n z c z
                                                                                                                                                                                        Scores:
                                                                                                                                                                                                                               Randomization group
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery sequence being compared:US-09-697-123B-1 (1-208)
Number of sequences searched:
26
Number of scores above cutoff:
24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Results file us-09-697-123b-1.res made by shanley on Wed 13 Nov 102 13:56:18-PST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FastDB - Fast Pairwise Comparison of Sequences Release 5.4\,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Results of the initial comparison of US-09-697-123B-1 (1-208) with: File : US09697123B.seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IntelliGenetics
                                                                                                                                                                                                                                                                                                                                               23
     Description
                                                                                                                                                                                                                                                                                                                                              46
                                                                                                                                              CPU
00:00:00.00
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157
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0.33
34
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                                                                                                                                                                                                          SEARCH STATISTICS
                                                                                                                                                                                                                                                                                                     PARAMETERS
                                                                                                                                                                                                                                                                                                                                             192
                                                                                                                                                                                                                                                           K-tuple
Joining penalty
Window size
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182
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26
24
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                                                                                                                                                                            Standard Deviation 49.98
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                                                                                                                                            Total Elapsed 00:00:00:00.00
Init. Opt.
Length Score Score Sig. Frame
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1
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30
208
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	X 10 20 30 40 50 60 70 TCAAGGAGAAGCTCACGACCTGGCCCGGGTAGGCCGCTACAAGGTCAAGAAGAAGCTCGGCCTGCACGTCG	Initial Score 200 Optimized Score 200 Significance 0.86 Residue Identity 96% Matches 200 Mismatches 8 Gaps 0 Conservative Substitutions 0	2. US-09-697-123B-1 (1-208) US-09-697-123B-3 Sequence 3, Application US/09697123B	150 160 170 180 200 x ACGAGGGCCAGCACGATGACCGTCCCGGGCGGCACCGAGGTGCGGTTGAGACCGACGACGACT	80 90 100 120 130 140 GCGATCGCATCACCAGCTGACCGAGGAGGAAGACGTCGTCGTCGCACCATCGATCG	X 10 20 30 40 50 FCAAGGAGAAGACGTACGCCCGGGTAGGCCGGCTACAGGTCACAAGAAGCTCGGCCTGCACGTCG	Initial Score = 208 Optimized Score = 208 Significance = 1.02 Residue Identity = 100% Matches = 208 Mismatches = 0 Gaps = 0 Conservative Substitutions = 0	1. US-09-697-123B-1 (1-208) US-09-697-123B-1 Sequence 1, Application US/09697123B	US-09-697-123B-1 Sequence 14, Application 214 136 169 -0 05-09-697-123B-7 Sequence 7, Application U 214 129 168 -0 US-09-697-123B-1 Sequence 18, Application 211 114 162 -0 US-09-697-123B-2 Sequence 21, Application 214 109 170 -0	8. US-09-697-123B-1 Sequence 12. Application 207 159 182 0.99. US-09-697-123B-9 Sequence 9, Application U 223 146 173 -0.0 US-09-697-123B-1 Sequence 13, Application 223 142 168 -0.0	5. US-UY-0Y-123B-2 Sequence 24, Application 208 175 175 0. 6. US-09-697-123B-2 Sequence 20, Application 205 172 184 0. 7. US-09-697-123B-4 Sequence 4, Application 11 207 162 180 0.	3. US-09-697-123B-2 Sequence 23, Application 208 181 181 0.	1. US-09-697-123B-6 Sequence 6, Application U 208 182 182 0. 2. US-09-697-123B-5 Sequence 5, Application U 208 182 182 0.	9. US-09-697-123B-1 Sequence 17, Application 208 182 182 0 0. US-09-697-123B-1 Sequence 17, Application 208 182 182 0 0. US-09-697-123B-1 Sequence 16, Application 208 182 182 0	. US-09-697-123B-1 Sequence 10, Application 208 186 186 0 . US-09-697-123B-1 Sequence 19, Application 208 184 184 0	US-09-697-123B-1 Sequence 15, Application 208 197 197 0 US-09-697-123B-1 Sequence 11, Application 208 189 189 0 US-09-697-123B-2 Sequence 2, Application U 208 189 189 0	ence Name Description Length Score Score Si	;	1. US-09-697-123B-1 Sequence 1, Application U 208 208 208 1.02
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Residue
Gaps
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Residue
Gaps
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Residue
Gaps
                                                US-09-697-123B-1
US-09-697-123B-2
                                                                                                                                                                                                       US-09-697-123B-1
US-09-697-123B-1
                                                                                                                                                                                                                                                                                                                                                            US-09-697-123B-1
US-09-697-123B-1
                                                                                                          GCGATCCGATCACCAGCTCCACGCTGACCGAAGAAGACGTCGTCGCCACCATCGAGTACCTGGTCCGTCTGC
                                                                                                                                                                                    Score Identity
                               Identity
                                                                                                                                                                                                                                                                                                                                           Identity
                                                                                                                                                                                                                                                                                                                                                 Score
                                                                                                                                                                                 6 0 0
                                                                                                                                                                                                                                                                                                                                       0 0 0
                                                (1-208)
Sequence
                                                                                                                                                                                                      Sequence 11,
                                                                                                                                                                                                            (1-208)
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Sequence 15,
                                                                                                                                                                                                                                                                                                                                                                                                                      90
                         189
90%
0
                                                                                                                                                                               189
90%
0
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948
0
                       Optimized Score = 189
Matches = 189
Conservative Substitutions
                                                                                                                                                                                          Optimized
                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                   Optimized Score = 197
Matches = 197
Conservative Substitutions
                                                                                                                                                                                     Matches
                                                Application
                                                                                                                                                                                                                                                                                                                                                                                                                      100
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                                                                                                                                                                                                                                                                                                                                                            Application US/09697123B
                                                                                                                                                                                           Score
                                                                                                                                                                                                                                                                                                                                                                                                                      110
                                                                                                                                                                               Substitutions
                                                US/09697123B
                                                                                                                                                                                                      US/09697123B
                                                                                                                                                                                    189
189
                                                                                                                                                                                                                                                                                                                                                                                                                      120
                              Significance
Mismatches
                                                                                                                                                                                    Significance
Mismatches
                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                Significance
                                                                                                                                                                                                                                                                                                                                                                                                                      130
                                                                                                                                                                                                                                                                                                  60
                                                                                                                                                                                                                                                                                                                                           1 1
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                       . 64
19
0
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Gaps
                                                                                                                                                                                                                                                            Gaps
                                                                                                                          Residue
                                                                                                                               Initial
                                                                                                                                                                                                                                                                                      .
                                                                                                                                                                                                                                                                 Residue Identity
                                                                                                                                                                                                                                                                       Initial Score
  US-09-697-123B-1
US-09-697-123B-8
                                                                                                                                         US-09-697-123B-1
US-09-697-123B-1
                                                                                                                                                                                                                                                                                US-09-697-123B-1
US-09-697-123B-1
                   TCAAGGAGAAGCGCTACGACCTGGCCCGGGTGGGCCGCTACAAGGTCAAGAAGAAGCTCGGTCTGAACGTCG
X 10 20 30 40 50 60 70
                                                                                                                              Score
                                                                                                                          Identity
                                                                                                                      . . .
 (1-208)
Sequence
                                                                                                                                                                                                                                                                                (1-208)
Sequence
                                                                                                                                        (1-208)
Sequence 19,
                                                                                                                   184
88%
0
                                                                                                                                                                                                                                                           186
89%
0
                                                                                                                        Optimized
Matches
                                                                                                                                                                                                                                                               Optimized
Matches
                                                                                                                   Conservative Substitutions
                                                                                                                                                                                                                                                           Conservative
 8, Application
                                                                                                                                                                                                                                                                                10,
                                                                                                                                         Application US/09697123B
                                                                                                                                                                                                                                                                                Application
                                                                                                                                                                                                                                                                3 Score
                                                                                                                             Score
                                                                                                                                                                                                                                                          Substitutions
US/09697123B
                                                                                                                                                                                                                                                                               US/09697123B
                                                                                                                        184
184
                                                                                                                                                                                                                                                               186
186
                                                                                                                        Significance
Mismatches
                                                                                                                                                                                                                                                               Significance
Mismatches
                                                                                                                    . . .
                                                                                                                                                                                                                                                            . . .
                                                                                                                             0
                                                                                                                                                                                                                                                                     0
                                                                                                                   .54
24
0
                                                                                                                                                                                                                                                          0 22 8
```

Initial Score Residue Identity

. .

183 87%

Optimized Matches

Score

183 183

Significance Mismatches

0

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Gaps
                                                                               Residue
                                                                                   Initial
                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                 Gaps
                                                                                               10.
                                                                                                                                                                                          Residue
                                                                                                                                                                                              Initial
US-09-697-123B-1
US-09-697-123B-1
                                                                                           US-09-697-123B-1
US-09-697-123B-1
                                                                                                           Identity
                                                                                   Score
                                                                                                                                                                                          Identity
                                                                                                                                                                                              Score
                                                                                                                                                                              10
                                                                           0 0 0
                                                                                                                                                                                                      (1-208)
Sequence 17,
                                                                                           (1-208)
Sequence 16,
                                                                              182
878
                                                                                                                                                                                          182
878
                                                                                                                                                                             20
                                                                           0
                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                 0
                                                                          Conservative Substitutions
                                                                              Optimized 
Matches
                                                                                                                                                                                     Conservative Substitutions
                                                                                                                                                                                          Matches
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                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                      Application US/09697123B
                                                                                           Application
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                                                                                                                                                                             40
                                                                                                                                                                                          8 8
                                                                                           US/09697123B
                                                                              182
182
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182
                                                                                                                                                                             50
                                                                              Significance
Mismatches
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Mismatches
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26
0
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26
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Initial
Residue
Gaps
                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                              Residue
                                                                                                                                                                                                                                                                                                                          12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Residue
                                                                                                                                                                                                                                                                                                     Initial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Initial
US-09-697-123B-1
US-09-697-123B-2
                                                                                                                                                80 90 100 120 130 140 GCGATCCGATCACCACCATCGACGATCACCACCACCACCACCATCGACGACCACCATCGACTACCACCATCGACGACCATCGACTACCACCATCGACTACCACCATCGACTACCACCATCGACTACCACCATCGACTGACCACCATCGACCATCGACCATCGACCACCACCATCGACCATCGACCATCGACCATCGCCTTCC 80 90 100 110 120 130 140
                                                                                                                                                                                                                                          US-09-697-123B-1 (1-208)
US-09-697-123B-5 Sequence
                                                                                                                                                                                                                                                                                                                                            US-09-697-123B-1
US-09-697-123B-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score - Identity -
                                                                                                 Identity
                                                                                                          Score
                                                                                                                                                                                                                                                                                            Identity
                                                                                                                                                                                                                                                                                                    Score
                                                                                             . . .
                                                                                                                                                                                                                                                                                        . . .
                                                                                                                    Sequence 23, Application US/09697123B
                                                                                                                               (1-208)
                                                                                            181
878
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (1-208)
Sequence 6,
                                                                                                                                                                                                                                                                                            182
878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 182
878
0
                                                                                                                                                                                                                                                                                       0
                                                                                       Optimized Score = 181
Matches = 181
Conservative Substitutions
                                                                                                                                                                                                                                                                                            Optimized Matches
                                                                                                                                                                                                                                                                                    Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Optimized
                                                                                                                                                                                                                                                                                                                5, Application US/09697123B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Application US/09697123B
                                                                                                                                                                                                                                                                                                  Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Substitutions
                                                                                                                                                                                                                                                                                            182
182
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182
                                                                                               Significance
Mismatches
                                                                                                                                                                                                                                                                                           Significance
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Significance
                                                                                                                                                                                                                                                                                                  0
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                                                                                                                                                                                                                                                                                   26
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26
                                                                                        0
```

ACGAGGGCCAGCACGATGACCGTCCCGGGCGCGCACGTGCCGGTTGAGACCGACGACATA

190

160

17.

```
Gaps
                                                                                                                                                                                                 Initial
Residue
Gaps
                                                             Residue
                                                                                                                                                                                                                                                                                                                                        Initial
Residue
Gaps
                                                                   Initial
                                                                                                                                                                                                                           15.
                                                                                                                                                                                                                                                                                                                                                                    14.
                      US-09-697-123B-1
US-09-697-123B-2
                                                                                               US-09-697-123B-1 (1-208)
US-09-697-123B-2 Sequence
                                                                                                                                                                                                                                                                         US-09-697-123B-1
US-09-697-123B-2
                                                                                                                                                                                                                                                                                                                                                                                       ATGAGGGTCAGTCGACGATGACCGTTCCAGGTGCCTCGAGGTGCCAGTGGATACTGACGACAT
                                                                                                                                                                                                     Score Identity
                                                             Identity
                                                                   Score
                                                                                                                                                                                                                                                                                                                                                    Score
                                                                                                                                                                                                                                                                                                                                              Identity
                                                                                                                                                                                      10
                                                         0 0 0
                                                                                                                                                                                                  0 0 9
                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                            (1-208)
Sequence
                                                                                                                                                                                                                                                                                                                                                             (1-208)
Sequence
                                                       172
918
3
                                             20
                                                                                                                                                                                                                                                                                                                                         181
878
0
                                                       Optimized Sco
Matches
Conservative
                                                                                                                                                                                                Conservative
                                                                                                                                                                                                     Matches
                                                                                                                                                                                                           Optimized Score
                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                   Optimized
                                                                                                                                                                                                                                                                                                                                                                                    170
                                                                            20,
                                                                                                                                                                                                                      24,
                                                                                                                                                                                                                                                                                                                                                            22, Application
                                                                            Application US/09697123B
                                                                                                                                                                                                                    Application US/09697123B
                                                                 Score
                                                                                                                                                                                                                                                                                                                                                   Score
                                                                                                                                                                                                                                                                                                                                                                                   180
                                                       Substitutions
                                                                                                                                                                                               Substitutions
                                                                                                                                                                                                                                                                                                                                        Substitutions
                                                             G 8
                                                                                                                                                                                                           p
                                                                                                                                                                                                                                                                                                                                                             US/09697123B
                                                            184
190
                                                                                                                                                                                                                                                                                                                                                                                   190
                                                                                                                                                                                                     175
175
                                                                                                                                                                                                                                                                                                                                             181
181
                                                           Significance
Mismatches
                                                                                                                                                                                                    Significance
Mismatches
                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                  Significance
                                                       0 0 0
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                                                                 0
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                                                      . 30
15
0
                                                                                                                                                                                             . 36
33
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27
```

16.

19.

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Initial
Residue
Gaps
                                     Residue
                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                   Residue
                                                                                                                                                                                                                                                                                                                                         Initial
                                                    US-09-697-123B-1 (1-208)
US-09-697-123B-9 Sequence
US-09-697-123B-1 (1-208)
US-09-697-123B-1 Sequence
                                                                                                                                                                                                                         US-09-697-123B-1
US-09-697-123B-4
                                                                                                                                                                                                                                                                                                                                                                       GCGAGCCGATCACCTGGACGCTGACCGAGGAAGACGTCGTCGCCACCATCGAGTACCTGGTGCGCCTGC 80 90 100 110 120 130 140
                                    Score
Identity
                                                                                                                                                                                   Score
                                                                                                                                                                                                                                                                                                                                  Identity
                                                                                                                                                                                                                                                                                                                                         Score
                                 . . .
                                                                                                                                                                                 . . .
                                                                                                                                   90
                                                                                                                                                                                                                                                                                                                                                   (1-208)
Sequence
                               146
83%
15
                                                                                                                                                                                                                                                                                                                                  162
93%
                                                                                                                                                                                          159
                                                                                                                                                                                  Optimized
Matches
                              Conservative Substitutions
                                    Matches
                                         Optimized
                                                                                                                                                                              Conservative Substitutions
                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                       Optimized
                                                    9
                                                                                                                                                                                                    12,
                                                                                                                                                                                                                                                                                                                                                   4
                                                    Application US/09697123B
                                                                                                                                                                                                                                                                                                                                                  Application
                                                                                                                                                                                                   Application US/09697123B
                                         Score
                                                                                                                                                                                         Score
                                                                                                                                                                                                                                                                                                                                       Score
                                                                                                                                                                                                                                                                                                                            Substitutions
                                                                                                                                                                                    . .
                                                                                                                                                                                                                                                                                                                                                  US/09697123B
                                   173
187
                                                                                                                                                                                   182
187
                                                                                                                                                                                  Significance
Mismatches
                                  Mismatches
                                        Significance
                                                                                                                                                                                                                                                                                                                                 Significance
Mismatches
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                                        ò
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                            21
0
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                                                                                                                                                                                                                                                                                                                           . 10
13
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18.

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Initial
Residue
                                                             Gaps
                                                                                  21.
                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                         Initial
Residue
                                                                                                                                                                                                                           20.
 140
         ACGACAT
                                                                              US-09-697-123B-1
US-09-697-123B-1
                                                                                                                      ACGACAT
                                                                                                                                                                                                                                                                                       US-09-697-123B-1
US-09-697-123B-1
                                                                                                                                                                                                                                                              ×
                                                                Score Identity
                                                                                                                                                                                                         Score
 150
                                                                                                                                                                                                                                                                                                                     10
                                                             0 0 0
                                                                           (1-208)
Sequence 14, Application US/09697123B
                                                                                                                                                                                                                     (1-208)
Sequence 13, Application US/09697123B
                                                             136
82%
6
                                                                                                                                                                                                     142
798
15
                                                                                                                                                                                                                                                                                                                     20
                                                           Optimized Score
Matches
Conservative Subs
                                                                                                                                                                                                         Optimized
Matches
                                                                                                                                                                                                    Conservative Substitutions
                                                                                                                                                                                                                                                                                                                    30
                                                                                                                                                                                                            Score
                                                           Substitutions
                                                                                                                                                                                                                                                                                                                    40
180
                                                               169 Significance
176 Mismatches
        120
                                                                                                                                                                                                       168 Significance
178 Mismatches
190
                                                                                                                                                                                                                                                                                                                   50
        130
                                                               . .
        140
                                                                                                                                                                                                            6
                                                           .42
32
                                                                                                                                                                                                   030
```

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Gaps
                                           Residue
                                                                                                                                                                                     Residue Identity Gaps
                                                                                                                                                                                                                                                                                                                                  Initial Score - Residue Identity - Gaps
                                                                                                                                                                                                Initial
                                                                                                                                                                                                                                                                                                                                                              22.
US-09-697-123B-1 (1-208)
US-09-697-123B-2 Sequence
                                                                             140
                                                                                                                                                                                                         US-09-697-123B-1
US-09-697-123B-1
                                                                                                                                                                                                                           US-09-697-123B-1
US-09-697-123B-7
                                                                                                                                                                                                                                                                                                                                                                           Identity
                                                Score
                                                                                                                                                                                                Score
                                      . . .
                                                                                                                                                                                                                                                                90
                                                                                                                                                                                                     (1-208)
Sequence 18, Application US/09697123B
                                    109
82%
6
                                                                                                                                                                                                                                                                                                                                                       (1-208)
Sequence 7,
                                                                                                                                                                                   114
79%
3
                                                                                                                                                                                                                                                                                                                                 129
81%
6
                                    Conservative
                                         Optimized Score -
Matches -
                                                                                                                                                                                  Conservative Substitutions
                                                                                                                                                                                            Optimized
                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                 Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                       Optimized 
Matches
                                                                                                                                                                                                                                                               100
                                                          21,
                                                         Application US/09697123B
                                                                                                                                                                                                                                                                                                                                                       Application US/09697123B
                                                                                                                                                                                             Score
                                                                                                                                                                                                                                                                                                                                            Score
                                   Substitutions
                                                                                                                                                                                                                                                               110
                                       170 Significance - 177 Mismatches -
                                                                                                                                                                                                                                                               120
                                                                                                                                                                                                                                                                                                                                     168 Significance
175 Mismatches
                                                                                                                                                                                       Significance
Mismatches
                                             ò
                                                                                                                                                                                                                                                                                                                                           6
                                                                                                                                                                                                                                                              140
                                                                                                                                                                                 000
                                                                                                                                                                                                                                                                                                                               33
```

GCGATCC---

80

140 GCCTGCACG GCCTGCACG 150	 CCAATCCGC 80
150 GAGGGCCAGCA 	
140	
170 GTCCCGGGCG GCCCCCGGCG	
180 GCACCGAGG7 GCGTCGAGG7 190	BAAGACGTCGT
190 TGCCGGTTGA(TGCCGGTGGA: 200	
200 GACCGACGACA: TGTGGACGACA: 210	
x 1 - 1 x	TIGC

```
Result
No.
              0 0 0 0 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Run
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Minimum DB
Maximum DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Minimum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Total number
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OM nucleic
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              00 4 0 V H
                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                     Score
         19
18.4
18.4
18.4
18.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq
                                                                                                                                                                                                                                                                                                                                                                             EST:*

1: en,

2: en,

3: em,

4: em,

5: em,

6: em,

7: em,

8: em,

110: c;

111: c,

113: d,

114: d,

115: d,

116: d,

117: d,

118: d,

129: d,

120: d,

130: d,

140: d,

150: d,

170: d,

180: d,

180: d,

190: d,

190:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nucleic search, using sw model
                                                                                                                                                                   Query
Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       length: 0
length: 2000000000
         95.0
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92.0
92.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16154066 seqs, 8097743376 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-697-123B-26
20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ggatgttgatcagggtctgc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gb_est1:*
gb_est2:*
                                                                                                                                                                                                                                                                                                                                                                        em_gss_other:*
em_gss_pro:*
em_gss_rod:*
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em_estro:*
em_htc:*
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em_gss_inv:*
em_gss_vrt:*
em_gss_vrt:*
em_gss_fun:*
em_gss_mam:*
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em_estfun:*
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         414
377
437
502
579
585
         10
9
9
13
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9
       AZ606523
AA143959
AW211046
AL045401
AI603914
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AA143959 ms13d11.r
AW211046 uo90e08 y
AL045401 DKFZP434D
AI603914 ms13d11 y
BI697763 603346856
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ALIGNMENTS

JOURNAL COMMENT REFERENCE AUTHORS ACCESSION VERSION KEYWORDS SOURCE RESULT 1 AZ606523 LOCUS DEFINITION ORGANISM TITLE plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Resea Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 414)
1 (bases 1414 bp DNA linear GSS 13-DEC-2000 clone UUGC1M0428B22 F, DNA sequence.
AZ606523 AZ606523.1 GI:11728629
GSS. Email: Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: Tel: 801 585 5606 Fax: 801 585 7177 house mouse. USA Biomedical Polymers Research Bldg., 0.00 20 ŝ 2030 . . SLC, G

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VERSION
KEYWORDS
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AA143959/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA143959 377 bp mRNA linear EST 12-FEB-199, ms13d11.r1 Stratagene mouse skin (#937313) Mus musculus cDNA clone IMAGE:606637 5' similar to TR:G498013 G498013 X104. ;, mRNA
                                                                                                  Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of Medicinep
Machington University School of Medicinep
                                                                                                                                                                                                                                                                            Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus
                                                                                                                                                                                                       Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 377)
                                                                                                                                                                                                                                 The WashU-HHMI Mouse EST Project
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High quality sequence stop: 414.
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Seq primer: CGTTGTAAAACGACGGCCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                          314 286 1800
314 286 1810
       clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWDA2 (g114732114[gb1AF129072.1), a copy-number inducible derivative of plasmid Rl. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli xL10 Gold (Stratagene) cells and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                               mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /lab_host**E. Coli strain XL10-Gold, T1-resistant, F-*/note**Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:10090"
/clone="UUGC1M0428B22"
/clone_11b="Mouse 10kb plasmid UUGC1M library"
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/strain="C57BL/6J"
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Pred. No.
royalty-free through LLNL; contact the
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AW211046/c
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AW211046
AW211046.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Colone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                         Seg primer: -40RP from Gibco High quality sequence stop: '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 437)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AW211046
437 bp mRNA linear EST 03-DEC-19
u090e08.yl NCI_CGAP_Mam3 Mus musculus cDNA clone IMAGE:2649830 59
similar to TR:092001 Q92001 TIGHT JUNCTION PROTEIN ZO-2. ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EST.
                                                                                                                                                                                                                                                                                                                                                                                      MGI:1030282
                                                                                                                                                                                                                                                                                                                                                                                                                                                    www-bio.llnī.gov/bbrp/image/image.html
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High quality sequence stop: 331.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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/clone="IMAGE:2649830"
/clone_lib="NCI_CGAP_Mam3"
/tissue_type="tumor, gross tissue"
                                                                                                            /organism="Mus musculus"
/strain="129,C57BL/6J,FVB/N"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="whole skin"
/dev_stage="11 weeks old"
/dev_stage="11 weeks old"
/lab.host="$OLR (kanamycin resistant)"
/note="Organ: skin; Vector: pBluescript SK-; Site_1: EcoRI
/note="Organ: Sting: Skin; Vector: pBluescript Skin; Ve
                                                                                                                                                                                                                                                                              Location/Qualifiers
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/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:606837"
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/sex="females"
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Pred. No. 2e+02;
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19; Conserv
                                                                                                                                        . Similarity
19; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de; sequenced by Qlagen (Hilden/Germany) within the cDNA sequencing consortium of the German Genome Project.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              No sl sequence available.
This clone (DKFZp434D055) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin- Charlottenburg, GERMANY; Email: clone@rzpd.de.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 502)
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DKFZp434D055 5', mRNA sequence.
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This is the 5' sequence of the clone insert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1999)
Contact: Duesterhoeft A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Duesterhoeft, A., Lauber, J., Mewes, H.W., Gassenhuber, J. and Wiemann
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                                                                                                                                                                                                                                                                                               /clone="DKFZP434D055"
/clone=11b="434 (synonym: htes3)"
/tissue_type="testis"
/dev_stage="adult"
/dev_stage="adult"
/lab_host="DHIOB"
/note="Vector: pSport1; Site_1: Noteators adults a
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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/lab_host="DH10B"
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                                                                                                                                                              Score 18.4; DB 9;
Pred. No. 2.2e+02;
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Pred. No. 2.1e+02;
0; Mismatches 1;
                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                                                                         GGATGTTGATGAGGGTCTGC
                                   mRNA sequence.
BI697763
BI697763.1 GI:15660392
                                                                                                                                  BI697763
603346856F1
house mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
TMAGE Consortium (info@image.llnl.gov) for further information.
This read is a RESEQUENCE of a previously sequenced mouse clone
This read has been verified (found to hit its original self in the sequence of the sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    579 bp mRNA linear EST 15-MAR-2000 ms13d11.yl Stratagene mouse skin (#937313) Mus musculus cDNA clone IMAGE:006837 5' similar to TR:P70625 P70625 ZONULA OCCLUDENS 2 A1603914
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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Mammalia; Eutheria;
l (bases 1 to 579)
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High quality sequence eton.
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/sex="females"
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/db_xref="taxon:10090"
/clone="IMAGE:606837"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 579;
                                                                                                                                                       linear
                                                                                                                         EST 18-SEP-2001
IMAGE:5374693 5',
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VERSION
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TITLE
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       National Institute on Aging/National Institutes of Health 333 Cassell Drive, Suite 3000, Baltimore, MD 21224-6820, USA Email: cdna@lgsun.grc.nia.nih.gov
This clone set has been freely distributed to the community. Please visit http://lgsun.grc.nia.nih.gov/cDNA/NIA_7_4k.html for details. plate: H4027 row: G column: 03
                                                                                                                                          Contact: Yong Qian 
Laboratory of Genetics
                                                                                                                                                                                Unpublished (2002)
Other_ESTs: H4027G03-3
                                                                                                                                                                                                                                                                       1 (bases 1 to 597)
VanBuren, V., Płao, Y., Dudekula, D.B., Qian, Y., Carter, M.G., Marti, P.R., Stagg, C.A., Bassey, U., Alba, K., Hamatani, T., Kargui, G.J.,
                                                                                                                                                                                                                         cDNA clone set
                                                                                                                                                                                                                                        Assembly, verification, and initial annotation of NIA 7.4K mouse
                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              H4027G03-5 NIA Mouse 7.4K cDNA Clone Set Mus musculus
        Seq primer: -21M13 Reverse
                                                                                                                                                                                                                                                          Luo, A.G. and Ko, M.S.H.
                                                                                                                                                                                                                                                                                                                                                                                                     house mouse
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Plate: LLAM11953 row: o column: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"

147 c 173 g 102 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Mus musculus"
/strain="FVB/N-3"
/db_xref="taxon:10090"
/clone="!MAGE:5374693"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_11b-"NCI_CGAP_Mam2"
/tissue_type-"tumor, biopsy sample"
/dev_stage="5 months"
/lab_host-"DH10B"
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Rodentia;
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Pred. No. 2.4e+02;
0; Mismatches 1;
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Sciurognathi; Muridae; Murinae; Mus
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RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
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                                                                                                                                                                                                                                           Seq F
                                                                                                                                                                                                                                                                                                                            Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 638)
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19; Conserv
                                                                                                                                                                                                                                                                           Possible reversed clone: similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1997)
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National Cancer Institute, Cancer Genome Anat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   xu20b08.x1
similar to
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     199
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Location/Qualifiers
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     Ф
                     /note="Organ: colon; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.7 kb. Life Technologies catalog #: 11531-019"
                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Vector: pSPORT1; Site_1: SalI; Site_2: NotI; This clone is among a rearrayed set of 7,407 clones from more than 20 cDNA libraries."

151 c 164 g 111 t
                                                                                        /tissue_type="moderately-differentiated adenocarcinoma"
/lab_host="DH10B"
                                                                                                                           /clone_lib="NCI_CGAP_Col4"
                                                                                                                                                   /clone="IMAGE:2800695"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /dev_stage="mixed"
/lab_host="DH10B"
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/db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Mus musculus"
/strain="C57BL/6"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         638 bp mRNA linear EST 03-JAN-
NCI_CGAP_Col4 Homo sapiens cDNA clone IMAGE:2800695
TR:Q15883 Q15883 x104; mRNA sequence.
                                                                                                                                                                                                          . 638
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 154
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Pred. No. 2.
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.4e+02;
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                                    1 GGATGTTGATCAGGGTCTGC 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. James Lin, Univeristy of Iowa
CDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
cDNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               706 bp mRNA linear EST 14-MAR-20
UI-M-EHOp-bvn-k-16-0-UI.rl NIH_BMAP_EHOp Mus musculus cDNA clone
IMAGE:5694471 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19:
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NIH-MGC http://mgc.nci.nih.gov/.
NATIONAL Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                              Similarity
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                        195
                                                                                            Conservative
                                                                                                                                                                      /Clone_lib="NIM_BMAP_EHOP"
/Clone_lib="whole brain"
/tissue_type="whole brain"
/dev_stage="embryo 18.5 dpc"
/lab_host="mbli0B (Tl phage resistant)"
/lab_nost="organ: brain: Vector: pyx-Asc; Site_1: EcoR I;
/note="organ: brain: Vector: pyx-Asc; Site_1: EcoR I;
/note="organ: brain: Vector: pyx-Asc; Site_1: EcoR I;
Site_2: Not I; The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured mRNa was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with Not I, and then cloned directionally into pyx-Asc vector. The library tag sequence located between the Not I site and the polyA tail, is CAGCCACGAC. This library was created for the university of Iowa Mouse Brain Molecular Anatomy Project (BMAP); 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        clone was contributed by the Brain Molecular Anatomy Project
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/strain="C57BL/6"
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95.0%;
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                                                                                                          Score 18.4;
Pred. No. 2.
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Pred. No. 2.5e+02;
                                                                                        Mismatches
                                                                                                      2.6e+02;
                                                                                                                          DB 14;
                                                                                                                          Length 706;
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                                                            REFERENCE
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BG385603/c
                          COMMENT
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                                                                                                                                                      Homo sapiens
Email: cgapbs-r@mail.nih.
                                                                                                                                                                                                                  BG385603.1
                                                                                                                                                                                                                                                mRNA sequence.
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BI697529
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1 GGATGTTGATCAGGGTCTGC 20
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Mammalia; Eutheria; Primates; Cat
1 (bases 1 to 759)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Ma
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                 BG385603 759
602453904F1 NIH_MGC_15 Homo
                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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http://image.llnl.gov
Plate: LLAM11958 row: 1 column:
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Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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Location/Qualifiers
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
/strain="FVB/N-3"
/db_xref="taxon:10090"
/clone="IMAGE:5376548"
/clone_1ib="NCI_CGAP_Mam2"
/tissue_type="tumor, biopsy sample"
/dev_stage="5 months"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Organ: mammary: Vector: pCMV-SPORT6; Site_1: Sal1; Site_2: Not1; Cloned unidirectionally. Primar: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH*

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95.0%;
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IMAGE:4582297 5',
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                                                                                                                                                                                                                                                                                                NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
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BI688003
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603315768F1 NCI_CGAP_Mam6
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                                                                                                                                                                                                              Plate: LLAM11904 row: g column: High quality sequence stop: 766.
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Mammalia; Eutheria;
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/tissue_type="adenocarcinoma cell line"
/tissue_type="adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: colon; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; CONA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5; adaptor: GGCACCAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of Callfornia, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)"
48 a 153 c 204 g 154 t
                                                                     /db_xref="taxon:10090"
/clone="IMAGE:5355689"
                                                                                                                  /organism="Mus musculus"
/strain="FVB/N"
                           /clone_lib="NCI_CGAP_Mam6"
/sex="female, virgin"
/tissue_type="infiltrating ductal carcinoma"
                                                                                                                                                                                          Location/Qualifiers
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/db_xref="taxon:9606"
/clone="IMAGE:4582297"
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95.0%;
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Rodentia;
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Pred. No. 2.7e+02;
0; Mismatches 1;
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Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                         l Similarity
19; Conserv
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (199)
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                                                                                                                                                                                                                                                                                                                                                                                                                     /Strain="FVB/N-3"
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/Clone="Imb="NCI_CGAP_Mam2"
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/dev_stage="5 months"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                         /note-"Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sa
Site_2: NotI: Cloned unidirectionally. Primer: Oligo of
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
208 c 208 g 130 t
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Site_2: NotI; Cloned unidirectionally. Primer: Oligo of
Library constructed by Life Technologies. Investigator
providing samples: Jeffrey Green, M.D., NIH"
a 206 c 204 g 126 t
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Pred. No. 2.7e+02;
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Pred. No. 2.7e+02;
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RESULT 14 BI155204/c

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Matches 19; Conserv
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TITLE
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                                                 Direct Submission
Submitted (23-APR-2002) National Institutes of Health, Mammalian Submitted (23-APR-2002) National Institutes of Health, Mammalian Sene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 4072)
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                       Strausberg, R.
                                                                                                                                                                                                                                                                                                     BC028426
BC028426.1 GI:20306365
                                                                                                                                                                                                                                                                                                                                           BC028426 4072 bp
Homo sapiens, clone IMAGE:4820998,
                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM11091 row: p column: 22
High quality sequence stop: 807.
                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Chu-xia Denocontal Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="NCI_CGAP_Mam3"
/tlssue_type="tumor, gross tissue"
/dev_stage="10 months"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism-"Mus musculus"
/strain-"129,C57BL/6J,FVB/N"
/db_xref-"taxon:10990"
/clone-"IMAGE:5032965"
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Pred. No. 2.8e+02;
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Search completed: November 13, Job time : 120.147 secs
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Series: IRAK Plate: 46 Row: h Column: 8
This clone has the following problem: frame shifted.
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Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI) 6
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             http://www.systemsbiology.org
contact: amadan@systemsbiology.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anuradha
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
                                                                                                                                                                                       Similarity
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                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                  /lab_host="DH10B"
/note="Vector: pBluescript"
957 c 1133 g 863 t
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/tissue_type="Brain, hippocampus"
/clone_lib="NIH_MGC_95"
                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
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Listing first 45 summaries
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Perfect score:
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           18.4
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Match
         IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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/cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
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/cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
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/cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
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    US-09-563-817-166
US-09-917-800A-1477
US-10-044-090-357
US-09-815-242-7923
US-09-864-761-21019
US-09-864-761-2613
US-09-960-352-4809
US-09-960-352-4809
US-09-964-761-5853
US-09-864-761-10561
US-09-864-761-27182
US-09-864-761-3455
US-09-864-761-3455
US-09-815-242-381
US-09-815-242-408
US-09-815-242-408
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Sequence 166, App Sequence 3477, App Sequence 357, App Sequence 21019, A Sequence 22613, A Sequence 22613, A Sequence 4266, Ap Sequence 4266, Ap Sequence 5853, Ap Sequence 27182, Ap Sequence 3712, Ap Sequence 381, Ap Sequence 381, Ap Sequence 408, App Sequence 408, Ap Sequence 361, App Sequence 361, App
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US-09-897-778-130	US-09-850-716A-130	TS-00-735-705-130	US-09-925-317	US-09-962-832-128	US-09-940-921B-10	US-09-815-242-4132	US-09-940-921B-8	US-09-822-830A-445	US-09-940-921B-6	US-09-938-842A-2333	US-09-728-952-61	US-09-833-381-553	US-09-998-598-1569	US-09-864-761-8234	US-09-864-761-8447	US-09-864-761-9973	US-10-007-805-248	US-09-339-338-248	-09	US-09-864-761-3510	-09	US-09-294-093B-2249	US-09-864-761-24969	US-09-350-874-3	US-09-350-874-7
Sequence 130, App	130,	110	, 071	100	1	Sequence 4, apprix	Section to a solid	Section of Appril	Sequence & Application	Today (To constant		550	1560		8447	9973		248	248	3510		2240	24969	Sequence 3, Appli	Sequence 7. Appli

ALIGNMENTS

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TYPE: DNA
OGANISM: homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(477)
OTHER INFORMATION: n = A,T,C or G
US-09-563-817-166
US-09-917-800A-1477/c; Sequence 1477, Application US/09917800A; Patent No. US20020119462A1; GENERAL INFORMATION:
; APPLICANT: Mendrick, Donna
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US-09-563-817-166/c
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Best Local Similarity 95.0
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/563,817
CURRENT FILING DATE: 2001-06-11
PRIOR APPLICATION NUMBER: US 60/132,343
PRIOR FILING DATE: 1999-05-04
NUMBER OF SEQ ID NOS: 1008
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 166
LENGTH: 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 166, Application US/09563817
Patent No. US20020095031A1
GENERAL INFORMATION:
APPLICANT: Nehls, Michael C.
APPLICANT: Zambrowicz, Brian
APPLICANT: Sands, Arthur T.
TITLE OF INVENTION: No. US20021095031A1el Human Polynucleotides
TITLE OF INVENTION: Polypeptides Encoded Thereby
FILE REFERENCE: LEX-0021-USA
                                                                                                                                                   92.0%;
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Johnson, Castle,

Arthur

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; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20020137081A1 364726.12
US-10-044-090-357
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US-10-044-090-357/c
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: LOCATION: (1)..(3339)
: OTHER INFORMATION: n = a or c or g
US-09-917-800A-1477
                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/10/044,090
CURRENT FILING DATE: 2002-01-09
NUMBER OF SEQ ID NOS: 850
SOFTWARE: PERL Program
SEQ ID NO 357
                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Olga Bandman
TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
FILE REFERENCE: PA-0028 US
      Query Match
Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                      Sequence 357, Application US/10044090 Patent No. US20020137081A1
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: US 60/297,457
PRIOR FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 60/298,884
PRIOR APPLICATION NUMBER: US 60/298,884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 60/292,336
PRIOR FILING DATE: 2001-05-22
PRIOR APPLICATION NUMBER: US 60/295,798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 60/222,880 PRIOR FILING DATE: 2000-11-02 PRIOR APPLICATION NUMBER: US 60/290,029 PRIOR FILING DATE: 2001-05-11 PRIOR APPLICATION NUMBER: US 60/290,645 PRIOR FILING DATE: 2001-05-15
                                                                                                                                                      ORGANISM: Homo sapiens
                                                                                                                                                                             LENGTH: 4530
TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR EILING DATE: 2000-07-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Molecular Toxicology Modeling FILE REFERENCE: 44921-5038-US CURRENT APPLICATION NUMBER: US/09/917,800A CURRENT FILING DATE: 2001-07-31
                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Genbank Accession No. US20020119462A1 U75916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
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FILING DATE: 2001-07-09
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l Similarity 95.0%;
19; Conservative
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    Conservative
                      92.0%;
95.0%;
  Score 18.4; D
Pred. No. 4.7;
0; Mismatches
    0;
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Pred. No. 4.
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                                      Length 4530;
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FILE REFERENCE ELITA, 011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR PELLING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,931
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-23
PRIOR FILING DATE: 2000-12-26
PRIOR FILING DATE: 2000-12-26
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
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; NAME/KEY: CDS
; LOCATION: (1)...(291)
US-09-815-242-7923
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                                                                                                                                                                                                                                        Sequence 21019, Application US/09864761 Patent No. US20020048763A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 7923
LENGTH ACC.
APPLICANT: Penn, Sharron G.
APPLICANT: Hanzel, David k.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID I
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Acomica-x-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith Wall, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 291
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1306 GGATGTTGATGAGGGTCTGC
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103 GGATGTTGTTCAGGGTCT 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity es 17; Conserv
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Yamamoto, Robert T.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            82.0%;
94.4%;
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Pred. No. 32;
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David K.

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OTHER INFORMATION: E
                                            WS-09-864-761-22613
Sequence 22613, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
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Best Local 9
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LENGTH: 76
APPLICANT: Penn, Sharron G. APPLICANT: Rank, David R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 76
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NUMBER OF SEQ ID NOS: 49117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 09/774,203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                   HER INFORMATION: EXPRESSED IN BT474, SIGNAL = 3.1
HER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 3.1
HER INFORMATION: EXPRESSED IN BEARIN, SIGNAL = 2.9
HER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.5
HER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.2
HER INFORMATION: EXPRESSED IN DULT LIVER, SIGNAL = 3.7
HER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.9
HER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.7
HER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.7
HER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.2
HER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.3
HER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.0
                                                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                 46 GGATGTTGGTCAGTGTCTG
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FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00661
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APPLICATION NUMBER: PCT/US01/00669
FILING DATE: 2001-01-30
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R APPLICATION NUMBER: US 09/632,366
R FILING DATE: 2000-08-03
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FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00664
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Pred. No. 55;
0; Mismatches
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RESULT 7
US-09-960-352-6294/c
; Sequence 6294, Application US/09960352
; Patent No. US20020137139A1
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Best Local S
Matches 17
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SOFTWARE: Annomax Sequence Lis
SEQ ID NO 22613
LENGTH: 237
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PRIOR FILING DATE: 2001-01-30
PRIOR PELICATION NUMBER: PCT/US01/00664
PRIOR PELICATION NUMBER: PCT/US01/00669
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
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OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 9.5

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 6.1

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 73

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2

OTHER INFORMATION: SWISSPROT HIT: Q64726, EVALUE 6.00e-27

OTHER INFORMATION: EST_HUMAN HIT: BF677910.1, EVALUE 1.00e-116

OTHER INFORMATION: NT HIT: X70170.1, EVALUE 1.00e-116
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PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
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CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR FILING DATE: 2000-10-04
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
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FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00663
FILING DATE: 2001-01-30
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FILING DATE: 2001-01-30
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17; Conserv
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Pred. No. 62;
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CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
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PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
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LENGTH: 280
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PRIOR FILING DATE: 2001-01-30
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PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
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APPLICANT: Tao, Nenghing
APPLICANT: Tao, Nenghing
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21.10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
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LOCATION: (115)
OTHER INFORMATION: unsure at
OTHER INFORMATION: Clone ID:
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         APPLICATION NUMBER: PCT/US01/00662
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00661
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FILING DATE: 2001-01-30
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Chen, Wensheng
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: 2001-01-30
NUMBER: PCT/US01/00661
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89.5%;
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Pred. No. 63;
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APPLICANT: Warren, Wesley C.
APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
FILE REFERENCE: 16511,006/37-21(10208)C
CURRENT FILLNG DATE: 2001-09-24
NUMBER OF SEQ ID NOX: 15112
SEQ ID NO 4809
LENGTH: 434
TYPE: DNA
ORGANISM: Bos taurus
OGGNASSM: Bos taurus
OGGNASSM: MOS CIone ID: 21-LIB3057-006-Q1-K1-F9
US-09-960-352-4809
                                 US-09-864-761-10561
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Sequence 10561, Application US/09864761 Patent No. US20020048763A1
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Matches
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LENGTH: 398
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                                                                                                                                                               l Similarity
17; Conser
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17; Conser
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EXPRESSED IN BT474
EXPRESSED IN BEAIN
EXPRESSED IN HELA,
EXPRESSED IN PLACE
EXPRESSED IN ADULT
EXPRESSED IN LUNG,
EXPRESSED IN BONE
EXPRESSED IN HEARI
EXPRESSED IN HEARI
EXPRESSED IN HEARI
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D IN HELA, SIGNAL = 2.9
D IN HELA, SIGNAL = 3.5
D IN PLACENTA, SIGNAL = 3.2
D IN ADULT LIVER, SIGNAL = 3.7
D IN LOUG, SIGNAL = 2.9
D IN LOUG, SIGNAL = 2.9
D IN HEART, SIGNAL = 3.2
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0; Mismatches
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                                                                                                                                                            0;
                                                                                                                                                                         Score 15.8;
Pred. No. 60
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GENERAL INFORMATION

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OTHER INFORMATION: EXPRESSED IN BRAIL
OTHER INFORMATION: EXPRESSED IN BONE
US-09-864-761-10561
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PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR APPLICATION NUMBER: PCT/US01/00668
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LENGTH: 483
                                                                                                                                                                                                                                                                                                             Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US
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CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
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TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Aeomica-x-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
                                                                                                                                                                                                              370 GGTTGTTGATCAGGGACTG
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                                                                                                                                                                                                                                                                                                                                    Local
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Rank, David R.
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Pred. No. 6
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BONE MARROW, SIG
                                                                                                                                                                                                                                                                                                        Mismatches
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OTHER INFORMATION: MAP TO ACOO6329.2

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.1

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 6.1

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 73

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = US-09-864-761-5853
                                                                                                                   RESULT 12
US-09-864-761-27182
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CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 60/32,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
                                                 GENERAL INFORMATION:
                                                                       Sequence 27182, Application US/09864761
Patent No. US20020048763A1
                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Annomax Sequence Listing Engine vers. SEQ ID NO 5853
                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
APPLICANT: Penn, Sharron G. APPLICANT: Rank, David R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
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PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
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PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
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PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
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PRIOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
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17; Conserv
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Chen, Wensheng
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                                                                                                                                                                                                                      279
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                                                                                                                                                                                                                                                                                                                                  Score 15.8;
Pred. No. 67
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Hanzel, David Chen, Wensheng

David K.

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US-09-864-761-3455/c

Sequence 3455, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
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                                                                                                                           RESULT 13
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                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
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SEQ ID NO 27182
LENGTH: 508
APPLICANT: Penn, Sharron G
                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: MAP TO AL121758.4

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.91

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.91

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.91

OTHER INFORMATION: EXT. HUMAN HIT: AU144395.1, EVALUE 1.20e-01

OTHER INFORMATION: NT HIT: AJ272265.1, EVALUE 5.00e+00

OTHER INFORMATION: SWISSPROT HIT: P21997, EVALUE 1.10e+00
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PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OR APPLICATION NUMBER: PCT/USO1/00662
OR FILING DATE: 2001-01-30
OR APPLICATION NUMBER: PCT/USO1/00661
OR APPLICATION NUMBER: PCT/USO1/00670
OR APPLICATION NUMBER: PCT/USO1/00670
OR FILING DATE: 2001-01-30
OR APPLICATION NUMBER: US 60/234,687
OR FILING DATE: 2000-09-21
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OR FILING DATE: 2001-01-30
OR APPLICATION NUMBER: PCT/US01/00665
OR FILING DATE: 2001-01-30
OR APPLICATION NUMBER: PCT/US01/00668
OR FILING DATE: 2001-01-30
OR APPLICATION NUMBER: PCT/US01/00663
OR FILING DATE: 2001-01-30
OR FILING DATE: 2001-01-30
OR FILING DATE: 2001-01-30
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OR FILING DATE: 2000-09-27
OR APPLICATION NUMBER: PCT/US01/00666
OR FILING DATE: 2001-01-30
OR APPLICATION NUMBER: PCT/US01/00667
OR FILING DATE: 2001-01-30
OR APPLICATION NUMBER: PCT/US01/00664
OR FILING DATE: 2001-01-30
OR FILING DATE: 2001-01-30
OR FILING DATE: 2001-01-30
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FILING DATE: 2000-10-04
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                                                                                                                                                                                                                                                                                                              Score 15.8;
Pred. No. 6
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                                                                                                                                                                                                                                                                                                                 67;
                                                                                                                                                                                                                                                                                                                                     DB
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RESULT 14
US-09-815-242-7772/c
Sequence 7772, Application US/09815242
Patent No. US20020061569A1
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PRIOR PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR PRIOR PRICIATION NUMBER: US 09/632,366
PRIOR PRICIATION NUMBER: US 09/632,366
PRIOR PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR PRICIATION NUMBER: US 60/236,359
PRIOR PRICIATION NUMBER: US 60/236,359
PRIOR PRICIATION NUMBER: PCT/US01/00666
PRIOR PRICIATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR PRICIAGION NUMBER: PCT/US01/00669
PRIOR APPLICATION NUMBER: PCT/US01/00669
                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
Matches 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 3455
LENGTH: 1976
                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:

FEATURE:

OTHER INFORMATION: MAP TO AC006116.1

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL

OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 60/234,687 PRIOR FILING DATE: 2000-09-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 19
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 49117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: Aeomica-x-1
CURRENT APPLICATION NUMBER:
CURRENT FILING DATE: 2001-0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                 1153 GATGTTGATCAAGGTATGC 1135
                                                                                                                                                                                                                                                                                                        Local Similarity hes 17; Conserv
                                                                                                                                                                                                                   2 GATGTTGATCAGGGTCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 09/608,408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: PCT/US01/00661 FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: PCT/US01/00662 FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: PCT FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: PCT/US01/00670 FILING DATE: 2001-01-30
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Chen, Wensheng
                                                                                                                                                                                                                                                                                                        Conservative
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David K.
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                                                                                                                                                                                                                                                                                                                             Score 15.8;
Pred. No. 77;
                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                         DB 10;
                                                                                                                                                                                                                                                                                                                                                      Length 1976;
                                                                                                                                                                                                                                                                                           0;
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GENERAL INFORMATION

APPLICANT:

Haselbeck, Robert

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APPLICANT: Shatla, Ajay
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Peter
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT APPLICATION DIACNOSIS OF CHLAMYDIAL INFECTION
FILE REFERENCE: 210121.469CB
CURRENT APPLICATION NUMBER: US/09/841,132
CURRENT FILING DATE: 2001-04-23
NUMBER OF SEQ ID NOS: 599
SOFTWARE: FRASESEQ FOR Windows Version 3.0/4.0
SEQ ID NO 381
LENGTH: 1995
TYPE: DNA
TYPE: DNA
ORGANISM: Chlamydia pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: 05/09/815,242

CURRENT FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/201,078

PRIOR FILLNG DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILLNG DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR FILLING DATE: 2000-05-26

PRIOR FILLING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR APPLICATION NUMBER: 60/205,93

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR FILING DATE: 2001-02-16

NUMBER: OF SEO ID NOS: 14110

SOPTWARE: FASTSEO for Windows Version 4.0

SEO ID NO 7772
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 381, Application US/09841132; Patent No. US20020061848A1; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : TYPE: DNA
: ORGANISM: Pseudomonas aeruginosa
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (1)...(1992)
US-09-815-242-7772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-841-132-381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      В
                                                         Query Match
Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 77.0%;
Best Local Similarity 94.1%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamotto, Robert T.
APPLICANT: Xu, H. Howard et T.
TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GGATGTTGATCAGGGTCTGC 20
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Zyskind, Judith W.
Wall, Daniel
                                                                     Conservative
                                                                                     76.0%;
85.0%;
                                                              Score 15.2; DB 10;
Pred. No. 1.5e+02;
0; Mismatches 3;
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Pred. No. 1.2e+02;
0; Mismatches 1;
                                                                                                      Length 1995;
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Db 393 GGATGGTGATCAGCCTCTGC 412
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Search completed: November 12, 2002, 16:59:33 Job time: 5.03468 secs

Sequence Seq

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1000.0 10

443, 446, 335, 221, 223,

Sequence Sequence

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18.4
118.4
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116.8
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
     GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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US-09-147-935A-8

US-09-147-935A-10

US-09-147-935A-11

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US-09-147-935A-13

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US-09-147-935A-18

US-09-147-935A-28

US-09-147-935A-31

US-09-147-935A-31

US-09-147-935A-31

US-09-147-935A-31

US-09-147-935A-31

US-09-147-935A-31

US-09-147-935A-31

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US-09-147-935A-33
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                                                    nucleic search, using sw model
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Listing first 45 summaries
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Query
Match Length D
                                                                             November 12,
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Perfect score:
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                                                                                                                                                          APPLICANT: PORTABLS, FRAN OISE
APPLICANT: PORTABLS, FRAN OISE
APPLICANT: MANNES, GEBER
APPLICANT: JANNES, GEBER
APPLICANT: JANNES, GEBER
TILLE OF INVENTION: METHOD FOR DETECTION OF THE ANTIBIOTIC
TITLE OF INVENTION: METHOD FOR SPECTRUM OF MYCOBACTERIUM SPECIES
KNUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                                                                                                                                                                                                                                                    .. micobacter ....uress:
STREET: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C. STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: WASHINGTON
COUNTRY.
                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: US
COUNTRY: US
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/750,088A
FILING DATE: 21-FEB-1997
CLASSIFICATION:
ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: GOLDSTEIN, JORGE A.
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 1657.0010000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEPHONE: 202-371-2640
                                                                                                   Sequence 69, Application US/08750088A
Patent No. 6329138
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 228 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               double
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Best Local Similarity
Matches 20; Conserv
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                                                      RESULT 1
US-08-750-088A-69/c
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1 GGATGTTGATCAGGGTCTGC 20

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Gaps

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GENERAL INFORMATION:

APPLICANT: KOOK, YOOD-HOH

APPLICANT: KOOK, YOOD-HOH

APPLICANT: KOOK, YOOD-HOH

APPLICANT: KOOK, YOOD-HOH

TITLE OF INVENTION: COMPARATIVE SEQUENCE ANALYSIS OF FOOB GENE

FILE REPERENCE: 0136/007425

CURRENT APPLICATION NUMBER: US/09/147,935A

CURRENT FILING DATE: 1999-03-19

PRIOR PAPLICATION NUMBER: PCT/KR98/00228

PRIOR FILING DATE: 1998-07-28

NUMBER OF SEQ ID NOS:
SOFTWARE: KOPATIN 1.0

SEQ ID NO 3

LENGTH: 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:

APPLICANT: KOOK, YOON-HOH

APPLICANT: KOOK, YOON-HOH

APPLICANT: KOOK, YOON-HOH

APPLICANT: KOOK, YOON-HOH

TITLE OF INVENTION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY

TITLE OF INVENTION: COMPARATIVE SEQUENCE ANALYSIS OF FROB GENE

FILE REFERENCE: 0136/00F425

CURRENT APPLICATION NUMBER: US/09/147,935A

CURRENT APPLICATION NUMBER: DCT/KR98/00228

PRIOR APPLICATION NUMBER: PCT/KR98/00228

PRIOR APPLICATION NUMBER: DCT/KR98/00228

PRIOR POSC ID NOS: 50

SOFTWARE: KOPATIN 1.0

SEQ ID NO 4

LENTH: 306
                                                                                                                                                                                    100.0%; Score 20; DB 4; Length 306; larity 100.0%; Pred. No. 1.1; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 20; DB 4; Length 306; 100.0%; Pred. No. 1.1; tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3, Application US/09147935A Patent No. 6242584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/09147935A Patent No. 6242584
          ; SOFTWARE: KOPATIN 1.0
; SEQ ID NO 1
; LENGTH: 306
; LENGTH: DNA
; ORGANISM: Mycobacterium abscessus US-09-147-935A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Mycobacterium asiaticum
                                                                                                                                                                                                                                                                                                          129 GGATGTTGATCAGGGTCTGC 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              129 GGATGTTGATCAGGGTCTGC 110
                                                                                                                                                                                                                                                                                   1 GGATGTTGATCAGGGTCTGC 20
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; ORGANISM: Mycobacterium aurum
US-09-147-935A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match 100.
Best Local Similarity 100.
Matches 20; Conservative
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Best Local Similarity
Matches 20; Conserv
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US-09-147-935A-4/C
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APPLICANT: KOOK, YOON-HOh
APPLICANT: KOOK, YOON-HOh
TITLE OF INVENTION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
TITLE OF INVENTION: COMPARATIVE SEQUENCE ANALYSIS OF FOOB GENE
TITLE OF INVENTION: COMPARATIVE SEQUENCE ANALYSIS OF FOOB GENE
CURRENT APPLICATION UNMBER: US/09/147,935A
CURRENT FILING DATE: 1999-03-19
PRIOR APPLICATION NUMBER: CCT/KR98/00228
PRIOR FILING DATE: 1998-07-28
NUMBER OF SEQ ID NOS: 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                     Sequence 37, Application US/08750088A
Patent No. 6129138
Patent No. 6129138
GENERAL INFORMATION:
APPLICANT: DE BEENHOUWER, HANS
APPLICANT: PORTAELS, FRAN OISE
APPLICANT: ACHTELINCKX, LIEVE
APPLICANT: JANNES, GERFT
APPLICANT: JANNES, GERFT
APPLICANT: GERFT
APPLICANT: RESISTANCE SPECTTON OF THE ANTIBIOTIC
TITLE OF INVENTION: RESISTANCE SPECTRUM OF WYCOBACTERIUM SPECIES
NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 20; DB 4; Length 254; 100.0%; Pred. No. 1.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           E: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C. 1100 NEW YORK AVENUE, SUITE 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIALS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PALENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION WUMBER: US/08/750,088A
FILING DATE: 21-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 1657.0010000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : Sequence 1, Application US/09147935A
; Patent No. 6242584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 202-371-2540
INFORMATION FOR SEO ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 254 base pairs
TYPE: nucleic acid
creanDEDNESS: double
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NAME: GOLDSTEIN, JORGE A.
REGISTRATION NUMBER: 29,021
88 GGATGTTGATCAGGGTCTGC 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: DNA (genomic)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 1100
TTY: WASHINGTON
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RY: US
20005-3934
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Best Local Similarity
Matches 20; Conserv
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                                                                                          RESULT 2
US-08-750-088A-37/c
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Matches 20; Conserv
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SEQ ID NO 10
LENGTH: 306
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Patent No. 6242584

GENERAL INFORMATION

APPLICANT: KOOK, YOON-HOH

APPLICANT: KIM, Bum-Joon

TITLE OF INVENTION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY

TITLE OF INVENTION: COMPARATIVE SEQUENCE ANALYSIS OF rpoB GENE

FILE REFERENCE: 0136/06425

CURRENT FILING DATE: 1999-03-19

PRIOR FILING DATE: 1999-03-19

PRIOR FILING DATE: 1998-07-28

SOFTWARE: KOPATIN 1.0

SEQ ID NOS: 50

SOFTWARE: KOPATIN 1.0
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                                                                                                                 Sequence 5, Application US/09147935A
Patent No. 6442584
GENERAL INFORMATION:
APPLICANT: KIM, Bum-Joon
TITLE OF INVENTION:
APPLICANT: KIM, Bum-Joon
TITLE OF INVENTION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
TITLE OF INVENTION: COMPARATIVE SEQUENCE ANALYSIS OF TOOB GENE
FILE REFERENCE: 0136/0F425
CURRENT FILING DATE: 1999-03-19
PRIOR APPLICATION NUMBER: 057/KR98/00228
PRIOR APPLICATION NUMBER: PCT/KR98/00228
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; Patent No. 6242584
: EBERRAL INFORMATION:
; APPLICANT: KOOK, Yoon-Hoh
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100.0%; Pr
ative 0;
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                129 GGATGTTGATCAGGGTCTGC 110
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100.0%;
Best Local Similarity 100.0%;
Matches 20; Conservative 0
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1 GGATGTTGATCAGGGTCTGC 20
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; ORGANISM: Mycobacterium avium
US-09-147-935A-5
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                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS:
SOFTWARE: KOPATIN
                                                                                                      US-09-147-935A-5/C
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LENGTH: 306
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Sequence 11, Application US/09147935A
Sequence 11, Application US/09147935A
GENERAL INFORMATION:
APPLICANT: KOOK, Yoon-Hoh
APPLICANT: KIM, Bum-Joon
TITLE OF INVENTION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
TITLE OF INVENTION: COMPARATIVE SEQUENCE ANALYSIS OF rpoB GENE
FILE REFERENCE: 0136/0F425
CURRENT APPLICATION NUMBER: US/09/147, 935A
CURRENT APPLICATION NUMBER: PCT/KR98/00228
PRIOR APPLICATION NUMBER: PCT/KR98/00228
NUMBER OF SEQ ID NOS: 50
SSEQ ID NO 11
APPLICANT: KIM, Bum-Joon
TITLE OF INVENTION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
TITLE OF INVENTION: COMPARATIVE SEQUENCE ANALYSIS OF rPOB GENE
FILE REFERENCE: 0136/OF425
CURRENT APPLICATION NUMBER: US/09/147,935A
CURRENT APPLICATION NUMBER: US/09/147,935A
PRIOR RILING DATE: 1999-03-19
PRIOR FILING DATE: 1999-07-28
NUMBER OF SEQ ID NOS: 50
SOFTWARE: KOPATIN 1.0
SEQ ID NO 9
LENGTH: 306
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Patent No. 6242584

GENERAL INFORMATION:
APPLICANT: KID, Bum-Joon
TITLE OF INVENTION:
TITLE OF INVENTION: COMPARATIVE SEQUENCE ANALYSIS OF rpoB GENE
FILE REFERENCE: 0136/0F425
CURRENT FILING DATE: 1999-03-19
PRIOR APPLICATION NUMBER: US/09/147,935A
PRIOR APPLICATION NUMBER: US/07/7K894/00228
PRIOR APPLICATION NUMBER: 1999-07-28
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Pred. No. 1.1;
// Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Mycobacterium celatum Type2
                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%; Some Best Local Similarity 100.0%; Protected 20; Conservative 0;
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SOFTWARE: KOPATIN 1.0
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Sequence 14, Application US/09147935A
Patent No. 6242584
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Mycobacterium fortuitum
            129 GGATGTTGATCAGGGTCTGC 110
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Best Local Similarity 100.
Matches 20; Conservative
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SOFTWARE: KOPATIN 1.0
SEQ ID NO 15
LENGTH: 306
                                                            RESULT 13
US-09-147-935A-14/c
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US-09-147-935A-17/C
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LENGTH: 306
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| Patent No. 6742584
| CENERAL INFORMATION:
| APPLICANT: KOOK, Yoon-Hoh
| APPLICANT: KIM, Bum-Joon
| TITLE OF INVENTION: COMPARATIVE SEQUENCE ANALYSIS OF FPOB GENE
| FILLE REFERENCE: 0136/0F425
| CURRENT APPLICATION NUMBER: US/09/147,935A
| CURRENT FILING DATE: 1999-03-19
| PRIOR PILING DATE: 1998-07-28
| NUMBER OF SEQ ID NOS: CONTAIN 1.0
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APPLICANT: KOOK, YOON-HOH
APPLICANT: KOOK, YOON-HOH
APPLICANT: KIM, BUM-JOON
ITTLE OF INVENTION: COMPARATIVE SEQUENCE ANALYSIS OF FPOB GENE
TITLE OF INVENTION: COMPARATIVE SEQUENCE ANALYSIS OF FPOB GENE
FILE REFERENCE: 0136/09428
CURRENT APPLICATION NUMBER: U5/99/147,935A
CURRENT APPLICATION NUMBER: U5/99-03-19
PRIOR APPLICATION NUMBER: PCT/KR98/00228
PRIOR APPLICATION NUMBER: 050
SOFTWARE: 1998-07-28
NUMBER OF SEO ID NOS: 50
SOFTWARE: ACOPATIN 1.0
SEO ID NO 13
LENGTH: 306
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100.0%; Score 20; DB 4; Length 306;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 20; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No.
:ive 0; Mismatch
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: Sequence 13, Application US/09147935A
; Patent No. 6242584
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                                                                                                                                                                             ; TYPE: DNA
; ORGANISM: Mycobacterium chitae
US-09-147-935A-11
                                                                                      100.0%;
ilarity 100.0%;
Conservative 0
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; ORGANISM: Mycobacterium fallax
US-09-147-935A-12
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Best Local Similarity
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Matches 20; Conserv
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LENGTH: 306
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LENGTH: 306
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US-09-147-935A-15/C

Sequence 15, Application US/09147935A

Patent No. 642584

GENERAL INFORMATION:
APPLICANT: KIOK, YOOO-HOH

TITLE OF INVENTION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
TITLE OF INVENTION: COMPARATIVE SEQUENCE ANALYSIS OF rpoB GENE
FILE REFERENCE: 0136/0F425

CURRENT APPLICATION NUMBER: US/09/147,935A

CURRENT FILING DATE: 1999-03-19

PRIOR APPLICATION NUMBER: PCT/KR98/00228

PRIOR APPLICATION NUMBER: PCT/KR98/00228

PRIOR ELING DATE: 1998-07-28
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Sequence 17, Application US/09147935A
Fatent NO. 6442584
GENERAL INFORMATION:
APPLICANT: KIM, Bum-Joon
TITLE OF INVENTION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
APPLICANT: KOOK, VOON-HOH
APPLICANT: KOOK, VOON-HOH
APPLICANT: KIM, Bum-Joon
TITLE OF INVENTION: COMPARATIVE SEQUENCE ANALYSIS OF rpoB GENE
TITLE OF INVENTION: COMPARATIVE SEQUENCE ANALYSIS OF rpoB GENE
FILE REFERENCE: 0136/06425
CURRENT APPLICATION NUMBER: US/09/147,935A
CURRENT FILING DATE: 1999-03-19
PRIOR PRILING DATE: 1998-07-28
NUMBER OF SEQ ID NOS: 50
SOFTMANE: KOPATIN 1.0
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100.0%; Score 20; DB 4; Length 306;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 20; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: DNA
; ORGANISM: Mycobacterium fortuitum 49403
US-09-147-935A-15
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1 GGATGTTGATCAGGGTCTGC 20

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### 7 TITLE OF INVENTION: COMPARATIVE SEQUENCE ANALYSIS OF TPOB GENE
| FILE REFERENCE: 0136,0F425
| CURRENT APPLICATION NUMBER: US/09/147,935A
| CURRENT FILING DATE: 1999-03-19
| PRIOR FILING DATE: 1998-07-28
| PROR FILING DATE: 1998-07-28
| PROR FILING DATE: 1998-07-28
| PROR FILING DATE: 1998-07-28
| SOFTWARE: COPATION NUMBER: PCT/KR98/00228
| SOFTWARE: COPATION NOS: 50
| SOFTWARE: NOD 17
| LENGTH: 306
| TYPE: DNA | 100.0%; Score 20; DB 4; Length 306; TYPE: DNA | 100.0%; Pred: No. 1.1; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Mismatches 20; Conservative 0; Mismatches 0; Indels 0; Caps 0; Copation of the copati
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Search completed: November 12, 2002, 21:03:47 Job time: 3.68208 secs

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(without alignments)
3438.621 Million cell updates/sec
                                                                                                                                 November 12, 2002, 15:44:35; Search time 13.0983 Seconds
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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4370478 Total number of hits satisfying chosen parameters: 2185239 seqs, 1125999159 residues 1 ggatgttgatcagggtctgc 20 IDENTITY_NUC Gapop 10.0 , Gapext 1.0 US-09-697-123B-26 20 Title: Perfect score: Scoring table: Searched: Sequence:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

**SIDS2/gcgdata/geneseq/geneseqn-embl/Nal980.DAT:*

\$\times_{\text{SIDS2}/\text{gcgdata}/\text{geneseqn-embl/Nal981.DAT:*}

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\$\times_{\text{SIDS2}/\text{gcdata}/\text{geneseqn-embl/Nal990.DAT:*}

\$\times_{\text{SIDS2}/\text{gcdata}/\text{geneseqn-embl/Nal990.DAT:*} N_Geneseq_101002:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Mycobacterium spec	Partial sequence o	Partial sequence o	Mycobacterium spec	RooB dene fragment	RooB gene fragment	RpoB gene fragment	RooB gene fragment	RpoB gene fragment
ΩI		AAT29617	AAT29615	AAS99529	AAX27208	AAX27209	AAX27210	AAX27211	AAX27212
80	22	17	17	24	19	19	19	19	19
Length	20	228	254	300	306	306	306	306	306
% Query re Match Length DB I	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
Score	20	20	20	20	20	20	20	20	20
Result No.	1	°	с С	C 4	0	o o	c 7	ထ ပ	6 0

c 10	20	100	306	19	AAX27213	RpoB gene fragment
	20	100	306	13	AAX27216	gene f
	20	100.	306	19	AAX27219	dene
	20	100	306	19	AAX27220	dene
	50	-	306	19	AAX27191	gene
	20	100	306	19	AAX27195	
	20	100.	306	19	AAX27200	dene
	20	100.	306	19	AAX27201	dene
	20	100.	306	19	AAX27202	dene
	20	100.	306	19	AAX27203	dene
	20	100.	306	13	AAX27204	gene
	20	100.	306	19	AAX27205	gene
	20	100.	306	19	AAX27206	gene
	20	100.	306	19	AAX27176	gene
	20	100.	306	19	AAX27177	dene
	20	100.	306	19	AAX27178	dene
	20	100.	306	19	AAX27181	
	20	100.	306	19	AAX27182	gene
	20	100	306	19	AAX27183	dene
	20	100.	306	19	AAX27184	dene
	20	100.	306	19	AAX27185	gene
c 31	50		306	19	AAX27186	gene
	20	100.	306	19	AAX27187	RpoB gene fragment
	20	100.	306	19	AAX27188	gene
	20	100	306	19	AAX27190	gene
	20	100	306	19	AAX27174	RpoB gene fragment
	20	100.	306	24	AAS99528	Mycobacterium spec
	20	100.	306	24	AAS99532	Mycobacterium spec
	20	100.	306	24	AAS99533	Mycobacterium spec
	20	100.	306	24	AAS99535	
	20	100.	306	24	AAS99536	Mycobacterium spec
	20	100.	306	24	AAS99537	Mycobacterium spec
	20	100.	306	24	AAS99540	
	20	_	306	24	AAS99541	ø
	20	100.	306	24		Mycobacterium spec
	20	100.	306	24	AAS99546	00
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					ALIGNMENIS	
RESULT 1	_					
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ID AAS	AAS05226	standard;	DNA;	20 B	BP.	
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Non-tuberculous mycobacteria; rpoB gene fragment; NTM; HIV; PRA; RFLP; PCR-restriction fragment length polymorphism analysis; PCR primer; ss. Park HJ; Mycobacterium species rpoB gene fragment PCR primer RPO3' Kim Y, Cho S, Lee H, Park YK, Bai G, Kim S, (ERUM-) ERUME BIOTECH CO LID. 27-OCT-2000; 2000WO-KR01223. 99KR-0046795. (first entry) WPI; 2001-300520/31. Mycobacterium sp WO200131061-A1. 27-0CT-1999; 07-SEP-2001 03-MAY-2001. AAS05226;

New DNA fragments from the rpoB gene of mycobacteria, useful for diagnosis and identification of many mycobacterial species by restriction fragment length polymorphism -

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                                      The present sequence for Mycobacterium species rpoB gene fragment PCR primer RP03' is used with PCR primer RP05' (AAS05225) to amplify the rpoB gene region from 24 rpoB gene fragments can be used in the diagnosis and identification of Mycobacterium species using a novel PCR-restriction fragment length polymorphism analysis (PRA) and identification of Mycobacterium species using a novel PCR-restriction fragment length polymorphism analysis (PRA) amplifying and digesting the DNA fragment from the microorganism to be identified and comparing the RFLP patterns from the microorganism to be identified and comparing the RFLP patterns from the known rpoB gene fragments with the unidentified fragment. The rpoB gene fragments are useful to identify a wide range of Mycobacterium species, e.g. for diagnosis or to obtain epidemiological and pathogenesis information for selection of appropriate therapies, including M. tuberculosis, M. leprae and non-tuberculous mycobacteria (MYM) encountered in subjects infected fragments is rapid, precise, simple and cost effective (only 1 PCR required), and can differentiate between many species in a single experiment, including those difficult to distinguish by usual biochemical cests.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Partial sequence of Mycobacterium MAC strain ITG 926 rpoB gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 20; DB 22; Length 20; 100.0%; Pred. No. 2.3; or Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antibiotic; resistance; spectrum; gene; mycobacterium; determination; amplification; MAC strain; rpoB; fragment; probe; differential; hybridisation; pattern; rifampicin; rifabutin; species identification; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Portaels F;
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                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 20 BP; 3 A; 3 C; 8 G; 6 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                             detecting specific Mycobacterial species.
            Disclosure; Page 13; 50pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mycobacterium MAC strain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 20; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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AAT29617/c
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Gaps
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antiblotic resistance spectrum (ARS) of a mycobacterium can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The antibiotic resistance spectrum (ARS) of a mycobacterium can be determined by amplifying the relevant part of the antibiotic resistance gene, hybridising it with at least 1 rpoB gene probe, detecting the hybrids formed and inferring the ARS, and opt. the spp. using species specific probes (i.e. AAT12146 derived from the present sequence, the partial nucleotide sequence of the presumptive M. scrofulaceum strain ITG 4979 rpoB gene) from the differential hybridisation patterns. The method is partic. useful for the detection of rifampicin and/or rifabutin resistance in M. leprae or M. tuberculosis, and mycobacterial spp.
            determined by amplifying the relevant part of the antibiotic resistance gene, hybridising it with at least 1 rpoB gene probe, detecting the hybrids formed and inferring the ARS, and opt. the SPP. using specific probes (1.e. AAT12148/49 derived from the present sequence, the partial nucleotide sequence of the presumptive Mycobacterium MAC strain ITG 926 rpoB gene) from the differential hybridisation patterns. The method is partic. useful M. leprae or M. tuberculosis, and mycobacterial spp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Partial sequence of M. scrofulaceum strain ITG 4979 rpoB gene.
                                                                                                                                                                                                                                                                                                 100.0%; Score 20; DB 17; Length 228; 100.0%; Pred. No. 3.1; 0; Indels (ive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antibiotic; resistance; spectrum; gene; mycobacterium; determination; amplification; scrofulaceum; rpoB; fragment; probe; differential; hybridisation; pattern; rifampicin; rifabutin; species identification; ss.
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                                                                                                                                                                                                                                                       Sequence 228 BP; 40 A; 76 C; 73 G; 37 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAT29615 standard; DNA; 254 BP
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                                                                                                                                                                                                                                                                                                                                                                              GGATGTTGATCAGGGTCTGC 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mycobacterium scrofulaceum.
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                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.
Matches 20, Conservative
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AAT29615/c
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BP.

(first entry)

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GGATGTTGATCAGGGTCTGC 110

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RpoB gene; mycobacteria; phylogenetic tree construction;
mycobacterial species identification; phylogenetic analysis; ss.
                1 GGATGTTGATCAGGGTCTGC 20
                                                                                                           RESULT 5
AAX27208/c
ID AAX27208 standard; DNA; 306
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                                                                                                                                                                                                                                                                                                                                                               Mycobacteria simiae
                                                                                                                                                                                                                                                                   RpoB gene fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-JUL-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-JUL-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a diagnostic kit for mycobacterial species dentification and drug resistance detection comprising an oligonuclectide chip including a species identification probe, a contrast group probe a mycobacterial drug resistance detection probe, a contrast group probe corresponding to each drug resistance detection probe, and a marker for detecting a hybridisation of the oligonuclectide chip and a specimen. The identification probe is comprised of species-specific DNA sequences of mycobacterial rpoB gene and the detection probe is comprised of one or more modified codons of mycobacterial rpoB gene. The method involves amplifying rpoB gene fragments of specimen by Polymerase Chain Reaction C PCR) and discriminating species by fluorescent intensity corresponding to a particular species. The specimen is preferably uncultured sputum, blood or cerebrospinal fillid of a patient. Sequences AAS99478-AAS99569
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kit for mycobacterial species identification and drug resistance detection, has oligonucleotide chip with species identification probe, a mycobacterial drug-resistance detection probe, and its contrast group
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drug resistance detection; mycobacterial species identification; probe; oligonucleotide chip; rpoB; sputum; blood; cerebrospinal fluid; ss;
                                                                                                                                              Gaps
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0
identification. The method is rapid and reliable and provides
                                                                                                 Ouery Match

100.0%; Score 20; DB 17; Length 254;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 20; Conservative 0; Mismatches 0; Indels
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                                                            Sequence 254 BP; 40 A; 84 C; 90 G; 39 T; 1 other;
                      simultaneous determn. of ARS and spp. identity.
                                                                                                                                                                                                                                                                                                                                                                                                                                Mycobacterium species identification primer #4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 21; 74pp; English.
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AAS99529 standard; DNA; 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mycobacterium avium.
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98KR-0000228 97KR-0035501

Kook Y;

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This sequence represents a mycobacterial rpoB gene fragment, that is amplified using the PCR primers of the invention. The primers form a method of detecting and identifying mycobacterial species by constructing a phylogenetic tree for the species. The use of the primers for sequence-specific amplification of the rpoB gene (encoding the beta subunit of RNA polymerse) from mycobacterial species provides an efficient way of characterising these species. In addition to phylogenetic analysis, the rpoB gene can be used as an alternative to the 165 RNA gene because it has four subunits, which are highly conserved throughout prokaryotes. The method is particularly useful for slow growing, fastidious or uncultivatable mycobacteria. Also, rifampin susceptibility can be simultaneously determined in M. tuberculosis.
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                                                           New pair of polymerase chain reaction (PCR) primers - for sequence-specific amplification of the rpoB gene from mycobacterial species, useful for detecting and identifying mycobacterial species
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Pred. No. 3.2;
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                                                                                                                                                                                    Claim 37; Page 73-74; 91pp; English.
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AAX27209 standard; DNA; 306
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WPI; 1998-539367/46.
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Mismatches

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Matches

Query Match Best Local Similarity

100.0%; Score 20; DB 24; Length 300; 100.0%; Pred. No. 3.2;

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(BION-) BIONEER CORP.
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                                Kim B,
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Matches
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            RpoB gene; mycobacteria; phylogenetic tree construction; mycobacterial species identification; phylogenetic analysis; ss.
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mycobacterial species identification; phylogenetic analysis; ss.
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Best Local Similarity 1000
                                                    Mycobacteria smegmatis
                                                                                                                                                                                 (BION-) BIONEER CORP.
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                                                                                                                                                                                                           Kook Y;
                                                                                                                               28-JUL-1998;
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                                                                            WO9905316-A1
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This sequence represents a mycobacterial rpoB gene fragment, that is amplified using the PCR primers of the invention. The primers form a method of detecting and identifying mycobacterial species by constructing a phylogenetic tree for the species. The use of the primers for sequence-specific amplification of the rpoB gene (encoding the beta subunit of RNA polymerse) from mycobacterial species provides an efficient way of characterising these species. In addition to phylogenetic analysis, the rpoB gene can be used as an alternative to the 16s TRNA gene because it has four subunits, which are highly conserved throughout prokaryotes. The method is particularly useful for slow growing, fastidious or uncultivatable mycobacteria. Also, rifempin susceptibility can be simultaneously determined in M. tuberculosis.
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                                                                           New pair of polymerase chain reaction (PCR) primers - for sequence-specific amplification of the rpoB gene from mycobacterial species, useful for detecting and identifying mycobacterial species
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ID AAX27211 standard; DNA; 306 BP.
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                                   WPI; 1998-539367/46.
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Kook Y;
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Pred. No. 3.2;

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Best Local Similarity

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method of detecting and identifying mycobacterial species by constructing a phylogenetic tree for the species. The use of the primers for sequence-specific amplification of the rpoB gene (encoding the beta subunit of RNA polymerase) from mycobacterial species provides an efficient way of characterising these species. In addition to phylogenetic analysis, the rpoB gene can be used as an alternative to phylogenetic analysis, the rpoB gene can be used as an alternative to conserved trnoughout prokaryotes. The method is particularly useful for slow growing, fastidious or uncultivatable mycobacteria. Also, rifampin susceptibility can be simultaneously determined in M. tuberculosis.
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mycobacterial species identification; phylogenetic analysis; ss.
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ID AAX27212 standard; DNA; 306 BP
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20; Conservative
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mycobacterial species identification; phylogenetic analysis; ss.
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    Mismatches
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                             1 GGATGTTGATCAGGGTCTGC
   20; Conservative
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hes 20; Conservative
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                                                                                                                                                                                                                          RpoB gene fragment.
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This sequence represents a mycobacterial rpoB gene fragment, that is amplified using the PCR primers of the invention. The primers form a method of detecting and identifying mycobacterial species by constructing a phylogenetic tree for the species. The use of the primers for sequence-specific amplification of the rpoB gene (encoding the beta subunit of RNA polymerse) from mycobacterial species provides an efficient way of characterising these species. In addition to phylogenetic analysis, the rpoB gene can be used as an atternative to phylogenetic analysis, the rpoB gene can be used as an atternative to conserved throughout prokaryotes. The method is particularly useful for slow growing, fastidious or uncultivatable mycobacteria. Also, rifampin susceptibility can be simultaneously determined in M. tuberculosis.
                                                                                                                                                                                           New pair of polymerase chain reaction (PCR) primers - for sequence-specific amplification of the rpoB gene from mycobacterial species, useful for detecting and identifying mycobacterial species
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Best Local Similarity 100.0
Matches 20; Conservative
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                                                                       (BION-) BIONEER CORP.
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                              28-JUL-1997;
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mycobacterial species identification; phylogenetic analysis; ss.
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                                                                                                                                               Mycobacteria vaccae.
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                                         RpoB gene fragment.
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27-MAY-1999
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AAX27219/C

RESULT 12

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Matches

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Gaps

Sequence 306 BP; 52 A; 101 C; 101 G; 52 T; 0 other;

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This sequence represents a mycobacterial rpoB gene fragment, that is amplified using the PCR primers of the invention. The primers form a method of detecting and identifying mycobacterial species by constructing a phylogenetic tree for the species. The use of the primers for sequence specific amplification of the rpoB gene (encoding the beta subunit of RNA polymerse) from mycobacterial species provides an efficient way of characterising these species. In addition to phylogenetic analysis, the rpoB gene can be used as an alternative to the 165 rRNA gene because it has four subunits, which are highly conserved throughout prokaryotes. The method is particularly useful for slow growing, fastidious or uncultivatable mycobacteria. Also, rifampin susceptibility can be simultaneously determined in M. tuberculosis.
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mycobacterial species identification; phylogenetic analysis; ss.
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Pred. No. 3.2;
Mismatches 0; Indels
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Matches 20; Conservative
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mycobacterial species identification; phylogenetic analysis; ss.
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                       ilarity 100.0%; P
Conservative 0;
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Query Match
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OM nucleic - nucleic search, using sw model Run on:

November 12, 2002, 16:50:46; Search time 61.1561 Seconds (Without alignments) 9517.553 Million cell updates/sec

US-09-697-123B-26 20 1 ggatgttgatcagggtctgc 20

Title: Perfect score: Sequence:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

2054640 seqs, 14551402878 residues Searched:

4109280 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

GenEmbl:* Database :

em_htg_hum:* em_htg_inv:* em_htg_other:* 9b_ba:*
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Description		A47855 Sequence 69	A47823 Sequence 37	AF057449 Mycobacte	AF057455 Mycobacte	AFOS/438 MYCODACTE	AF057458 Mycobacte	AF057459 Mycobacte	AF057460 Mycobacte	AFUS/461 Mycobacte	AF05/402 Mycobacte	AF057464 Mycobacte	AF057465 Mycobacte	AF03/40/ Mycobacte AF057468 Mycobacte	AF057472 Mycobacte	AF057477 Mycobacte	AFUS/4/8 Mycobacte	AF057480 Mycobacte	AF057481 Mycobacte	AFUS/462 Mycobacte	AF057484 Mycobacte	AF057485 Mycobacte	AF057487 Mycobacte	AFUS/488 Mycobacte AFUS7489 Mycobacte	AF057490 Mycobacte	AF057492 Mycobacte	AF057494 Rhodococc	Mycobac	Sequenc	Sedneuc	Seg	ARISTON SEQUENCE	ט נ	AR157011 Sequence	U2	ט נט	ARIS/014 Sequence ARIS7015 Sequence				linear PAT 0/-MAR-199/					Jannes, G. and Rossau, R.	ISTANCE	
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SUMMARIES		A47855	A47823	AF057449	AFU3/455	AF057457	AF057458	AF057459	AF057460	AF057461	AF057463	AF057464	AF057465	AF057468	AF057472	AF057477	AF057479	AF057480	AF057481	AF057483	AF057484	AF057485	AF05/487	AF057489	AF057490	AF057492	AFUS/494 AFUS/494	AF173087	AR157002	AR157004	AR15/005	AR157009	AR157010	AR157011	AR157012	AR15/013	AR157015	ALIGNMENT		2	220 DP nt WO9533851					Machtelinckx, L.		69 14-DEC-199
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Mycobacterium asiaticum RNA polymerase beta (rpoB) gene, partial
      Kook,Y.H., Kim,B.J., Lee,S.H., Lyu,M.A., Kim,S.J., Ba1,G.H., Kim,S.J., Chae,G.T., Kim,E.J. and Cha,C.Y. Direct Submission
Submitted (06-ARR-1998) Microbiology, Seoul National University College of Medicine, 28 Youngon-dong, Chongno-gu, Seoul 110-799,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kim, B.J., Lee, S.H., Lyu, M.A., Kim, S.J., Bai, G.H., Chae, G.T., Kim, B.J., Lee, S.H., Lyu, M.A., Kim, S.J., Bai, G.H., Chae, G.T., Kim, E.C., Cha, C.Y. and Kook, Y.H.
Identification of mycobacterial species by comparative sequence analysis of the RNA polymerase gene (rpoB)
J. Clin. Microbiol. 37 (6), 1714-1720 (1999)
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Kook,Y.H., Kim,B.J., Lee,S.H., Lyu,M.A., Kim,S.J., Bai,G.H.,
Kim,S.J., Chee,G.T., Kim,E.J. and Cha,C.Y.
Direct Submission
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Actinomycetales; Corynebacterineae; Mycobacteriaceae;
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/organism="Mycobacterium abscessus"

    306
    /organism="Mycobacterium asiaticum"

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100.0%; Pred. No. 26;
iive 0; Mismatches
                                                                                                                                                         /strain="CAP97E-03"
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<1. .>306
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/gene="rpoB"
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Berling, B. H., Machtelinckx, L., Jannes, G. and Rossau, R. METHOD FOR THE DETECTION OF THE ANTIBIOTIC RESISTANCE SPECTRUM OF MYCOBACTERIUM SPECIES
MYCOBACTERIUM SPECIES
MYCOBACTERIUM SPECIES
TO 953 14-DEC-1995;
INNOGENETICS NV (BE)
Other publication AU 2789695 960104.
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Mycobacterium abscessus RNA polymerase beta (rpoB) gene, partial
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1 (bases 1 to 306)
Kim,B.J., Lee,S.H., Lyu,M.A., Kim,S.J., Bai,G.H., Chae,G.T.,
Kim,E.C., Cha,C.Y. and Kook,Y.H.
Identification of mycobacterial species by comparative sequence
analysis of the RNA polymerase gene (rpoB)
J. Clin. Microbiol. 37 (6), 1714-1720 (1999)
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Mycobacterium abscessus
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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INNOGENETICS NV (BE)
Other publication AU 2789695 960104.
Location/Qualifiers
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Sequence 37 from Patent WO9533851.
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AF057458
AF057458.1 GI:5902503
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Mycobacterium avium RNA polymerase beta (rpoB) gene, partial cds.
AF057457
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(Lae, S. I. to 306)

Klin, B. J., Lee, S. H., Lyu, M.A., Klim, S. J., Bal, G. H., Chae, G. T., Klim, E. C., Cha, C. Y. and Kook Y. H.

Identification of mycobacterial species by comparative sequenanalysis of the RNA polymerase gene (rpoB)

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Direct Submission
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/organism="Mycobacterium
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/db_xref="taxon:1764"
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10.6 c
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Kim, B.J., Lee, S.H., Lyu, M.A., Kim, S.J., Bai, G.H., Chae, G.T.,

Kim, E.C., Cha, C.Y. and Kook, Y.H.

Identification of mycobacterial species by comparative sequence analysis of the RNA polymerase gene (rpoB)

J. Clin. Microbiol. 37 (6), 1714-1720 (1999)
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Kook, Y.H., Kim, B.J., Lee, S.H., Lyu, M.A., Kim, S.J., Bai, G.H.,
Kim, S.J., Chae, G.T., Kim, E.J. and Cha, C.Y.

Direct Submission
Submitted (19-JUN-2000) Microbiology, Seoul National University
College of Medicine, 28 Youngon-dong, Chongno-gu, Seoul 110-799,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (06-APR-1998) Microbiology, Seoul National University College of Medicine, 28 Youngon-dong, Chongno-gu, Seoul 110-799
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Kook,Y.H., Kim,B.J., Lee,S.H., Lyu,M.A., Kim,S.J., Bai,G.H.,
Kim,S.J., Chae,G.T., Kim,E.J. and Cha,C.Y.
Direct Submission
Submitted (06-APR-1998) Mirrolling
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On Jun 19, 2000 this sequence version replaced gi:5902499,
Location/Qualifiers
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Actinomycetales; Corynebacterineae; Mycobacteriaceae;
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100.0%; Pred. No. 26;
ive 0; Mismatches
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BCT 17-SEP-1999
Kim.S.J., Chae.G.T., Kim.E.J. and Cha.C.Y.
Direct Submission
Submitted (06-APR-1998) Microbiology, Seoul National University
College of Medicine, 28 Youngon-dong, Chongno-gu, Seoul 110-799,
Korea
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Kim, B.-J., Lee, S.H., Lyu, M.A., Kim, S.J., Bai, G.H., Chae, G.T.,
Kim, B.-C., Cha, C.Y. and Kook, Y.H.
Identification of mycobacterial species by comparative sequence
analysis of the RNA polymerase gene (rpoB)
J. Clin. Microbiol. 37 (6), 1714-1720 (1999)
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Submitted (06-APR-1998) Microbiology, Seoul National University
College of Medicine, 28 Youngon-dong, Chongno-gu, Seoul 110-799,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mycobacterium chelonae RNA polymerase beta (rpoB) gene, partial
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Kook,Y.H., Kim,B.J., Lee,S.H., Lyu,M.A., Kim,S.J., Bai,G.H.,
Kim,S.J., Chae,G.T., Kim,E.J. and Cha,C.Y.
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Actinomycetales; Corynebacterineae; Mycobacteriaceae;
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Pred. No. 26;
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    .306
    .70ganism="Mycobacterium celatum"
/strain="APCC51130"
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                                                                                    | (bases 1 to 306)
| Kim, B.J., Cha, C.S.H., Lyu, M.A., Kim, S.J., Bai, G.H., Chae, G.T.,
| Kim, E.C., Cha, C.Y. and Kook, Y.H.
| Identification of mycobacterial species by comparative sequence
analysis of the RNA polymerase gene (rpoB)
J. Clin. Microbiol. 37 (6), 1714-1720 (1999)
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Kim,B.J., Lee,S.H., Lyu,M.A., Kim,S.J., Bai,G.H., Chae,G.T.,

Kim,E.C., Cha,C.Y. and Kook,Y.H.

Tdentification of mycobacterial species by comparative sequence analysis of the RNA polymerase gene (rpoB)

J. Clin. Microbiol. 37 (6), 1714-1720 (1999)
                                                                                                                                                                                                                                                                                                                  Seoul National University
Chongno-gu, Seoul 110-799,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Direct Submission
Submitted (06-APR-1998) Microbiology, Seoul National Univers
College of Medicine, 28 Youngon-dong, Chongno-gu, Seoul 110-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10325313
2 (bases 1 to 306)
Kook,Y.H., Kim,B.J., Lee,S.H., Lyu,M.A., Kim,S.J., Bai,G.H.,
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              Mycobacterium celatum.
Mycobacterium celatum
Bacteria: Firmicutes; Actinobacteriae, Actinobacteridae, Actinomycetales; Corynebacterineae, Mycobacteriaceae,
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Pred. No. 2
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KEYWORDS
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BCT 17-SEP-1999

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AF057462 306 bp DNA linear BCT 17-SEP-199
Mycobacterium fallax RNA polymerase beta (rpoB) gene, partial cds
AF057462
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108 c 98 g 51 t
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Kim, B.J., Lyu, M.A., Kim, S.J., Bai, G.H., Chae, G.T.,
Kim, E.C., Cha, C.Y. and Kook, Y.H.
Identification of mycobacterial species by comparative sequence
analysis of the RNA polymerase gene (rpoB)
J. Clin. Microbiol. 37 (6), 1714-1720 (1999)
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Chongno-gu, Seoul 110-799,
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Rim, S.J., Chae, G.T., Kim, E.J. and Cha, C.Y.
Submitsion
Submitted (06-APR-1998) Microbiology, Seoul National Univers.
College of Medicine, 28 Youngon-dong, Chongno-gu, Seoul 110-7
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Actinomycetales; Corynebacterineae; Mycobacteriaceae;
                                                                                                                                                                                                                                                                                   100.0%; Score 20; DB 1; Length 306;
.larity 100.0%; Pred. No. 26;
Conservative 0; Mismatches 0; Indels
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110 c 101 g 45 t
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Mycobacterium flavescens RNA polymerase beta (rpoB) gene, partial
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                                   Kim, B.J., Lee, S.H., Lyu, M.A., Kim, S.J., Bai, G.H., Chae, G.T., Kim, B.J., Lee, S.H., Lyu, M.A., Kim, S.J., Bai, G.H., Chae, G.T., Kim, E.C., Cha, C.Y. and Kook, Y.H. Identification of mycobacterial species by comparative sequence analysis of the RNA polymerase gene (rpoB) J. Clin. Microbiol. 37 (6), 1714-1720 (1999)
                                                                                                                                                                                                                                                                                                                                                            Seoul National University
Chongno-gu, Seoul 110-799,
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1 (bases 1 to 306)
Kim, B.J., Lee, S.H., Lyu, M.A., Kim, S.J., Bai, G.H., Chae, G.T.,
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Nook,Y.H., Kim,B.J., Lee,S.H., Lyu,M.A., Kim,S.J., Bal,G.H.,
Kim,S.J., Chae,G.T., Kim,E.J. and Cha,C.Y.
Direct Submission
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Mycobacterium flavescens
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae;
Mycobacterium.
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26;
                                                                                                                                                                                                                                                                                                                                                    Submitted (06-APR-1998) Microbiology, College of Medicine, 28 Youngon-dong,
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Pred. No. 2
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AR057465.1 GI:5902517
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Kook Y.H., Kim.B.J., Lee.S.H., Lyu.M.A., Kim,S.J., Bai,G.H.,
Kim,S.J., Chae,G.T., Kim,E.J. and Cha,C.Y.

Direct Submission
Submitted (06-APR-1998) Microbiology, Seoul National University
College of Medicine, 28 Youngon-dong, Chongno-gu, Seoul 110-799,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mycobacterium.

1 (bases 1 to 306)

1 (bases 1 to 306)

Kim, B.J., Lee, S.H., Lyu, M.A., Kim, S.J., Bai, G.H., Chae, G.T.,

Kim, B.J., Lee, S.H., Lyu, M.A., Kim, S.J., Bai, G.H., Chae, G.T.,

Kim, E.C., Cha, C.Y. and Kook, Y.H.

Identification of mycobacterial species by comparative sequence
analysis of the RNA polymerase gene (rpoB)
J. Clin. Microbiol. 37 (6), 1714-1720 (1999)
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae;
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    306
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<1. .>306
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AF057465/c
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inf c 100 g 51 t
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Mycobacterium fortuitum strain ATCC6841 RNA polymerase beta (rpoB)
AP057464
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Kim.E.C., Cha.C.Y. and Kook,Y.H.
Identification of mycobacterial species by comparative sequence
analysis of the RNA polymerase gene (rpoB)
J. Clin. Microbiol. 37 (6), 1714-1720 (1999)
                                                                                                                                                                                                                      Seoul National University
Chongno-gu, Seoul 110-799,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    I (bases I to 306)
Kim,B.J., Lee,S.H., Lyu,M.A., Kim,S.J., Bai,G.H., Chae,G.T.,
Kim,B.J., Lee,S.H., Lyu,M.A., Kim,S.J., Bai,G.H., Chae,G.T.,
Kim,E.C., Cha,C.Y. and Kook,Y.H.
Identification of mycobacterial species by comparative sequence
analysis of the RNA polymerase gene (rpoB)
J. Clin. Microbiol. 37 (6), 1714-1720 (1999)
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Kim, S.J., Chae, G.T., Kim, E.J. and Cha, C.Y.

Byircet Submission

Submitted (06-ARR-1998) Microbiology, Seoul National University College of Medicine, 28 Youngon-dong, Chongno-gu, Seoul 110-799,
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    /organism="Mycobacterium fortuitum"

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Pred. No. 26;
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                                                                                                                                                                                                                                                                                                                                    /strain="ATCC14474"
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<1. .>306
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a 99 c 105 g 51 t
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Mycobacterium genavense RNA polymerase beta (rpoB) gene, partial
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(bases 1 to 306)

Kim, B. J., Lee, S. H., Luy, M. A., Kim, S. J., Bai, G. H., Chae, G. T.,

Kim, E. C., Cha, C. Y. and Kook, Y. H.

Identification of mycobacterial species by comparative sequence
analysis of the RNA polymerase gene (rpob)
J. Clin. Microbiol. 37 (6), 1714-1720 (1999)
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Kook Y. H., Kim, B. J., Lee, S. H., Lyu, M. A., Kim, S. J., Bai, G. H.,
Kim, S. J., Chae, G. T., Kim, E. J. and Cha, C. Y.
Direct Submission
Submitted (06-APR-1998) Microbiology, Seoul National University
College of Medicine, 28 Youngon-dong, Chongno-gu, Seoul 110-799,
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae;
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Query Match
100.0%; Score 20; DB 1; Length 306;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels
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Job time : 63.8561 secs
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AF057467.1 GI:5902521
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A1948950 wq18b12.x

BH648296 BOMY48TF

H06751 y183a07.r1

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BH717250 BOMFN3GTF

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B178039 BM7030

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B178038 B17803

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B178183 C2H2-314T H

AN787398 945008C12

BM51789 TEXA00

BM51789 TEXA00

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BM71789 BM7103 Y

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BM71895 1700166 BM712 Y

AM724941 FØ55mm. FI

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Mycobacterium smegmatis.
Mycobacterium smegmatis
Bacteria, Actinobacteria, Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
1 (bases 1 to 1282)
Whurugasu-061,B., Tay,A. and Dick,T.
Upregulation of stress response genes and ABC transporters in anaerobic stationary-phase Mycobacterium smegmatis
20092472
20092472
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Mycobacterium Laboratory
Institute of Molecular and Cell Biology
My Medical Drive, Singapore 117609, Republic of Singapore
Tel: 65 874 3011
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Insert Length: 1282 Std Error: 0.00
Seq primer: T3 Forward; T7 Backward.
1. .1282
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BG714670
B1168616
BM377270
BQ465913
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BQ466189
AL598382
AG086517
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AW718755
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TITLE
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A1770311 42 Mycoba
AQ575881 nbxb0088A
BF495134 AT03975.5
BM427436 pgf2n.pk0
BF504233 AT05552.5
BF498268 AT12651.5
                                                                                                                  November 12, 2002, 16:59:42 ; Search time 101.315 Seconds (without alignments) 3037.202 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                              32308132
          GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                    16154066 seqs, 8097743376 residues
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                                                                                    using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum Match 100%
Listing first 45 so
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19
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em_gss_hum:*
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gb_est4:*
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em_estfun:*
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gb_est2:*
gb_htc:*
                                                                                    nucleic search,
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Match Length
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Perfect score:
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Maximum DB :
                                                                                  nucleic
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                                                                                             /clone_lib="Mycobacterium anaerobic stationary phase
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/organism="Mycobacterium smegmatis"
/strain="mc2155"
/db_xref="taxon:1772"
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/clone_lib="CGOT Rice BAC Library"
/tissue_type="Leaf"
/lab_host="E. coll DH108"
                                                                                                                                                          /lab_host="E. coli XL1-Blue MRF'"
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/organism="Oryza sativa"
/strain="Japonica"
/cultivar="Nipponbare"
/db_xref="taxon:4530"
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High quality sequence stop: 336.
Location/Qualifiers
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AQ575881.1 GI:4976366
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DEFINITION
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AQ575881/c
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TITLE
JOURNAL
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SOURCE
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world. Half of the world population especially those inhabiting highly populated areas of the humid tropics and subtropics, rely on rice as their primary source of carbohydrate. Monocctyledonous rice is a diploid plant (2n-24) with a haploid genome equivalent of 431 Mbp (Arumaganathan and Earle, 1991). The relatively small genome of rice, three times larger than that of Arabidopsis, makes it suitable for genomic studies. In order to facilitate positional cloning, physical mapping and genome sequencing of rice, we have constructed a BAC library from Oryza sativa, Nipponbare variety. The library contains 36.864 clones with an average insert size of 128.5 Kb providing 10.9 haploid genome equivalents. The deep coverage allows the isolation a particular sequence with a probability of 99.9 %. Two high density filters, each containing 18,432 clones (doubly spotted), represent the whole library for colony screening."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa, Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Edopterygota; Diptera; Brachycera; Muscomorpha;
Neoptera; Edopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 609)
S Stapleton, M., Brokstein, P., Hong, L., Agbayani, A., Baxter, E., Berman, B., Carlson, J., Champe, M., Chew, M., Dorsett, V., Farfan, D., Frise, E., George, R., Gonzalez, M., Guarin, H., Harris, N., Li, P., Liao, G., Miranda, A., Misra, S., Mungall, C.J., Nunoo, J., Pacleb, J., Paragas, V., Park, S., Phouanenavong, S., Wan, K., Yu, C., Lewis, S. E., Celniker, S. and Rubin, G.M.

BDGP/HHMI AT Drosophila EST Project
Unpublished (2000)
On Dec 6, 2000 this sequence version replaced gi:11578435.
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/sex="male"
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AT03975.5prime AT Drosophila melanogaster adult testes poTB7

Drosophila melanogaster cDNA clone AT03975 5 similar to Med:
FBan0001775 'transcription factor' located on: 3R 100D1-100D1;:
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One Cyclotron Rd, Berkeley, CA 94720, USA
Eax: 510 486 6798
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
hit genomic AE003779: arm:3R [27296749,27528812]
estImated-cyto:100B:1100B:3 04/07/2001
Plate: AT.39 row. G column: 3
High quality sequence stop: 595.
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/lab_host="Plates AT.10-AT.120: DH5-alpha. Plates
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94.7%; Score 18; DB 17; Length 705; 100.0%; Pred. No. 2.46+02; ive 0; Mismatches 0; Indels
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/db_xref~"taxon:7227"
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BF495134
BF495134.2 GI:13685621
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EST 19-APR-2001

659 bp

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fruit fly.

Evaryota: Metanogaster

Eukaryota: Metanogaster

Eukaryota: Metanogaster

Eukaryota: Metanogaster

Bukaryota: Metanogaster

Roppera: Endopterygota: Diptera: Brachycera: Muscomorpha:

Ephydroidea: Drosophilidae; Drosophila.

Ephydroidea: Drosophilidae; Drosophila.

Stapleton.M., Brokstein.P., Hong.L., Agbayani.A., Baxter.E., Berman S. B., Carlson.J., Champe.M., Chavez.C., Chew.M., Dorsett.V., Farfan D., Frise,E., George, R., Gonzalez.M., Guarin,H., Harits,N., Li.P., Liao,G., Miranda.A., Misra.S., Mungall.C.J., Nunco.J., Pacleb.J., Callikor.S. and Rubin.G.M.

BDCP/HHMI AT Drosophila EST Project

Unpublished (2000)

On Dec G. 2000 this sequence version replaced gi:11587534.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="AT05552"
/clone_lib="AT Drosophila melanogaster adult testes pOTB7"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BF498268

100 mRNA linear EST 19-APR-2001

112651.5prime AT Drosophila melanogaster adult testes porfer

112651.5prime AT Drosophila melanogaster cDNA 6712651 5 similar to Medi

112651.5prime AT 10001.1001;

112651.5prime AT 10001.1001;
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//dev_arge="0-3 day old Ore-R males"
//dev_arge="0-3 day old Ore-R males"
//dev_arge="13-9 bib-alpha TonA"
//note="0-4-3.39 bib-alpha TonA"
//note="0-4-3.34 bib-argen ADULT testess, Vector: poTB7; Site_1: EcoR1;
Site_2: Xhol; The mRNA for the testis library was made
from testes and seminal vessicles hand dissected from 0-3
day old Ore-R males. RNA kindly provided by the lab of
Margaret Fuller. Sized fractionated cDNAs were directly
ligated into poTB9: Plasmid cDNA library."
                                                                                                                                 AT05552.5prime AT Drosophila melanogaster adult testes porB7
Drosophila melanogaster cDNA clone AT05552 5 similar to Med:
FBan0001175 'transcription factor' located on: 3R 100D1-100D1;:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
hit genomic AE003779: arm:3R [27296749,27528812]
estimated-cyto:100D1:100E3: 04/07/2001
Plate: AT.55 row: E column: 4
High quality sequence stop: 657.
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/db_xref-"taxon:7227"
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One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
                                                                                                                                                                                                     04/07/2001, mRNA sequence.
BF504233
                                                                                                                                                                                                                                                       BF504233.2 GI:13686863
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BF498268/c
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AT.121-AT.319: DH5-alpha TonA"

//note="Organ: A@ULT testes: Vector: pOTB7; Site_1: ECORI;
Site_2: Xhol; The mRNA for the testis library was made
from testes and seminal vessicles hand dissected from 0-3
day old Ore-R males. RNA kindly provided by the lab of
Margaret Fuller. Sized fractionated cDNAs were directly
liqueed into porB7. Plasmid cDNA library."
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Gallus gallus cDNA clone pgf2n.pk006.ml2 5' similar to gill4091760
ref[NP_114461.1| APP-binding protein 1 [Rattus norvegicus]
gb[AAD09247.1| (U90829) APP-binding protein 1 [Rattus norvegicus],
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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Eukaryota; Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria: Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus
1 (bases 1 to 647)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Vector: pcMvSPORT6; Library made from equivalent pools of total RNA isolated from each developmental age (across strains); Single pass sequencing from 5'-end" 133 c 1159 g 165 t 13 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="Abdominal Fat"
/dev_stage="Embryonic (d18,d19); post-hatch (d1,w3,w7,w9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cogburn, L.A., Morgan, R. and Burnside, J. ESTs from Normalized Chicken fat CDNA library-USDA/IFAFS Animal
                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cogburn@udel.edu, www.chickest.udel.edu.
Location/Qualifiers
1.647
/organism="Gallus gallus"
/strain="Commercial broiler, Ottawa Research Centre,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:9031"
/clone="pgf2n.pk006.m12"
/clone_lib="Normalized Chicken Abdominal Fat Library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                             Length 609;
                                                                                                                                                                                                                                      91.6%; Score 17.4; DB 12; Length 94.7%; Pred. No. 4.5e+02; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (2002)
Contact: Larry A. Cogburn
University of Delaware
Townsend Hall, Newark, DE 19717, USA
Tel: 302-831-1335
Fax: 302-831-2822
Email: cogburn@udel.edu, www.chickest.
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/lab_host="E. coli EMDH10B"
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/sex="Male and Female"
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BM427436
BM427436.1 GI:18432610
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94.78;
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Gaps

663 bp

04/09/2001, mRNA sequence. BF498268

ACCESSION

40 TCAAGGAGCAGCGCTACGA 58

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Gaps

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Indels

Length 667;

Score 17.4; DB 9; Pred. No. 4.6e+02;

91.6%;

0; Mismatches

1 others

169 t

170 g

141 c

. 667

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Martinistr. 52, 20251 Hamburg, Germany
Email: URL: http://genetics.hpi.uni-hamburg.de/dt40est.html.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                  /cell_type="bursal lymphocyte"
/dev_stage="2-3 weeks old"
/note="CB inbred strain"
                                                                                                                                                                        /organism="Gallus gallus"
/db_xref="taxon:9031"
/clone="27g6r1"
/clone_lib="riken1"
                Heinrich-Pette-Institute
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Matches 18; Conservative
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Matches 17; Conserv
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                                                                                                                  Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Rukaryota; Metazoa; Arthropoda; Brachycera; Muscomorpha;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

E 1 (bases 1 to 663)
Stapleton, M., Brokstein, P., Hong, L., Agbayani, A., Baxter, E., Berman, B., Carlson, J., Change, M., Chavez, C., Chew, M., Dorsett, V., Farfan, D., Frise, E., George, R., Gonzalez, M., Guarin, H., Harris, N., Li, P., Liao, G., Miranda, A., Misra, S., Mungall, C.J., Nunoo, J., Pacleb, J., Parages, V., Park, S., Phouanenavong, S., Wan, K., Yu, C., Lewis, S.E., Celniker, S. and Rubin, G.M.

BDGP/HHMI AT Drosophila EST Project
Unpublished (2000)
On Dec 6, 2000 this sequence version replaced gi:11581569.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lawrence Berkeley National Lab
Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
hit genomic AE003779: arm:3R [27296749,27528812]
est.lamted-cyto:1001-100E3: 04/09/2001
Plate: AT. 126 row: E column: 3
High quality sequence stop: 624.
Location/Oualifiers
1. .663
/organism-"Drosophila melanogaster"
/db.xref="taxon:7227"
/clone="AT12551"
/sex="male"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /dev_mage="0-3 day old Ore-R males"
/lab_host="Plates AT.10-AT.120: DH5-alpha. Plates
/lab_host="Plates AT.10-AT.120: DH5-alpha. Plates
/AT.121-AT.319: DH5-alpha TonA"
/AT.121-AT.319: DH5-at.319: DH5-at
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Phrosauria; Aves; Neognathae; Galliformes; Phasianidae;
1 (bases 1 to 667)
Buerstedde,J.M.
Gallus gallus bursal lymphocyte EST
Unpublished (2002)
Contact: Buerstedde JM
Cellular Immunology
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BF498268.2 GI:13690169
                                                            fruit fly.
Drosophila melanogaster
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Best Local Similarity 94.7%;
Matches 18; Conservative 0
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fzmb0l3f050e10k0 fzmb filtered library 2ea mays genomic clone
BH785787
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maize
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/clone="fzmb013f050e10"
/clone="fzmb013f050e10"
/clone="lb=fzmb filtered library"
/note="Organ: leaf; Vector: pBCSK(-); Site_1: HincII; DNA prepared from purified nuclel was randomly sheared, end-repaired, size fractionated to enrich for the 0.5 to 5 kb fraction, ligated into HincII-digested pBCSK(-) vector and electroporated into E. coli cells."
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                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Lillopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 558)
Budiman, M.A., Freese, R.G., Bedell, J.A., Nunberg, A.N. and Lakey, N.D. GeneThresher methylation filtered genomic sequences from maize Unpublished (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                            Orion Genomics, LLC
404 Forest Park Ave, St. Louis, MO 63108, USA
14 615 6979
Fax: 314 615 5975
Email: jbedelleoriongenomics.com
Plate: framb013f050 row: e column: 10
Seq primer: SK reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      High quality sequence stop: 558.
Location/Qualiflers
1. .558
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/cultivar="MO17"
                                                                                                          BH785787.1 GI:19790828
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1 (bases 1 to 265)
Anderson, O.D., Chao, S., Han, P.S., Hsia, C.C., Johnson, R.R., Kang, Y., Lazo, G.R., Miller, R., Rausch, C.J., Seaton, C.L., Tong, J.C., Verhey, S.D. and Walker-Simmons, M.K.
The structure and function of the expressed portion of the wheat genomes - ABA-treated embryo library Unpublished (2000)
Unpublished (2000)
US Department of Agriculture, Agriculture Research Service, Pacific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WHEO615_H12_P23ZA Wheat ABA-treated embryo cDNA library Triticum aestivum cDNA clone WHEO615_H12_P23, mRNA sequence.
BE517162
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                                 BH424101 249 bp DNA linear GSS 12-DEC-2001
BOGOY49TR BOGO Brassica oleracea genomic clone BOGOY49, DNA
                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
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Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M. Whole genome shotgun sequencing of Brassica oleracea Other_GSSS: BOGOV40TF
Contact: Chris Town
                                                                                                                                                                                                                                                                                                                                                                                                             Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
                                                                                                                                                                                                                                                                                                                                                       9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-3523
Fax: 301-838-0208
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Pred. No. 9.8e+02;
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/clone="BOGOY49"
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Class: sheared ends.
Location/Qualifiers
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                                                                                                       вн424101.1 GI:17609829
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1 Similarity 94.4%;
17; Conservative
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Brassica oleracea
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Best Local Similarity
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BE517162/c
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RESULT 9
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 290)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NATional Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

The Strausberg, Ph.D.

Contact: Robert Strausberg, P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lhb="Wheat_ABA-treated embryo cDNA library"
/clone_lhb="Wheat_ABA-treated embryo cDNA library"
/tissue_type="Seed embryo"
/dev_atage="Mature dormant seeds"
/lab_host="E. col! DH12s"
/lab_host="Embryos were cut from mature, dormant seeds and imbibed in Embryos were cut from mature, dormant seeds and imbibed in 25 microM ABA (abscisic acid) in 5 mM Mes buffer, pH 5.7, for 12 hr at 22 C. The tissue, total RNA, and poly(A)
RNA were prepared by Steven Verhey in M.K.
Walker-Simmons's lab (USDA-ARS, Washington State Univ., Walker-Simmons's lab (USDA-ARS, Washington State Univ., Walker-Simmons and Oligo dr primers. Library was plated and archived by Russell Johnson (Colby College, ME/Walker-Simmons' lab). Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors).

16 a 101 c 87 g 60 t lothers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. 265
/organism="Triticum aestivum"
/organism="Triticum aestivum"
/oultiva="Brevor (soft, white, winter, common wheat)"
/db_xref="taxon:4565"
/clone="WHE0615_H12_P23"
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800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
Fax: 5105595818
Email: oandersn@pw.usda.gov
Sequence have been trimmed to remove vector sequence and low quality sequence with phred score less than 20
Seq primer: Clontech Matchmaker 3' AD primer.
Location/Qualifiers
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Insert Length: 880 Std Error: 0.00
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Seq primer: -400P from Gibco
High quality sequence stop: 273.
Location/Qualifiers
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Matches 17; Conserv
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source

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RESULT 13
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                                /clone="INAGE: 2471615"
/clone="INAGE: 2471615"
/clone="INAGE: 2471615"
/clone="Lype="2 pooled tumors (clear cell type)"
/lab_host="DH108"
/note="Organ: kidney; Vector: pT773D-pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA from the normalized library NCI_CGAP_Kid5 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (clonelDs 132912-1325831, 1471368-1472903 and 1492104-1493255). Subtraction by Bento Soares and M. Fatima Bonaldo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BH648296 375 bp DNA linear GSS 19-FEB-2002 BOMFY48TF BO_2_3_KB Brassica oleracea genomic clone BOMFY48, DNA
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
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/clone_llb="BO_2 3 kB"
/note="Vector: pH0S1; Site_l: BstXI; 2-3 kb sheared
genomic DNA inserted into pH0S1 using BstXI linkers"
7 c 92 g 94 t
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                                                                                                                                                                                                                                                                                                                                                                      Score 16.4; DB 9; Length 290;
Pred. No. 1e+03;
0; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 301-838-522.
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seg primer: TF
Class: sheared ends.
Location/Qualifiers
Location/Qualifiers
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Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M. Whole genome shotgun sequencing of Brassica oleracea (Unpublished (2001)
Contact: Chris Town
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9712 Medical Center Drive, Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                  58 t
/organism-"Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /strain="TO1000DH3"
/db_xref="taxon:3712"
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BH648296.1 GI:18705920
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94.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                 17; Conservative
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Brassica oleracea
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TITLE
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105 CAAGGAGAAGGGCTACGA 122

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H06751 A32 bp mRNA linear EST 21-JUN-1995
                                                                                                                                                                                                                                                                                            L Unpublished (1995)

L Unpublished (1995)

Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

Insert Size: 1388

High quality sequence stops: 265

Source: IRMAGE Consortium, LLNL

This clone is available royaly/free through LLNL; contact the
IMAGE Consortium (info@image.linl.gov) for further information.

Insert Length: 1388

Std Error: 0.00

Seq primer: M13RP1

High quality sequence stop: 265.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BM375873 437 bp mRNA linear EST 23-JUL-2002 EBem06 SQ004_K13_R embryo, 21 DPA, no treatment, cv Optic, EBem06 Hordeum vulgare cDNA clone EBem06_SQ004_K13 5', mRNA sequence. BM375873. GI:21935809
                                                                                                                                                                              (Research 1 (Dases 1 to 432)
Hiller, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hullman, M., Kucaba, T., Le, M., Lannon, G., Marra, M., Parsons, J., Rikin, L., Rohhifing, T., Soares, M., Tan, F., Trevaskis, E., Waterston R., Williamson, A., Wohldmann, P. and Wilson, R.
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                                                                                                                             Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/clone="IMAGE:44512"
/clone="Lib="Soares infant brain INIB"
/sex="female"
/dev_stage="73 days post natal"
                                 MAGE: 44512 5', mRNA sequence
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                                                                       H06751.1 GI:870283
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Best Local Similarity 94.4
Matches 17; Conservative
                                                                                                               human.
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BM375873
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VERSION
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KEYWORDS
SOURCE
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101
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                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Hodeum.

    (bases 1 to 437)

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                                                                                                                                                   Hedley, P., Liu, H., Caldwell, D., McCallum, N., Mudie, S., Cardle, L., Ramsay, L., Machray, G., Marshall, D.F.M. and Waugh, R. Development of Barley Transcriptome Resources Unpublished (2001)
On Jan 10, 2002 this sequence version replaced g1:18119263.
Contact: Waugh R, Marshall DF Genome Dynamics/Computational Biology
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/db_xref="taxon:4513"
/db_xref="taxon:4513"
/clone="EBem06_SQ004_K13"
/clone_llb="embryo, 21 DPA, no treatment, cv Optic, EBem06"
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                                                                                                                                                                                                                                                                                                             Scottish Crop Research Institute
Invergowrle, Dundee, DD2 5DA, Scotland, UK
Tel: 00 44 1382 562731
Fax: 00 44 1382 562426
Email: est@scri.sari.ac.uk
All sequence has a Phred quality score of 20 or over
Seq primer: M13 reverse.
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Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M. Whole genome shotgun sequencing of Brassica oleracea Unpublished (2001)
Other_GSSs: BOMFM36TR
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9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
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/organism="Hordeum vulgare"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="embryo"
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/lab_host="DH10B"
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BH717250.1 GI:18814189
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Conservative
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                  Hordeum vulgare.
                                            Hordeum vulgare
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Matches 17; Conserv
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Gaps
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Pred. No. 1.2e+03;
0; Mismatches 1; Indels 0
Fax: 301-838-0208
Email: cdtcwn@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Class: sheared ends.
                                                                                                                                                                                                                                                                    Indels
                                                                                                 /organism="Brassica oleracea"
                                                                                                                                                                                                                                                                                                                                                                 Search completed: November 13, 2002, 04:01:02 Job time: 114.815 secs
                                                                       Location/Qualifiers
                                                                                                                                                                                                                                        86.3%;
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                                                                                                                                                                                                                                                                                              2 CAAGGAGAAGCGCTACGA 19
                                                                                                                                                                                                                                    Query Match
Best Local Similarity 94.4
Matches 17; Conservative
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TYPE: DNA ORGANISM: Homo sapiens
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                                                                                                                                                                                                       November 12, 2002, 16:05:40 ; Search time 1.93295 Seconds (without alignments) 3487.380 Million cell updates/sec
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/cgn2_6/ptodata/2/pubpna/US00_NEW_PUB.seq:*
5.1.3
Compugen Ltd
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US-09-294-0938-4362

US-09-224-0977

US-09-815-242-9077

US-09-80-107-2432

US-09-960-152-9053

US-09-960-152-9068

US-09-960-152-9068

US-09-960-152-12378

US-09-960-152-11556

US-09-960-152-11566

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US-09-960-152-1425
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GenCore version Copyright (c) 1993 - 2002
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                            OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Match Length
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Perfect score:
Sequence:
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US-09-981-363-356
US-09-981-263-336
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US-09-974-300-4785
US-09-974-978-6201
US-09-294-0938-6201
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US-09-80-356-31965
US-09-80-356-31970
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APPLICANT: Lalgudi, Raghunath, V.
APPLICANT: Ito, Laura, Y.
APPLICANT: Sherman, Bradley, K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN TASSEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
Sequence 29, Application US/09833381
Patent No. US20020132090A1
GENERAL INFORMATION:
APPLICAMT: Robison, Keith E.
TITLE OF INVENTION: No. US20020132090Alel Nucleic Acid and Protein Homologs
FILE REFREENCE: 5800-119
CURRENT APPLICATION NUMBER: US/09/833,381
CURRENT FILING DATE: 2001-04-11
PRIOR APPLICATION NUMBER: 09/516,448
PRIOR FILING DATE: 2000-02-29
NUMBER OF SEQ ID NOS: 2050
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 29
LENGTH: 212
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Pred. No. 20;
0; Mismatches 3; Indels
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; Patent No. US20010051335A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match 84.2%;
Best Local Similarity 84.2%;
Matches 16; Conservative
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Yamamoto, Robert T.
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         Wall, Daniel
Trawick, John D.
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Best Local Similarity 89.5
Matches 17; Conservative
                                                      Carr, Grant
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US-09-815-242-9077
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LOCATION: (1)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: INCOMENDATION.
APPLICANT: Lagudi, Raghunath, V.
APPLICANT: Ito, Laura, Y.
APPLICANT: Sherman, Bradley, K.
TITLE OF INCOMENDATE.
FILE REFERENCE: PL.0009 US
CURRENT APPLICATION NUMBER: US/09/294,093B
CURRENT APPLICATION NUMBER: US/09/294,093B
CURRENT APPLICATION NUMBER: 60/082.567
PRIOR FILING DATE: April 21, 1998
NUMBER OF SEQ ID NOS: 6207
SOFTWARE: PERL PROGram
SEQ ID NO 5081
LENGTH: 281
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                                                                                                                                                                                                                                                               : NAME/KEY: misc_feature

: OTHER INFORMATION: Incyte ID No. US20010051335A1 700353887H1

: NAME/KEY: unsure

: LOCATION: 69, 75, 80, 87, 206

: OTHER INFORMATION: a, t, c, g, or other

US-09-294-093B-4362
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: OTHER INFORMATION: Incyte ID No. US20010051335A1 700355754H1

: NAME/KEY: unsure

: LOCATION: 178, 205, 215

: OTHER INFORMATION: a, t, c, g, or other

US-09-294-093B-5081
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89.5%; Pred. No. 25;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                   / Match 83.2%; Score 15.8; I Local Similarity 89.5%; Pred. No. 25; Pred. 17; Conservative 0; Mismatches
FILE REFERENCE: PL-0009 US
CURRENT APPLICATION NUMBER: US/09/294,093B
CURRENT FILING DATE: 1999-04-16
PRIOR APPLICATION NUMBER: 60/082,567
PRIOR FILING DATE: APFIL 21, 1998
NUMBER OF SEQ ID NOS: 6207
SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 5081, Application US/09294093B
Patent No. US20010051335A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 9077, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               140 TCAAGGAGAAGGGCTCCGA 158
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Best Local Similarity 89.5
Matches 17; Conservative
                                                                                                                                                                                                TYPE: DNA
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-294-093B-5081
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                                                                                                                                                     SEQ ID NO 4362
LENGTH: 265
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US-09-880-107-2432/c

Sequence 2432, Application US/09880107

Sequence 2432, Application US/09880107

Sequence 2432, Application US/09880107

Sequence 2432, Application US/09880107

GENERAL INFORMATION:

APPLICANT: HORNATION:

APPLICANT: Scherf, Uwe

APPLICANT: Gene Logic, Inc.

TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer

FILE REFERENCE: 44921-5028-WO

CURRENT FILING DATE: 2000-06-14

PRIOR APPLICATION NUMBER: US 60/211,379

PRIOR APPLICATION NUMBER: US 60/211,379

PRIOR APPLICATION NUMBER: US 60/211,379

PRIOR PILING DATE: 2000-06-14

PRIOR PILING DATE: 2000-10-02

NUMBER OF SEQ ID NOS: 3950

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 2432
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US-09-880-107-2432
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TITLE OF INVENTION: Identification of Essential Genes in CURRENT FILLS ELITRA.011A
CURRENT FILING DATE: 2001-03-21
PRIOR PAPLICATION NUMBER: 60/2019, 078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR PAPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-12-22
PRIOR FILING DATE: 2001-12-22
PRIOR FILING DATE: 2001-12-26
PRIOR FILING DATE: 2001-12-16
NUMBER OF SEQ ID NOS: 14110
SUPPRARE: ESSESSE FOR WINDOWS VERSION 4.0
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89.5%; Pred. No. 29;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Streptococcus pneumoniae
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Best Local Similarity
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APPLICANT: Tao, Nengring
APPLICANT: Byatt, John C
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 9968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Nengbing
APPLICANT: Tao, Nengbing
APPLICANT: Tao, Nengbing
APPLICANT: Mathialagan, Magappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: NUCLEIC ACID AND FAT DEPOSITION
TITLE OF INVENTION: NUGLEIC ACID AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-7(10298)
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
LENGTH: 375
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US-09-960-352-8128/c
Sequence 8128, Application US/09960352
Patent No. US20020137139A1
GENERAL INFORMATION:
APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Mongbing
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICANTION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
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                                                                                                                                                                                                                                                                                                                                                                                    Length 370;
                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                            ) ORGANISM: Bos taurus
) OTHER INFORMATION: Clone ID: 43-LIB3057-006-01-K1-C12
US-09-960-352-9968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 53-LIB3057-014-Q1-K1-F10
US-09-960-352-12378
                                                                                                                                                                                                                                                                                                                                                                                    10;
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Pred. No. 42;
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Pred. No. 42;
                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
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94.1%;
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94.1%;
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Best Local Similarity 94.1
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 94.1
Matches 16; Conservative
  GENERAL INFORMATION:
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US-09-960-352-12378/c
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                                                                                                                                                                                                                                                           LENGTH:
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                                                                                                                                                                                                                     APPLICANT: Warren, Wesley C.
APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Nengbing
APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: WOLCLEC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: WISCLE ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEO ID NOS: 15112
SEO ID NO 9053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 6002, Application US/09960352
Facent No. US2002013713941
GENERAL INFORMATION:
APPLICANT: Waster, Wesley C.
APPLICANT: Tao, Nengbing
APPLICANT: Tao, Nengbing
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MUSCLE AND EAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 6002
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  Indels
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; ORGANISM: Bos taurus

; OTHER INCRMATION: Clone ID: 26-LIB3057-001-Q1-K1-G9

US-09-960-352-6002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Clone ID: 39-LIB30S7-003-01-K1-B4 US-09-960-352-9053
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Pred. No. 41;
0; Mismatches 1;
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Pred. No. 42;
0; Mismatches
Mismatches
                                                                                                                                                                                    Sequence 9053, Application US/09960352 Patent No. US20020137139A1
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; Patent No. US20020137139A1
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94.1%;
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Best Local Similarity 94.1%;
Matches 16; Conservative
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                                         1 TCAAGGAGAAGCGCTACGA
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Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
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                                                                                                                                                                     US-09-960-352-9053/c
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17;
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Matches
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Gaps

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Indels

Length 390;

Score 15.4; DB 10; Pred. No. 42; 0; Mismatches

81.1%; 94.1%;

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298 CAAGGACAAGCGCTACG 314
                                                                                           2 CAAGGAGAAGCGCTACG 18
                                                    Conservative
    Query Match
Best Local Similarity
Matches 16; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATIONS-09-960-352-14725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 14725
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Sequence 50302, Application US/09960352
Patent No. US200201373941
GENERAL INFORMATION:
APPLICANT: WATHEN, Wesley C.
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
APPLICANT: Mathialagan, Nagappan
APPLICANT: Mathialagan, Nagappan
APPLICANT: MATHIAN: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
LENGTH: 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Nengbing
APPLICANT: Tao, Nengbing
APPLICANT: Tao, Nengbing
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
TITLE OF STORE TO TOOK 37-24
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
LENGTH: 386
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                                                                                                                                                                                                                                              Length 384;
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                                                                                                                                  .: LOCATION: (9)
.: OTHER INFORMATION: unsure at all n locations
.: OTHER DEPREMATION: Clone ID: 35-LIB3057-006-01-K1-A12
US-09-960-352-8128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ) ORGANISM: Bos taurus
) OTHER INFORMATION: Clone ID: 50-LIB3057-003-Q1-K1-E10
US-09-960-352-11656
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; OTHER INFORMATION: Clone ID: 22-LIB3057-005-Q1-K1-F9
US-09-960-352-5030
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Pred. No. 42;
0; Mismatches
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Pred. No. 42;
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Best Local Similarity 94.1%;
Matches 16; Conservative
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94.1%;
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Best Local Similarity 94.1
Matches 16; Conservative
                                                             ORGANISM: Bos taurus
FEATURE:
                                                                                                              NAME/KEY: unsure
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US-09-960-352-11656
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US-09-960-352-5030
SEQ ID NO 8128
LENGTH: 384
                                                TYPE: DNA
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APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Mengbing
APPLICANT: Tao, Mengbing
APPLICANT: Tao, Mengbing
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
                                                                       APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Nengbing
APPLICANT: Tao, Nengbing
APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REPRESENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT PILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
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OTHER INFORMATION: Clone ID: 63-LIB3057-002-01-K1-H4
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81.1%; Score 15.4; DB 10;
Best Local Similarity 94.1%; Pred. No. 42;
Matches 16; Conservative 0; Mismatches 1;
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Patent No. US20020137139A1
GENERAL INFORMATION:
Sequence 8824, Application US/09960352
Patent No. US20020137139A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 312 CAAGGACAAGCGCTACG 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 CAAGGAGAAGCGCTACG 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Bos taurus
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Best Local Similarity
Matches 16; Conserv
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RESULT 15

US-09-960-352-4589/C

US-09-960-352-4589/C

Sequence 4589, Application US/09960352

Sequence 4589, Application US/09960352

Sequence 4589, Application US/09960352

Sequence 4589, Application US/09960352

Septiment: Warran, Wesley C.

APPLICANT: Byatt, John C.

APPLICANT: Byatt, John C.

APPLICANT: Byatt, John C.

APPLICANT: Byatt, John C.

TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION

FILE REPERENCE: 1551.006/37-21(10298)C

CURRENT FILING DATE: 2001-09-24

NUMBER OF SEQ ID NOS: 15112

SEQ ID NO 4589

LENGTH: 422
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : TYPE: DNA
DOGANISM: Bos taurus
: OTHER INFORMATION: Clone ID: 20-LIB3057-020-Q1-K1-E11
US-09-960-352-4589
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US-08-961-527-317

US-07-971-096-3

US-08-175-096-3

US-08-175-096-3

US-08-175-096-3

US-08-171-3378-4

US-08-944-151-13

US-08-131-1338-57

US-08-940-0868-57

US-08-940-0868-57

US-08-961-57-1058-57

US-08-961-57-1058-57

US-09-648-797-57

US-09-641-597-37

US-09-221-0178-911

US-09-221-0178-911

US-09-21-0178-911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Mueting, Ann M.
REGISTRATION NUMBER: 33,977
REERENE/POCKET NUMBER: 150.105US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-339-031
TELEFAX: 612-339-3061
INFORMATION FOR SEQ ID NO: 1:
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LENGTH: 970 base pairs
TYPE: nucleic acid
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812
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3240
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Matches 19; Conserv
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 US-08-250-030-1
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                                                              2002, 15:56:36 ; Search time 2.54798 Seconds (without alignments) 2286.857 Million cell updates/sec
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Sequence 208, 1
Sequence 178, 2
Sequence 105, 1
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Sequence 57
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Sequence 5
Sequence 5
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/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/Packfiles1.seq:*
/cgn2_6/ptodata/1/ina/backfiles1.seq:*
      GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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US-09-233-527-1
PCT-US93-05651-1
US-08-998-416-125
US-09-221-0178-476
US-09-494-151-6
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US-09-724-864-24
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US-08-434-418-3
US-08-433-288-3
US-08-174-739A-3
US-08-434-256-3
US-08-658-207A-1
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US-08-434-418-5
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Maximum Match 100%
Listing first 45 summaries
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19
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Maximum DB seq length: 200000000
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Patent No. 5643723
GENERAL INFORMATION:
APPLICANT: Persint Detection of a Genetic Locus Encoding
TITLE OF INVENTION: Resistance to Rifampin in Mycobacterial Cultures and
TITLE OF INVENTION: Clinical Specimens
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schwegman, Lundberg & Woessner
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Pred. No. 1.2;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/250,030
FILING DATE: 26-MAY-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
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STREET: 3500 IDS Center
CITY: Minneapolis
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/313,185
FILING DATE: 12-0CT-1994
ATTORNEY/AGENT INFORMATION:
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Patent No. 6124098
GENERAL INFORMATION:
APPLICANT: Heym, Beate
APPLICANT: Cole, Stewart
                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: DNA (genomic)
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94.7%;
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Best Local Similarity 94.7 Matches 18; Conservative
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STATE: D.C.
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                                   APPLICANT: Mayo Foundation for Medical Education and Research APPLICANT: and Hoffmann-La Roche Inc.
TITLE OF INVENTION: Detection of a Genetic Locus Encoding TITLE OF INVENTION: Resistance to Rifampin NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schwegman, Lundberg & Woessner
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APPLICANT: Heyn Beate
APPLICANT: COLe, Stewart
APPLICANT: Young, Douglas
APPLICANT: Zhang, Ying
APPLICANT: Honore, Nadine
APPLICANT: Honore, Nadine
APPLICANT: Bodmer, Thomas
TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
TITLE OF INVENTION: in Mycobacterium Tuberculosis
CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06790
FILING DATE: 26-MAY-1995
CLASSIFICATION:
                                                                                                           STREET: 3500 IDS Center CITY: Minneapolis CTATE: MN
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Sequence 1, Application PC/TUS9506790 GENERAL INFORMATION:
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NAME: RABACCL, Kevin W.
REGISTRATION NUMBER: 35,651
REFRENCE/DOCKET NUMBER: 150.1
TELEPHONE: 612-339-0331
TELEPHONE: 612-339-3061
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 970 base pairs
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1300 I Street, N.W.
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Best Local Similarity 100.0%;
Matches 19; Conservative (
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APPLICANT: Young, Douglas
APPLICANT: Zhang, Ying
APPLICANT: Telenti, Amalio
APPLICANT: Telenti, Amalio
APPLICANT: Bodmer, Thomas
TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
TITLE OF INVENTION: in Mycobacterium Tuberculosis
CORRESPONDENCE, 66
CORRESPONDENCE ADDRESS:
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STREET: 1300 I Street, N.W.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FO Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/313,185
FILING DATE: 12-OCT-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/082,614A
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Pred. No. 8.2;
0; Mismatches 1;
                                                                                                                                                                                                                                       REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 02356.0068-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-400
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 3447 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
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Query Match
Best Local Similarity
Matches 17; Conserva
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COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-961-527-208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Charles Kunsch
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
NUMBER OF SEQUENCES: 391
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
REFERENCE/DOCKET NUMBER: 02356.0068-00000
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Pred. No. 46;
0; Mismatches
                                                                                                                                                                                                                                        Ouery Match 91.6%; Score 17.4; D
Best Local Similarity 94.7%; Pred. No. 8.2;
Matches 18; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue CITY: Rockville STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,527
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Brookes, A. Anders
RECISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: 9B340P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8512
INFORMATION FOR SEQ ID NO: 360: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 360, Application US/08961527 Patent No. 6420135
             TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 3447 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                MOLECULE TYPE: DNA (genomic)
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                                                                                                                                                                                                                                                                                                                    1 TCAAGGAGAAGCGCTACGA 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 1958 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match
Best Local Similarity 89.53
Matches 17; Conservative
                                                                                                                                                                      linear
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STRANDEDNESS:
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US-08-961-527-360
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Sequence 208, Application US/08961327

Pathent, No. 620135

GENERAL, INFORMATION.
APPLICATION.
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Gaps

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US-08-961-527-108/c

Sequence 108, Application US/08961527

Sequence 108, Application US/08961527

Patent No. 6420135

GENERAL INFORMATION:

TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences NUMBER OF SEQUENCES: 391

CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc.

STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Watson, James D
APPLICANT: Watson, James D
APPLICANT: Watson, James G.
TITLE OF INVENTION: Polynucleotides, polypeptides expressed
TITLE OF INVENTION: By the polynucleotides and methods for their use.
TITLE REFERENCE: 11000.105001
CURRENT APPLICATION NUMBER: US/09/724,864
CURRENT FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: U.S. No. 6380362 60/171,678
PRIOR FILING DATE: 1999-12-23
NUMBER OF SEQ ID NOS: 72
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                  Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: 1058cette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS Version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,527
FILING DATE:
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Pred. No. 55;
0; Mismatches
              Mismatches
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NAME: Brookes, A. Anders
REGISTRATION UNDER: 36,373
REFERENCE/DOCKET NUMBER: 98340
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 108:
SEQUENCE CHRACTERISTICS:
LENGTH: 11309 base pairs
TYPE: nucleic acid
STRANDENNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 24, Application US/09724864
Patent No. 6380362
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89.5%;
                                                1 TCAAGGAGAGCGCTACGA 19
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Best Local Similarity 89.59
Matches 17; Conservative
          17; Conservative
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                     STREET: 9410 Key CITY: Rockville STATE: Maryland COUNTRY: USA
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US-08-961-527-108
          Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Charles Kunsch
TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
NUMBER OF SEQUENCES: 391
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Indels
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MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CAPRICATION DATA:
FILING DATE:
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89.5%; Pred. No. 50;
Live 0; Mismatches
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Pred. No. 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue CITY: Rockville STATE: Maryland COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB340P1
TELECOMMUNICATION INPORMATION:
TELEPAX: (301) 309-8512
INPORMATION FOR SEQ ID NO: 105: SEQUENCE CHARACTERISTICS:
LENGTH: 6516 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                PB340P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 105, Application US/08961527 Patent No. 6420135 GENERAL INFORMATION:
                                                                                                               NAME: BLOOKES, A. Anders
REGISTRATION NUMBER: 36,373
REFRENCE/DOCKET NUMBER: PB34C
TELECOMMUNICATION INFORMATION:
TELEFAX: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 178:
SEQUENCE CHARACTERISTICS:
LENGTH: 4854 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100 TCAAAGAGAAGCACTACGA 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       83.2%;
89.5%;
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                                                                                              ATTORNEY/AGENT INFORMATION
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Matches 17; Conservative
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                           linear
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Best Local Similarity
                                                                                FILING DATE:
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US-08-961-527-178
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5725 CAAGGAGAAGTGCTAAGA 5742
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 88.9°
Matches 16; Conservative
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Matches 16; Conservative
                 PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 14
US-08-998-416-125/c
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APPLICANT: HOTVIZ, H. ROBERT
TITLE OF INVENTION: GENE WHICH PROTECTS CELLS FROM PROGRAMMED CELL DEATH AND
TITLE OF INVENTION: GENE WHICH PROTECTS CELLS FROM PROGRAMMED CELL DEATH AND
TITLE OF INVENTION: USES THEREOF
TITLE OF INVENTION: UNBER: US/09/234,186
CURRENT FILING DATE: 1999-01-20
EARLIER APPLICATION NUMBER: 07/927,681
EARLIER PILING DATE: 1992-06-12
EARLIER PILING DATE: 1992-08-10
EARLIER PILING DATE: 1997-08-10
EARLIER FILING DATE: 1997-02-19
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FASLESO FOR WINDOWS VERSION 4.0
EARLIER FILING DATE: 1997-02-19
NUMBER OF SEQ ID NOS: 8
SEQ ID NO 1
EARLIER FILING DATE: 1997-02-19
EARLIER FILING DATE: 1997-02-19
EARLIER FILING DATE: 1997-02-19
EARLIER FILING DATE: 1997-02-19
EARLIER FILING DATE: USWARD VERSION 4.0
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Patent No. 6465617
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL HORVILZ, H. Robert
APPLICANT: Hengartner, Michael
TITLE OF INVENTION: GENE WHICH PROTECTS CELLS FROM PROGRAMMED CELL DEATH AND
TITLE OF INVENTION: USES THEREFOR
FILE REFERENCE: 01997/201004
CURRENT APPLICATION NUMBER: US/09/233,527
CURRENT FILING DATE: 1999-01-20
PRIOR FILING DATE: 1992-06-12
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                                                                                                                                                                        Length 2395;
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                                                                                                                                                                     Score 14.8; DB 4;
Pred. No. 1.4e+02;
0; Mismatches 2;
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Pred. No. 1.6e+02;
0; Mismatches 2;
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 24
LENGTH: 2395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : NAME/KEY: misc_feature
: LCCATION: (1)...(6559)
: OTHER INFORMATION: n = A,T,C or G
US-09-234-186-1
                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/09234186
Patent No. 6312947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Caenorrhabditis elegans
                                                                                                                                                                Ouery Match 77.9%; Soc
Best Local Similarity 88.9%; Prr
Matches 16; Conservative 0;
                                                                                                                                                                                                                                                                                       Db 1796 CAAGGAGAACTCTACGA 1779
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88.98;
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Matches 16; Conservative
                                                                TYPE: DNA
CRGANISM: MOUSE
US-09-724-864-24
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US-09-233-527-1
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PCT-US93-05651-1
Sequence 1, Application PC/TUS9305651
Sequence 1, Application PC/TUS9305651
Sequence 1, Application PC/TUS9305651
SEQUENCE 1, Application PC/TUS9305651
TITLE OF INVENTION:
NUMBER OF EXQUENCES: 5
CURPUTER READABLE FORM:
MEDIUM TYPE: diskette
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/05651
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LEMRACTER: 6560 base pairs
TYPE: nucleic acid
STANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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88.9%; Pred. No. 1.6e+02;
iive 0; Mismatches 2;
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88.9%; Pred. No. 1.6e+02;
tive 0; Mismatches 2;
PRIOR FILING DATE: 1992-08-10
PRIOR APPLICATION NUMBER: 08/288,295
PRIOR FILING DATE: 1994-08-10
PRIOR APPLICATION NUMBER: 08/801,248
PRIOR FILING DATE: 1997-02-19
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 6559
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 125, Application US/08998416
| Sequence 125, Application US/08998416
| Patent No. 623954
| GENERAL INFORMATION:
| APPLICANT: Philippsen, Peter APPLICANT: Pohlmann, Rainer APPLICANT: Stelner, Sablne APPLICANT: Mont, Christine APPLICANT: Mendland, Jurgen APPLICANT: Rebischung, Corinne TITLE OF INVENTION: GENOMIC DNA SEQUENC: TITLE OF INVENTION: GENOMIC DNA SEQUENC: TITLE OF INVENTION: AND USES THEREOF NUMBER OF SEQUENCES: 1152
| CORRESPONDENCE ADDRESS: STREEDF: STREEDF: NO. 6239264artte correspondences.
                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature

LCCATION: (1)...(6559)

COTHER INFORMATION: n = A,T,C or G

US-09-233-527-1
                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Caenorrhabditis elegans
FEATURE:
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: MOLECULE TYPE: DNA (genomic)
PCT-US93-05651-1
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Score 14.4; DB 4; Length 711;
Pred. No. 2e+02;
0; Mismatches 1; Indels (
                                                                                                            FILING DATA
ATTORNEY AGENT INFORMATION.
NAME: MOLECY, Gladys H
REGISTRATION NUMBER: 32,430
REFRENCE/DOCKET NUMBER: 27340-20021.00
TELEPHONE: 650-813-5600
TELEFAX: 650-494-0792
TELER: 706141
INFORMATION FOR SED ID NO: 476:
SEQUENCE CHARACTERISTICS:
LENGTH: 711 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: UNKNOWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Search completed: November 12, 2002, 21:03:46 Job time : 8.54798 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORIGINAL SOURCE:
ORGANISM: PORYPHYROMONAS GINGIVALIS
                              APPLICATION NUMBER: PP2911
FILING DATE: 09-APR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU98/01023
FILING DATE: 10-DEC-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   75.8%;
93.8%;
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US-09-221-017B-476
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Sequence 476, Application US/09221017B
Patent No. 6444799
GENERAL INFORMATION:
APPLICANT: Ross, Bruce C.
TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF NUMBER OF SEQUENCES: 1120
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CTITY: Palo Alto
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Pred. No. 1.9e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                        COMPUTER: FLORPY disk

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM:
PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/998,416

FLING DATE: 24-DEC 1997

CLASSIFICATION DATE: 1957

PRIOR APPLICATION DATE: 31-DEC-1996

ATTORNEY/AGENT INFORMATION:
NAME: Medigs, J. Timothy
REGISTRATION NUMBER: 38,241

REFERENCE/DOCKET NUMBER: 38,241

REFERENCE/DOCKET NUMBER: 39-541-8689

INFORMATION FOR SEQ ID NO: 125:
SEQUENCE CHARACTERISTICS:
LENGTH: 515 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIF: 94304-10108
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: Windows
SOFTWARE: FastSEQ for Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/221,017B
FILING DATE: 23-DEC-1998
Research Triangle Park
No. 6239264th Carolina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 31-DEC-1997
PRIOR APPLICATION NUMBER: PP1546
FILING DATE: 30-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
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93.8%;
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Best Local Similarity 93.8
Matches 15; Conservative
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                                                                               COMPUTER READABLE FORM:
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US-08-998-416-125
                                         USA
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Drosophila melanog
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      Mycobacterium
Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptococcus
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AAT09676
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ABL04469
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AAA89994
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(without alignments)
3438.621 Million cell updates/sec
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| SIDSZ/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*
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| SIDSZ/gcgdata/geneseq-geneseqn-embl/NA1999.DAT:*
| SIDSZ/gcgdata/geneseq-geneseqn-embl/NA20018.DAT:*
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        GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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                                                                                     New DNA fragments from the rpoB diagnosis and identification of
                                                                     restriction fragment length
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                                                                                                                                                                                                                                                                                                                                              Mycobacterium gordonae type IV
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                                                                                                                                                              Park YK, Bai G,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                         99KR-0046795.
                                                                                                                                                                                                                                                                                                                                                                       mycobacteria; rpoB gene fragment; NTM; HIV; PRA; RFLD; fragment length polymorphism analysis; ds.
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                                                                                  gene of mycobacteria, useful for many mycobacterial species by
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The present sequence for Mycobacterium gordonae type IV rpoB gene fragment is 1 of 24 rpoB gene fragments (AAS05201-AAS05224) from

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Best Local
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The present sequence for Mycobacterium szulgai rpoB gene fragment is 1 of 24 rpoB gene fragments (ANSO$201-ANSO$224) from various Mycobacterial species. These rpoB gene fragments can be used in the diagnosis and identification of Mycobacterium species using a novel PCR-restriction fragment length polymorphism analysis (PRA) method. The method comprises obtaining a restriction fragment length polymorphism (RPLP) pattern of the 24 rpoB gene fragments; isolating, amplifying and digesting the DNA fragment from the microorganism to
                                                                                                                                                                                                       New DNA fragments from the rpoB gene of mycobacteria, useful for diagnosis and identification of many mycobacterial species by
                                                                                                                                                                Claim 1;
                                                                                                                                                                                                  restriction
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Non-tuberculous mycobacteria; rpoB gene fragment; NTM; HIV; PRA; RFLP; PCR-restriction fragment length polymorphism analysis; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Non-tuberculous
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                                                                                                                                                           Page 43-44; 50pp; English.
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Best Local :
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          The present sequence for Mycobacterium gordonae type I rpoB gene fragment is 1 of 24 rpoB gene fragments (AAS05201-AAS05224) from various Mycobacterial species. These rpoB gene fragments can be used in the diagnosis and identification of Mycobacterium species using a movel PCR-restriction fragment length polymorphism analysis (PRA) method. The method comprises obtaining a restriction fragment length polymorphism (RFLP) pattern of the 24 rpoB gene fragments; isolating, amplifying and digesting the DNA fragment from the microorganism to be identified and comparing the RFLP patterns from the known rpoB gene fragments with the unidentified fragment. The rpoB gene fragments are useful to identify a wide range of Mycobacterium species, e.g. for diagnosis or to obtain epidemiological and pathogenesis information for selection of appropriate therapies, including M. tuberculosis, M. Leprae
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                                                                                                                                                                                                                                                                                                   New DNA fragments from the rpoB diagnosis and identification of
                                                                                                                                                                                                                                                       Claim 1;
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                                                                                                                                                                                                                                                                                     restriction fragment length
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     non-tuberculous mycobacteria (NTM)
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Pred. No.
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encountered in subjects infected
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RESULT 5
AAS05202
CC The present sequence for Mycobacterium gordonae type II rpoB gene CC fragment is 1 of 24 rpoB gene fragments (AASO5201-AASO5224) from CC various Mycobacterial species. These rpoB gene fragments can be used CC in the diagnosis and identification of Mycobacterium species using a CC novel PCR-restriction fragment length polymorphism analysis (PRA) CC method. The method comprises obtaining a restriction fragment length CC polymorphism (RFLP) pattern of the 24 rpoB gene fragments; isolating, CC amplifying and digesting the DNA fragment from the microorganism to be identified and comparing the RFLP patterns from the known rpoB gene CC fragments with the unidentified fragment. The rpoB gene fragments CC are useful to identify a wide range of Mycobacterium species, e.g. for CC diagnosis or to obtain epidemiological and pathogenesis information for Selection of appropriate therapies, including M. tuberculosis, M. leprae CC and non-tuberculous mycobacteria (NTM) encountered in subjects infected CC with human immunodeficiency virus (HIV) Analysis of the rpoB gene CC required), and can differentiate between many species in a single experiment, including those difficult to distinguish by usual biochemical CC detecting specific Mycobacterial species
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Best Local S
Matches 19
                                                                                                                                                                                                                                                                                                                                                                     New DNA fragments from the rpoB gene of mycobacteria, useful for diagnosis and identification of many mycobacterial species by restriction fragment length polymorphism \,
                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 40;
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19; Conserv
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7.5;
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specific

species

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RESULT 6
AAS05203
                                                                                                        The present sequence for Mycobacterium gordonae type III rpoB gene CC fragment is 1 of 24 rpoB gene fragments (AASO5201-AASO5224) from CC various Mycobacterial species. These rpoB gene fragments can be used CC in the diagnosis and identification of Mycobacterium species using a CC novel PCR-restriction fragment length polymorphism analysis (PRA) CC method. The method comprises obtaining a restriction fragment length polymorphism (RFLP) pattern of the 24 rpoB gene fragments; isolating, CC amplifying and digesting the DNA fragment from the microorganism to comparifying the RFLP patterns from the known rpoB gene CC digeners with the unidentified fragment. The rpoB gene fragments (PRA) gene CC are useful to identify a wide range of Mycobacterium species, e.g. for CC diagnosis or to obtain epidemiological and pathogenesis information for CC diagnosis or to obtain epidemiological and pathogenesis information for CC diagnosis or to obtain epidemiological and pathogenesis information for CC diagnosis or to obtain epidemiological and pathogenesis information for CC diagnosis or to obtain epidemiological and pathogenesis information for CC diagnosis or to obtain epidemiological and pathogenesis information for CC diagnosis or to obtain epidemiological and pathogenesis information for CC diagnosis or to obtain epidemiological and pathogenesis information for CC and non-tuberculous mycobacteria (NTM) encountered in subjects infected CC with human immunodeficiency virus (HTV). Analysis of the rpoB gene CC required), and can differentiate between many species in a single comparation described are oligonucleotide probes (AASO5227-AASO5242) for detecting specific Mycobacterial species.
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Best Local Similarity
Matches 19; Conserv
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                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New DNA fragments from the rpoB gene of mycobacteria, useful diagnosis and identification of many mycobacterial species by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 41; 50pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      restriction fragment length polymorphism
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ilarity 100.0%;
Conservative (
                                                                     BP;
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                                                                     46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bai G,
                                                                                                     Mycobacterial species.
                                                                   A.
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                                                                     69 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         English.
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   Score 19; DE
Pred. No. 7.5
0; Mismatches
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                                                                     63 G;
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Pred. No.
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                                                                   30 T;
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                                                                   0 other;
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                                 Length 208;
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Gaps
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Query Match Best Local Matches 1

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Conservative

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Mismatches

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Score 19; Pred. No.

DB 22; Length 208

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                                                                                                                                                  polymorphism (RFLP) pattern of the 24 rpoB gene fragments: isolating, amplifying and digesting the DNA fragment from the microorganism to be identified and comparing the RFLP patterns from the known rpoB gene fragments with the unidentified fragment. The rpoB gene fragments are useful to identify a wide range of Mycobacterium species, e.g. for diagnosis or to obtain epidemiological and pathogenesis information for selection of appropriate therapies, including M. tuberculosis, M. leprae
                          and non-tuberculous mycobacteria (NTM) encountered in subjects infected with human immunodeficiency virus (HIV). Analysis of the rpoB gene fragments is rapid, precise, simple and cost effective (only 1 PCR required), and can differentiate between many species in a single experiment, including those difficult to distinguish by usual biochemical tests. Also described are oligonucleotide probes (AAS05227-AAS05242) for detecting specific Mycobacterial species.
                                                                                                                                                                                                                                                                                   The present sequence for Mycobacterium tuberculosis rpoB gene fragment is 1 of 24 rpoB gene fragments (AAS05201-AAS05224) from various Mycobacterial species. These rpoB gene fragments can be used in the diagnosis and identification of Mycobacterium species using a novel PCR-restriction fragment length polymorphism analysis (PRA) method. The method comprises obtaining a restriction fragment length polymorphism comprises obtaining a restriction fragment length polymorphism.
   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 41; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New DNA fragments from the rpoB gene of mycobacteria, useful for diagnosis and identification of many mycobacterial species by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-300520/31.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          restriction fragment length polymorphism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lee H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (ERUM-) ERUME BIOTECH CO LTD
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   208
   ВP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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46 A; 62 C;
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67 G;
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33 T; 0 other;
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AAS05208
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                                                                             RESULT 9
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AAS05206
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CC fragment is 1 of 24 rpoB gene fragments (AASO5201-AASO5224) from
CC various Mycobacterial species. These rpoB gene fragments can be used
CC in the diagnosis and identification of Mycobacterium species using a
CC movel PCR-restriction fragment length polymorphism analysis (PRA)
CC method. The method comprises obtaining a restriction fragment length
CC polymorphism (RFLP) pattern of the 24 rpoB gene fragments; isolating,
CC amplifying and digesting the DNA fragment from the microorganism to
CC be identified and comparing the RFLP patterns from the known rpoB gene
CC fragments with the unidentified fragment. The rpoB gene fragments
CC are useful to identify a wide range of Mycobacterium species, e.g. for
CC diagnosis or to obtain epidemiological and pathogenesis information for
CC diagnosis or to obtain epidemiological and pathogenesis in subjects infected
CC and non-tuberculous mycobacteria (NTM) encountered in subjects infected
CC with human immunodeficiency virus (HIV). Analysis of the rpoB gene
CC required), and can differentiate between many species in a single
CC experiment, including those difficult to distinguish by usual biochemical
CC tests. Also described are oligonucleotide probes (AASO5227-AASO5242) for
CC detecting specific Mycobacterial species.
                                                                                                                                                                                           Matches
                                                                                                                                                                                                                        Query Match
             AAS05208
                                           AAS05208 standard; DNA;
                                                                                                                                                                                                                                                        Sequence 208 BP; 46 A; 62 C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI;
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                                                                                                                                                      TCAAGGAGAAGCGCTACGA 19
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                                                                                                                                                                                         19;
                                                                                                                                                                                                        Similarity
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                                                                                                                                                                                                                                                                                    specific Mycobacterial species.
                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           fragment length polymorphism
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                                                                                                                                                                                                     100.0%;
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                                           208 BP
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                                                                                                                                                                                                       Score 19; 1
Pred. No. 7
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                                                                                                                                                                                                                    Length 208;
                                                                                                                                                                                        Indels
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                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                  RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                converted with the control of proposition of appropriate the patterns using a control of the method. The method comprises obtaining a restriction fragment length composition fragment length composition of the 24 rpoB gene fragment; isolating, compilitying and digesting the DNA fragment from the microorganism to be identified and comparing the RPIP patterns from the known rpoB gene fragments with the unidentified fragment. The rpoB gene fragments comparing the range of Mycobacterium species, e.g. for control of appropriate therapies, including M. tuberculosis, e.g. for control of appropriate therapies, including M. tuberculosis, M. leprae and non-tuberculous mycobacteria (NTM) encountered in subjects infected with human immunodeficiency virus (HIV). Analysis of the rpoB gene control of ragments is rapid, precise, simple and cost effective (only 1 PCR crequired), and can differentiate between many species in a single control of the poB gene control of th
                                                                                                                                                                                                                                                                                                                                                                                  Best Loc
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New DNA fragments from the rpoB gene of mycobacteria, useful for diagnosis and identification of many mycobacterial species by restriction fragment length polymorphism \,
                                                   Mycobacterium ulcerans rpoB gene fragment.
                                                                                                                                             AAS05210;
                                                                                                                                                                                   AAS05210 standard; DNA; 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence for Mycobacterium kansasii rpoB gene fragment is 1 of 24 rpoB gene fragments (AAS05201-AAS05224) from various Mycobacterial species. These rpoB gene fragments can be used in the diagnosis and identification of Mycobacterium species using a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mycobacterium kansasii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (ERUM-) ERUME BIOTECH CO LTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PCR-restriction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mycobacterium kansasii rpoB gene fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Non-tuberculous
                                                                                                                                                                                                                                                                                                                                                                                                      Local
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                                                                                                                                                                                                                                                                                                                                     1 TCAAGGAGAAGCGCTACGA 19
                                                                                                                                                                                                                                                                                             TCAAGGAGAAGCGCTACGA 19
                                                                                                                                                                                                                                                                                                                                                                                    19;
                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Park YK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Page 42;
                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000WO-KR01223
                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99KR-0046795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mycobacteria; rpoB gene fragment; NTM;
fragment length polymorphism analysis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                51 A; 65 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bai G,
                                                                                                                                                                                                                                                                                                                                                                                                 100.0%;
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                                                                                                                                                                                     ВP
                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            65 G; 27 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                      Score 19;
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                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                               7.5;
                                                                                                                                                                                                                                                                                                                                                                                                                   DB 22; Length 208;
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                                                                                                                                                                                                                                                                                                                                                                             0
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                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Non-tuberculous mycobacteria; rpoB gene fragment; NTM; HIV; PRA; RFLP; PCR-restriction fragment length polymorphism analysis; ds.

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RESULT 11
AAS05211
ID AAS05
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                                                                                                                                                                                                                                                                                                                                                                      Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         polymorphism (RFLP) pattern of the 24 rpoB gene fragments; isolating, amplifying and digesting the DNA fragment from the microorganism to be identified and comparing the RFLP patterns from the known rpoB gene fragments with the unidentified fragment. The rpoB gene fragments are useful to identify a wide range of Mycobacterium species, e.g. for diagnosis or to obtain epidemiological and pathogenesis information for selection of appropriate therapies, including M. tuberculosis, M. leprae and non-tuberculous mycobacteria (NTM) encountered in subjects infected with human immunodeficiency virus (HIV). Analysis of the rpoB gene fragments is rapid, precise, simple and cost effective (only 1 PCR required), and can differentiate between many species in a single experiment, including those difficult to distinguish by usual biochemical tests. Also described are oligonucleotide probes (AAS05227-AAS05242) for detecting specific Mycobacterial species.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence for Mycobacterium ulcerans rpoB gene fragment is 1 of 24 rpoB gene fragments (AASO5201-AASO5224) from various Mycobacterial species. These rpoB gene fragments can be used in the diagnosis and identification of Mycobacterium species using a novel PCR-restriction fragment length polymorphism analysis (PRA) method. The method comprises obtaining a restriction fragment length polymorphism comprises obtaining a restriction fragment length polymorphism.
                             WO200131061-A1
                                                        Mycobacterium marinum
                                                                                       Non-tuberculous
PCR-restriction
                                                                                                                                   Mycobacterium marinum rpoB gene fragment.
                                                                                                                                                                  07-SEP-2001 (first entry)
                                                                                                                                                                                                  AAS05211;
                                                                                                                                                                                                                              AAS05211 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 43; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     restriction fragment length polymorphism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New DNA fragments from the rpoB gene of mycobacteria, useful for diagnosis and identification of many mycobacterial species by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lee H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-OCT-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mycobacterium ulcerans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (ERUM-) ERUME BIOTECH CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                       TCAAGGAGAAGCGCTACGA 19
                                                                                                                                                                                                                                                                                                                                                                      19;
                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                    BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000WO-KR01223
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                                                                                      mycobacteria; rpoB gene fragment; NTM;
fragment length polymorphism analysis;
                                                                                                                                                                                                                                                                                                                                                                                                                                  45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bai G,
                                                                                                                                                                                                                                DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                 A; 68 C;
                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kin
                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                 67 G; 28 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                   Score 19; L
Pred. No. 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'n
                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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                                                                                                                                                                                                                                                                                                                                                                             DB 7.5;
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                                                                                                                                                                                                                                                                                                                                                                                                  22;
                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                Length 208;
                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                       HIV; PRA; RFLP ds.
                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                 Gaps
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cc novel pcr-restriction fragment length polymorphism analysis (PRA)
CC method. The method comprises obtaining a restriction fragment length
CC polymorphism (RFLP) pattern of the 24 rpoB gene fragments; isolating,
CC amplifying and digesting the DNA fragment from the microorganism to
CC be identified and comparing the RFLP patterns from the microorganism to
CC are useful to identify a wide range of Mycobacterium species, e.g. for
CC diagnosis or to obtain epidemiological and pathogenesis information for
CC selection of appropriate therapies, including M. tuberculosis, M. leprae
CC and non-tuberculous mycobacteria (NYM) encountered in subjects infected
CC with human immunodeficiency virus (HIV). Analysis of the rpoB gene
CC fragments is rapid, precise, simple and cost effective (only 1 pcR
CC required), and can differentiate between many species in a single
CC experiment, including those difficult to distinguish by usual biochemical
CC detecting specific Mycobacterial species.

Ax

Common the composition of the probes (AASO5227-AASO5242) for
CX
CA detecting specific Mycobacterial species.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 12
AAS05215
AC XXX AC
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Matches
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                                                                                                       27-OCT-2000;
                                                                                                                                                               03-MAY-2001
                                                                                                                                                                                                                       WO200131061-A1
                                                                                                                                                                                                                                                                         Mycobacterium avium
                                                                                                                                                                                                                                                                                                                                 PCR-restriction
                                                                                                                                                                                                                                                                                                                                                           Non-tuberculous
                                                                                                                                                                                                                                                                                                                                                                                                           Mycobacterium avium rpoB gene fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAS05215;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAS05215 standard; DNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 TCAAGGAGAAGCGCTACGA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCAAGGAGAAGCGCTACGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fragment length polymorphism
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BP;
                                                                                                       2000WO-KR01223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first
                                                                                                                                                                                                                                                                                                                        mycobacteria; rpoB gene fragment; NTM;
fragment length polymorphism analysis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99KR-0046795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  45 A; 69 C; 68 G; 26 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entry)
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of mycobacteria, useful for mycobacterial species by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ś
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               . 7.5;
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                                                                                                                                                                                                                                                                                                                           HIV; PRA; RFLP; ds.
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(ERUM-) ERUME BIOTECH CO LTD

27-OCT-1999;

99KR-0046795

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RESULT 13
AASO5216
ID AASO5
XX AASO5
XX AASO5
XX O7-SE
XX NON-t
XW PCR-r
XX PCOb
XX PCOC
XX PC
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CC fragment is 1 of 24 rpoB gene fragments (AASO5201-AASO5224) from
CC various Mycobacterial species. These rpoB gene fragments can be used
CC in the diagnosis and identification of Mycobacterium species using a
CC novel PCR restriction fragment length polymorphism analysis (PRA)
CC method. The method comprises obtaining a restriction fragment length
CC polymorphism (RFLP) pattern of the 24 rpoB gene fragments; isolating,
CC amplifying and digesting the DNA fragment from the microorganism to
CC be identified and comparing the RFLP patterns from the known rpoB gene
CC fragments with the unidentified fragment. The rpoB gene fragments
CC are useful to identify a wide range of Mycobacterium species, e.g. for
CC diagnosis or to obtain epidemiological and pathogenesis information for
CC selection of appropriate therapies, including M. tuberculosis, M. leprae
CC required, and can differentiate between many species in a single
CC experiment, including those difficult to distinguish by usual biochemical
CC tests. Also described are oligonucleotide probes (AASO5227-AASO5242) for
CC detecting specific Mycobacterial species.
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  New DNA fragments from
                                                     WPI; 2001-300520/31
                                                                                                                                                                                                        27-OCT-1999;
                                                                                                                                                                                                                                                                                                        03-MAY-2001.
                                                                                                                                                                                                                                                     27-OCT-2000; 2000WO-KR01223
                                                                                                                                                                                                                                                                                                                                                             WO200131061-A1
                                                                                                                                                                                                                                                                                                                                                                                                             Mycobacterium bovis
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Non-tuberculous PCR-restriction
                                                                                                                                                     (ERUM-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mycobacterium bovis rpoB gene fragment.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAS05216 standard; DNA; 208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI;
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                                                                                                                                                     ERUME BIOTECH CO LTD
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                                                                                                  YK,
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                                                                                                                                                                                                        99KR-0046795
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fragment length polymorphism analysis;
                                                                                                  Bai
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100.0%; F
itive 0;
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the rpoB gene of mycobacteria, useful
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Pred. No.
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7.5;
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                                                                                                  픤
                                                                                                                                                                                                                                                                                                                                                                                                                                                          HIV; PRA; RFLP; ds.
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В Ş

Sequence 208 BP; 46 A; 62 C;

67 G; 33 T; 0 other;

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CC The present sequence for Mycobacterium bovis rpoB gene
CC fragment is 1 of 24 rpoB gene fragments (AASO5201-AASO5224) from
CC various Mycobacterial species. These rpoB gene fragments can be used
CC in the diagnosis and identification of Mycobacterium species using a
CC novel PCR-restriction fragment length polymorphism analysis (PRA)
CC method. The method comprises obtaining a restriction fragment length
CC polymorphism (RFLP) pattern of the 24 rpoB gene fragments; isolating,
CC amplifying and digesting the DNA fragment from the microorganism to
CC be identified and comparing the RPLP patterns from the known rpoB gene
CC fragments with the unidentified fragment. The rpoB gene fragments
CC diagnosis or to obtain epidemiological and pathogenesis information for
CC selection of appropriate therapies, including M. tuberculosis, M. leprae
CC diagnosis or to obtain epidemiological and pathogenesis information for
CC selection of appropriate therapies, including M. tuberculosis, M. leprae
CC with human immunodeficiency virus (HIV). Analysis of the rpoB gene
CC required), and can differentiate between many species in a single
CC experiment, including those difficult to distinguish by usual blochemical
CC detecting specific Mycobacterial species
CC detecting specific Mycobacterial species
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        diagnosis and identification of many mycobacterial species by restriction fragment length polymorphism \, -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 45; 50pp; English
                                                specific Mycobacterial species.
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RESULT 14
AAS05217
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New DNA fragments from the rpoB gene of mycobacteria, useful for diagnosis and identification of many mycobacterial species by restriction fragment length polymorphism \,
                                                                    WPI; 2001-300520/31.
                                                                                                     Lee
                                                                                                                                                                27-OCT-1999;
                                                                                                                                                                                             27-OCT-2000; 2000WO-KR01223
                                                                                                                                                                                                                              03-MAY-2001
                                                                                                                                                                                                                                                           WO200131061-A1
                                                                                                                                                                                                                                                                                       Mycobacterium celatum.
                                                                                                                               (ERUM-) ERUME BIOTECH CO LTD.
                                                                                                                                                                                                                                                                                                                                                                Mycobacterium celatum rpoB gene fragment.
                                                                                                                                                                                                                                                                                                                                                                                                    07-SEP-2001
                                                                                                                                                                                                                                                                                                                       PCR-restriction
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                                                                                                                                                                                                                                                                                                                                      Non-tuberculous
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                                                                                                 Park YK,
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                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                99KR-0046795
                                                                                                                                                                                                                                                                                                                 mycobacteria; rpoB gene fragment; NTM; HIV; PRA; RFLP; fragment length polymorphism analysis; ds.
                                                                                                 Bai G,
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                                                                                                 Kin
                                                                                           Υ,
                                                                                                Park HJ
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The present sequence for Mycobacterium celatum rpoB gene

Claim 1; Page 45; 50pp; English.

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RESULT 15
AAS05219
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Best Local
The present sequence for Mycobacterium fortuitum rpoB gene fragment is 1 of 24 rpoB gene fragments (AAS05201-AAS05224) from various Mycobacterial species. These rpoB gene fragments can be used in the diagnosis and identification of Mycobacterium species using a novel PCR-restriction fragment length polymorphism analysis (PRA) method. The method comprises obtaining a restriction fragment length polymorphism (RFLP) pattern of the 24 rpoB gene fragments; isolating,
                                                                                                                                                                                                                                           Claim 1; Page 46;
                                                                                                                                                                                                                                                                                                  restriction
                                                                                                                                                                                                                                                                                                                New DNA fragments from the rpoB gene of mycobacteria, useful diagnosis and identification of many mycobacterial species by
                                                                                                                                                                                                                                                                                                                                                                                                               WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lee
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19; Conser
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                                                                                                                                                                                                                                                                                            fragment length
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                                                                                                                                                                                                                                  50pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; 71 C;
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                                                                                                                                                                                                                                                                                            polymorphism
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Pred. No. 7.5;
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Best Local
                                                                                                                                                                                   amplifying and digesting the DNA fragment from the microorganism to be identified and comparing the RFLP patterns from the known rpoB gene fragments with the unidentified fragment. The rpoB gene fragments with the unidentified fragment. The rpoB gene fragments are useful to identify a wide range of Mycobacterium species, e.g. for diagnosis or to obtain epidemiological and pathogenesis information for selection of appropriate theraples, including M. tuberculosis, M. leprae and non-tuberculous mycobacteria (NTM) encountered in subjects infected with human immunodeficiency virus (HTV). Analysis of the rpoB gene fragments is rapid, precise, simple and cost effective (only 1 PCR required), and can differentiate between many species in a single experiment, including those difficult to distinguish by usual biochemical tests. Also described are oligonucleotide probes (AASO5227-AASO5242) for detecting specific Mycobacterial species.
                                                                                                                                                        Sequence
1 TCAAGGAGAAGCGCTACGA
                                 TCAAGGAGAAGCGCTACGA 19
                                                                              19;
                                                                                            Similarity
                                                                                                                                                    208 BP; 43 L; 69 C;
                                                                          Conservative
                                                                                            100.0%;
19
                                                                          0;
                                                                                                                                                  69 G; 27 T;
                                                                                            Score 19;
Pred. No.
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                                                                                                             DB 22;
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Search completed: November 12, Job time: 14.4434 secs 2002, 16:50:33

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November 12, 2002, 16:50:46; Search time 58.0983 Seconds (without alignments) 9517.553 Million cell updates/sec
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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em_htg_inv:*
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11. 9b_ba:*

2. 9b_btg;*

31. 9b_om:*

41. 9b_om:*

9b_pb!:*

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Pred. No. is the number of results predicted by chance to have a

em_htgo_other:*

em_htgo_hum:*

em_htg_vrt:*

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description		ycobac	AJ318819 Mycobacte	AJ318813 Mycobacte	AJ318815 Mycobacte	AJ31881/ Mycobacte	AJJIBBIA Mycobacte	AJJIBBID MYCODACTE	AJJIBBZI MYCODACTE	Tanynp Sedneuce I	AXIII339 Sequence	U24494 Mycobacteri	U12205 Mycobacteri	L27989 Mycobacteri	AE006964 Mycobacte	295972 Mycobacter1	AF019754 Drosophil	AF057162 Drosoph11	AF041439 Drosoph11	AF019753 Drosophil	AY069496 Drosoph11	AF039232 Drosoph11	AF027729 Drosophil	AR067447 Sequence	AF242549 Amycolato	AF039233 Drosoph11	AE011788 Xanthomon	214314 M.leprae qe	AC017309 Drosophil	AC019900 Drosophil	AP003504 Oryza sat	AC008310 Drosophil	AC010214 Drosophil	AE003779 Drosophil	AE003638 Drosoph11	AL583923 Mycobacte	D55629 Sea lamprey	BC026311 Homo sap1	AC014154 Drosophil	AE005712 Caulobact		Pseudomo	AFUZ9344 BULKNOIDE	ALDIZON SCIEDTOMY	ALIZAZI MALLUS NO ALO31124 Streptomy	Š		SO HOU THE PROPERTY OF THE PRO				gene.		teridae; Actinomy	: Mycoba	
ΙĐ		MTU318818	8 6	7:	7 :	100	ቷ :	ב כ	ž	130/00	AKILISS	MSU24494	MT012205	MSGRPOB	AE006964	MTC1376	AF019754	AF057162	AF041439	AF019753	AY069496	AF039232	AF027729	AR067447	AF242549	AF039233	AE011788	MLB1790G	AC017309	AC019900	AP003504	AC008310	AC010214	AE003779	AE003638	MLEPRTN7		₹;	CU1415	E005/1	35	AE0046/4	י הר	;;	C1C2	ALIGNMENTS		610 hn	tuberculosis partial	1415-97.	~	bun.	tuberculosis.	ria; Actinob	corynebacterineae; Mycobacteriaceae tuberculosis complex	
DB	:	Η,	-	٠,	٦.	٠,	٠,	- ا	4 4	٥ (۰ م	٠,	-	Н,	-	-	ო	m	٣	m	m	٣	m	9	Н	m	-	-	(1	~	ω .	m i	n (7) (.	٠,	s o	א ע	٧,		٦,	٦,	٠.	٠,					ercu	late	084	62	מינים בי	icte:	έà	5
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Query Match	-	98	100.0	3 6	36	36	3 6	38	38	38	38	100.0	100.0	100.0	100.0	100.0	91.6	91.6	91.6	91.6	91.6	91.6	91.6	91.6	91.6	91.6	91.6	91.6	91.6	91.6	91.6	91.6	91.0	0.1.0	91.0	91.0	200	000	000	9 0		86.3	86.3	86.3	86.3			MTU318818	Mycobacterium	a subuni	18818.1	ројуше	bacter	Bacteria; Actir	nebacte	
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Gaps

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QPSQFMGQNNPLSGLHKRRLSALGPGGLSRERAGLEVRDVHP"
191 C 202 g 95 t
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Molecular analysis of rifampin-resistant Mycobacterium tuberculosis
isolated in Spain (1996-2001). Description of new alleles into rpoB
gene and review
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RLSOFITEMDONNPLSGLTHKRLSALGPGGLSRERAGLEVRDVHP"
1910.
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Mycobacterium tuberculosis.
Mycobacterium tuberculosis
Mycobacterium tuberculosis
Bacteria, Actinobacteria; Actinobacteridae; Actinomycetales;
Corymebacterinae; Mycobacteriaceae; Mycobacterium; Mycobacterium tuberculosis complex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (07-AUG-2001) Herrera L., Servicio Bacteriologia, Nacional Microbiología., Ctra. Majadahonda-Pozuelo, Km 2.5, Majadahonda. Madrid. 28220, SPAIN Location/Qualifiers
                                                                                                                                                                                                                                                                                Length 610
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    616
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36;
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Pred. No. 36;
; Mismatches
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Herrera, L.
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Molecular analysis of rifampin-resistant Mycobacterium tuberculosis isolated in Spain (1996-2001). Description of new alleles into rpoB
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RLRTVGELIONQIRVGMSRMERVYRERMTTQDDVEAITPOTLINIRPVVAAIKEFFGTS
QPSOFMGONPLESCHTKRRLSALGPGGLSRERAGLEVRDVHP"
191 c 202 g 55 t
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Location/Qualifiers
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Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium
tuberculosis complex.
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                                                                                                                     Direct Submission
Submitted (07-AUG-2001) Herrera L., Servicio Bacteriologia,
Nacional Microbiologia., Ctra. Majadahonda-Pozuelo, Km 2.5,
Majadahonda. Madrid. 28220, SPAIN
Location/Qualifiers
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RNA POLYMETASE beta subunit; rpoB gene.
Mycobacterium tuberculosis.
Mycobacterium tuberculosis.
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Submitted (07-AUG-2001) Herrera L.,
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Herrera, L.
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Herrera,L., Jimenez,M.S. and Saez,J.A.
Molecular analysis of rifampin-resistant Mycobacterium tuberculosis
isolated in Spain (1996-2001). Description of new alleles into rpoB
gene and review
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FFGTSQPSGFMGQNNBLSGLTHKRLSALGPGGLSRERAGLEVRDV"
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Molecular analysis of rifampin-resistant Mycobacterium tuberculosis
isolated in Spain (1996-2001). Description of new alleles into rpoB
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Mycobacterium tuberculosis.
Mycobacterium tuberculosis.
Mycobacterium tuberculosis.
Mycobacterium tuberculosis.
Gotvinobacterium Actinobacteria; Actinobacteriums, Mycobacteriums, Mycobacteriums, Hycobacteriums, Hycobacteriums, Hycobacteriums, Hycobacteriums, Hycobacterium, Hycobacte
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Submitted (07-AUG-2001) Herrera L., Servicio Bacteriologia, a
Nacional Microbiologia, Ctra. Majadahonda-Pozuelo, Km 2.5,
Majadahonda. Madrid. 28220, SPAIN
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Submitted (07-AUG-2001) Herrera L., Servicio Bacteriologia,
Nacional Microbiologia., Ctra. Majadahonda-Pozuelo, Km 2.5,
Majadahonda. Madrid. 28220, SPAIN
Location/Qualifiers
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/organta="Mycobacterium tuberculosis"
/isolate="2348-98"
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    633
/organism="Mycobacterium tuberculosis"
/isolate="1058-97"

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AJ318815.1 GI:22208406
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Molecular analysis of rifampin-resistant Mycobacterium tuberculosis isolated in Spain (1996-2001). Description of new alleles into rpoggene and review
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Mycobacterium tuberculosis.
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/db_xref="taxon:1773"
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Herrera, L., Jimenez, M.S. and Saez, J.A.
Molecular analysis of rifampin-resistant Mycobacterium tuberculosis
isolated in Spain (1996-2001). Description of new alleles into rpoB
gene and review
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a 202 c 212 g 99 t
                                                                                                                                                   DNA circular BCT 09-AUG-2002 rpoB gene for RNA polymerase
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Submitted (07-AUG-2001) Herrera L., Servicio Bacteriologia, Centro
Nacional Microbiologia., Ctra. Majadahonda-Pozuelo, Km 2.5,
Majadahonda. Madrid. 28220, SPAIN
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Wycobacterium tuberculosis partial rpoB gene for RNA polymerase beta subunit, isolate 1071-98.

AJ318821

AJ318821. G1:22208418

RNA polymerase beta subunit; rpoB gene.

Wycobacterium tuberculosis.

Bacteria; Actinobacteria; Actinobacteriase, Actinomycetales; Corynebacterium away wycobacterium; Mycobacteriase, Mycobacteriase, Hycobacteriase, Hycobacteriase, Hycobacteriase, Hycobacteriase, Hycobacteriase, Hycobacteriase, Hycobacteriase, Hycobacteriase, Hycobacteriase, Hycobacteriasese, Hycobacteriasese, Hycobacteriasese, Hycobacteriasese, Hycobacteriasese, Hycobacteriasese, Hycobacteriasese, Hycobacteriasese, Hycobacterium
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Persing, D.H., Hunt, J.J., Young, K.K.Y., Felmlee, T.A., Roberts, G.D.
and Whelan, A.Christian.
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/isolate="1071-98"
/db_xref="taxon:1773"
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red. No. 36;
Mismatches 0
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150706
150706.1 GI:2472409
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/gene="rpoB"
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Matches 19; Conserv
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I50706
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RYGRYKVKKKLKLGLHYGEPITSSTLTEEDVVATIEYLVRLHEGQTTMTVPGGVEVPVE
TDDIDHFGNRRLRTVGELIQNQIRVGMSRMERVVRERMTTQDVEAITPQTLINIRPVV
AAIKREFGTSQLSQFMDONPLESGLTYKRRLSALGFGGLSRERAGLEVRDV"
195 c 210 g 99 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MTU318816 637 bp DNA circular BCT 09-AUG-2002 Mycobacterium tuberculosis partial rpoB gene for RNA polymerase beta subunit, isolate 1255-98.
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GRYNVRKLGLHVGEPITSSTLTEEDVVATIEYLVRLHEGGTTMTVPGGVEVPVETDD
IDHFGNRRLRTVGELIONOIRVGMSRMERVYRERMTTQDVEATTPQTLINIRPVVAAI
KEFFGTSGLSGFMDQNNPLSGLTHKRMFALGPGGLSRERAGLEVRDVHPSH"
198 c 101 g 101 t
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Submitted (07-AUG-2001) Herrera L., Servicio Bacteriologia, Centro
Nacional Microbiologia., Ctra. Majadahonda-Pozuelo, Km 2.5,
Majadahonda. Madrid. 28220, SPAIN
Location/Qualifiers
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Corynebacterineae: Mycobacteriaceae; Mycobacterium; Mycobacterium
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                                                 /transl_table=11
/product="RNA polymerase beta subunit"
/protein_id="CACA97031.1"
/db_xref="G1:22208405"
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/transl_table=11
/product="RNA polymerase beta subunit"
/protein_id="CAC87033.1"
/db_xref="G1:22208409"
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Pred. No. 36;
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AJ318816.1 GI:22208408
RNA Polymerase beta subunit; rpoB gene.
Mycobacterium tuberculosis.
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      /gene="rpoB"
/codon_start=1
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ilarity 100.0%;
Conservative 0;
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Herrera, L.
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/transl_table=11
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/gene="rpoB"
194. .3703
/gene="rpoB"
/codon_start=1
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Imboden, P.
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Best Local Similarity 100.
Matches 19; Conservative
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U12205
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Mycobacterium tuberculosis.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaeae;
Actinomycetales; Corynebacterium tuberculosis complex.

(bases 1 to 3534)
Bergeron, M.G., Boissinot, M., Huletsky, A., m Nard, C., Ouellette, M., Picard, F.J. and Roy, P.H.
Highly conserved genes and their use to generate probes and primers for detection of microorganisms
Patent: WO 0123604-A 2072 05-APR-2001;
Infectio Diagnostic (1.D.) INC. (CA)

Location/Qualifiers
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Hetherington, S.V., Watson, A.S. and Patrick, C.C.
Sequence and analysis of the rpoB gene of Mycobacterium smegmatis Antimicrob. Agents Chemother. 39 (9), 2164-2166 (1995)
Detection of a genetic locus encoding resistance to rifampin in mycobacterial cultures and in clinical specimens
Patent: US 5643723-A 1 01-JUL-1997;
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Mycobacterium smegmatis DNA polymerase (rpoB) gene, complete cds
U24494
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Actinomycetales; Corynebacterineae; Mycobacteriaceae;
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Pred. No. 36;
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Sequence 2072 from Patent WO0123604.
AX111339
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1081 c 1188 g
                                               Location/Qualifiers
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/organism="unknown"
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Best Local Similarity 100.
Matches 19; Conservative
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AX111339
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LUVQTOSFERLYGERRAYGALINGSERNPYGGLEEVLAELSFIEDESGSMSLSFSDPR
LUVQTOSFERLYGERRAYGALINGSERPPYGGLEEVLAELSFIEDESGSMSLSFSDPR
FDEYKASVDECKDKDWTYAAPLFVTAEFINNNTGEIKSGTVEWGDFPWATEKGTFIN
GTERVYVSQLVSRSCYYFDETIDKSFERTHSYKVIEGRGAMLEPDVBRADTEKGTFIN
GTERVYVSQLVSRSCYYFDETIDKSFERTHSYKVIEGRGAMLEPDVBRADTEKGTFIN
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ERWTTQDVAITPOGCYGERVASHDIDHFGNRRLFTGGSLGSVTARVNPFGFIETPVR
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PGGLSRERAGLEVRDVHPSHVGANAIKEFFGNSHGLIGJIGSLGSVTARVNPFGFIETPVR
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GRVXYVARAYRSAIVRGENTPERFERENTENGESTATTINSDDTV
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Mycobacterium tuberculosis H37Rv RNA-polymerase beta subunit (fpoB)
Hetherington,S.V.
Direct Submission
Submitted (lli-APR-1995) Seth V. Hetherington, Infectious Diseases,
St. Jude Children's Research Hospital, 332 N. Lauderdale, Memphis,
TN 38101, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Mycobacterium tuberculosis
Bacteria: Firmicutes; Actinobacteria: Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae;
Mycobacterium; Mycobacterium tuberculosis complex.
I (bases 1 to 3853)
Imboden, P., Troller, R., Marchesi, F., Telenti, A., Bodmer, T.,
Cole, S., Schopfer, K. and Burkart, T.
The robB gene of Mycobacterium tuberculosis
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    .3752
    /organism="Mycobacterium smegmatis"
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/protein_id="AAA91426.2"
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EDELPAGVNELVRVYVAQKRKISDGDKLAGRHGNKGVIGKILPVEDMPFLADGTPVDI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ANGCPIVDAGDRVEAGQVIADGPCTDDGEMALGKNLLVAIMPWEGHNYEDAIILSNRL
VEEDVLTSIHIEEHEIDARDTRLGAEEITRDIPNISDEVLADLDERGIVRIGAEVRDG
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KLHHLVDDKIHARSTGPYSMITQQPLGGKAQFGGQRFGEMAMQAYGAAYTLQELL
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Mycobacterium tuberculosis (strain Rv) DNA.
Mycobacterium tuberculosis
Bacteria: Actinobacteria: Actinobacteriae;
Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium
Luberculosis complex.
1 (bases 1 to 5084)
Miller, L. P., Crawford, J.T. and Shinnick, T.M.
The rpoB gene of Mycobacterium tuberculosis
Antimicrob. Agents Chemother. 38 (4), 805-811 (1994)
Submitted (11-JUL-1994) Paul Imboden, Institute for Medical
Microbiology, University of Berne, Friedbuehlstrasse 51, Berne,
3010, Switzerland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                  /organism-"Mycobacterium tuberculosis"
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/protein_id="AAA20242.2"
/db_xref="G1:7144499"
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/strain="Rv"
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576. .>3853
                                                Location/Qualifiers
1. .3853
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/transl_table=11
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576. .>3853
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Matches 19; Conservative
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/ULTAIS LA LION-"MINEGILADSRQSKTAASPSPSRPQSSSNNSVPGAPNRVSFAKL
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RDTVGYRIDKRRRQPVTVLLAALGAFFSEQIVERFGESEIMSGTLEKONTVGTDEALLD
IYRKLERGERPTRESAQTLENLFFKEKRYDLARVGRYKVNKKLGLHVGEPITSSTLT
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ANQCPTYDAGDNYRVAGACVITECPERALLGRIFTRIPIPINGSGRYVEDINGTRYFREBE
DILJOKTYTPKGGYCTYGRAEITRDIPINISDEVLADHFRINGENY
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KLHHLVDDKIHARSTGPYSMITQQPLGKROAFGERFRULKAISF
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HIWYEKGVPSRLGYLLDLAPKDLEKIIYFAAYVITSVDEEMRHNEL"
1534 c 1691 g 890 t
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[ tbases 1 to 1932]
Fleischmann, R.D., Alland, D., Elsen, J.A., Carpenter, L., White, O., Peterson, J., DeBoy, R., Dodson, R., Gwinn, M., Haft, D., Hickey, E., Kolonay, J.F., Nelson, W.C., Umayam, L.A., Ermolaeva, M.,
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Mycobacterium tuberculosis CDC1551
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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AE006964 AE000516
AE006964.1 GI:13880217
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                       1065. .4598
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1065. .4598
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Best Local Similarity 100.
Matches 19; Conservative
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REFERENCE AUTHORS

JOURNAL

TITLE

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FEATURES

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CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 / CLAINS Lat Con-MLEGGILADSROSKTAASPSPSRPOSSSNNSVPGAPNRVSFAKL
REPLEVPGLLDVQTDSFEWLIGSPRWRESAAERGDVNPVGGLEEVLYELSPIEDFSGS
MSLSFSPRRPDVKAPVDECKROWTYAAFLETNNWTGEIR GSGTVFWADFPMA
TERGTFI INGTERVVAPDECKROWTYAELETNNWTGEIR GSGTVFWADFPMA
TEKGTFI INGTERVVAPOKARPDECKROWTYAELESTUNGFEILD
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EVEYVESEVOYWOVSDEIVYLTADEEDRHVVVQANSPIDAORFRYBRRAGG
EVEYVESEVOYWOVSENGIVILTANDEDRHALMALGALILLSN
LVGTGMELRAAIDAORDAVAARAIPFLEHDDANRALMGANWORQAVPLVRSRAG
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LVGTGMELRAAIDAORGVROHOSTUNGTONIGTROT VRRUF
CANOCPI VDAGGRYGAGGATILLSNIF
CANOCPI VDAGGRYGAGARGNOKOVIGIRVESRE
DEDLELAGGURLANDYOFRGRYSTSRODKLAGRHGKAVPHGESGKVIGIRVFSRE
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I ILMTHGVPRRMNIGOLLETHLGWAHSGMKVDAAKGVPDMAARLPDELLEAQPNAIV
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LTIKSDDTVGRANTYGENIPEPGIPESFKVLLKELQSLCINVEVLSSDGAAIE
LTIKSDDTVGRANTYGGEIPPEGIPESFKVLLKELQSLCINVEVLSSDGAAIE
LTIKSDDTVGRANTYGGGA
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GLFCEKIFGPTRDWECYGGYYKRRYRFKGIICERCGVEVTRAKVRRERMHIELAAPVT
HIWYFKGVPSRLGYLLDLAPKDLEKIIYFAAYVITSVDEEMRHNELSTLEAEMAVERK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LEDIWSTFTKLAPKÖLIVDENLYRELVDRYGEYFTGAMGAESIGKLIENFDIGAEAES
LRDVIRNGKGGKKLRALKRLKVVAAFQGSGNSPMGMVLDAVPVIPPELRPMVQLDGGR
FATSDLNDLYRRVINRNNRLKRLIDLGAPEIIVNNEKRMLQESVDALFDNGRRGRPVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GPGNRPLKSLSDLLKGKQGRFRQNLLGKRVDYSGRSVIVVGPQLKLHQCGLPKLMALE
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Salzberg,S.L., Delcher,A., Utterback,T., Weidman,J., Khouri,H.,
Milli,M. Wikula,A. and Bishai,W.
Whole genome comparison of Mycobacterium tuberculosis clinical and
laboratory strains
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="similar to GB:L27989 GB:L05910 GB:U12205 SP:P47766
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Fleischmann,R.D., Alland,D., Eisen,J.A., Carpenter,L., White,O., Peterschmann,R.D., Alland,D., Eisen,J.A., Carpenter,L., White,O., Peterson,J., Debby,R., Dodson,R., Gwinn,M., Haft,D., Hickey,E., Kolonay,J.E., Nelson,W.C., Umayam,L.A., Ermolaeva,M., Salzberg,S.L., Delcher,A., Utterback,T., Weidman,J., Khouri,H., Gill,J., Mikula,A. and Bishai,W.
Submission
Submitted (25-APR-2001) The Institute for Genomic Research, 9712 Medical Center Dr. Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /transl_table=11
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3744. 7694
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163. .3699
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                                                                                                                                                              Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        source
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gene

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SIFAALGVVSGTQLDPCQSPRPVSVIHIHGTADPLVRYHGGPGAGFARIDGPPVPDLN
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1585. 2664
//gene="Rv0655"
1585. 2664
//gene="Rv0655"
1585. 2664
//gene="Rv0655, (MTC1376.21), len: 359, abc transporter,
FASTA score: FREE_ECOLI F45393 hypothetical abc
transporter atp-binding (269 aa) opt: 644 z-score: 721.8
E(): 3.4e-33 (38.5% identity in 244 aa overlap); contains
FS00017 AFP/CTP-binding site motif A, PS00211 ABC
transporters family signature, highly similar to M. leprae
MKL_MYCLE P30769 possible ribonuclectide transport atp-
(347 aa) opt: 2021 z-score:2244.4 E(): 0, (92.2% identity
in 335 aa overlap). Also similar to many otherM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                available on the World Wide Web.

(URL, http://www.sanger.ac.uk/Projects/M_tuberculosis/) CDS have been renumbered from the original cosmid submissions but the old gene designations are in brackets after the new gene numbers. Gene prediction was based on a Hidden Markov Model of TB genes implemented in TBparse (Krogh) supplemented with visual inspection of positional base preference in codons, especially where there is an increase in the observed/expected third position G + C. CAUTION: In some cases we may not have predicted the correct initiation codon. Where possible we choose an initiation codon (atg, gtg, or ttg) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon; if this cannot be identified we choose the most upstream initiation codon.
                                                                                                                                                                                                                  Submitted (11-JUN-1998) Submitted on behalf of the Mycobacterium tuberculosis sequencing and mapping teams, Sanger Centre, Wellcome Trust Genome Campus, Hinkton, Cambridge CB10 15A Unite de Genetique Moleculaire Bacteriene, Institut Pasteur, 28 rue du Docteur Roux, 75724 Paris Cedex 15, France E-mail: parkhill@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Rv0654, (MTC1376.22), len: 501. unknown, FASTA
score: 053353 LIGNOSTILBENE-ALPHA, BETA-DTOXYGENASE (485
aa) opt:280 z-score: 330.11 E(): 2.39-11, (28.5% identity
in 523 aaoverlapp, Also similar to M. tuberculosis protein
MTCY21C12.07c (29.5% identity in 522 aa overlap)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  / LTAIRS LATION—"MITTAGA AESONDY LEGELA PUSTEUTATO LPUTGRIPEHLOGRY
LRNGPRIPVAE LODAT THWFT AGA AESONDY LEGELA PUSTEUTATO LPUTGRIPED THA CHARLA LEGENT WITH AGA THA CHARLA 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Details of M. tuberculosis sequencing at the Sanger Centre are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="agga, possible rbs upstream of Rv0654"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
1. .19770
Acrganism=Mycobacterium tuberculosis H37Rv=
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57. .61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product-"hypothetical protein Rv0654"
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Nature 393 (6685), 537-544 (1998)
98295987
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="Rv0654"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="Rv0654"
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                                                                                                                      (bases 1 to 19770)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68. .1573
                                                                                                                                                                                        Direct Submission
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                                                                                                                                            Parkhill, J.
                                                                                        9634230
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                                                                                                              REFERENCE
AUTHORS
                                                                                                                                                                                 TITLE
JOURNAL
       JOURNAL
MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene
                                                                                 PUBMED
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                                                                                                                                                                                                                                                                                                                                                                                                    COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               / LTAINSTALT LION- "MSDTHVVTNQVPPLENYNPASSPVLIEALIOEGGWGLDEVNEV
GAISASCOAGNRGELADRNRPTLHTHDAYGYRVDEVEYDPAYHELMRTAITHGMHAAP
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VLADLAVEARAAT IT IEBWLAGATDNAVRGNETEALLRIGLAAAKYWVCKSTAHAAE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PEPADLDERTERLVARIAALPVNQLIMYKLALNSALLQQGVATSRMYSTVFDGAARHT
PEGHAFVADAVEHGFRDAVRRNDEPFGDYGRQASRV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
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Mycobacterium; Mycobacterium tuberculosis complex.

I (bases 1 to 19770)

Cole,S.T., Brosch,R., Parkhill,J., Garnier,T., Churcher,C.,
Harris,D., Gordon,S.V., Eiglmeier,R., Gas,S., Barry III,C.E.,
Tekaia,F., Badcock,K., Basham,D., Ebrown,D., Chillingworth,T.,
Connor,R., Davies,R., Devlin,K., Feltwell,T., Gentles,S.,
Hamlin,N., Holroyd,S., Hornsby,T., Jagels,K., Krogh,A., McLean,J.,
Rajandream,M.A., Rogers,J., Rutter,S., Seeger,K., Skelton,S.,
Squares,S., Sqares,R., Sulston,J.E., Taylor,K., Whitehead,S. and
Barrell,B.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MTC1376
Mycobacterium tuberculosis H37Rv complete genome; segment 32/162.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Mycobacterium tuberculosis H37Rv
Bacteria; Firmicutes: Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 19; DB 1; Length 19352;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
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13498. .14436
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/gene="MT0702"
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/gene="MT0703
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295972.1 GI:3261790
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Best Local Similarity
Matches 19; Conserv
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DEFINITION
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// Gene="Rv0657c"

// Complement(3530. 3885)

// Complement(3530. 3885)

// Gene="Rv0657c"

// Note="Rv0657c"

// Note="Rv
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ALARSRE"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="PS00017 ATP/GTP-binding site motif A" 2074. 2118
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/note="Rv6656"
/gene="Rv6656c"
/gene="Rv6656c"
/note="Rv6656c"
tuberculosis ABC transporters eg. MTCY253.24 (33.6% identity in 241 aa overlap)"
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complement(3761, .4477)
/gene="Rv0658c"
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/gene="Rv0658c"
/note="Rv0658c, (MTC1376.18), len: 238,
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CDS

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SAGVLALALAAPTVVAAGLAILITRLRGNGLRTDLRLRWSWRGLRLGLWFGFGGMLVT
IPASLVYTAIVGPEANSAVNRIFGGGRRASWRWALLVVVEVAPLCEEIIYRGLLWG
YDD:RWGRWAALLVYTVVYFALAHLEFARAPLLVVVAIPIALARFYSGGLLASIVTHOV
TNLLPGIVLLLGCITGLRGTSLP"
COMPLement(4480. .4483)
Anote="possible RBS upstream of Rv0658c"
Complement(4753. .5061)
/gene="Rv0659c"
                                                                                                                                                                                                    complement(4753..5061)
/gene="Rv0659c"
/note="Rv0659c, (MTC1376.17), len: 102; unknown, similar
to YWAS WYCTU 010867 hypothetical 12.3 kd protein cy39.28
(114 aa), fasta scores; opt: 144 z-score: 213.2 E():
7.3e-05, 30.8% identity in 107 aa overlap. Also similar to
MTCV09F9.22 (32.7% identity in 101 aa overlap)*
//cransl_table=11
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LVSELELTAVENRVPSDCVVNFDNIHTLPRTAFRRRITRLSPARLHEACQTLRASTGC
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complement(5048. .5293)
/gene="Rv0660c"
/note="Rv0660c"
/note="Rv0660c, (MTC1376.16), len: 81, some similarity la RAD16485_130 Halobacterium sp; NRC-1 plasm (100 aa), /codon_start
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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19; Conserv
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Best Local Si
Matches 19;
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CDS

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Minimum DB
Maximum DB
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Waximum Match 100%
Listing first 45 summaries
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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length: 2000000000
                                                          IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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208
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em_gss_vrt:*
em_gss_fun:*
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                                                                                em_gss_mus:*
em_gss_other:*
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em_gss_inv:*
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	æ			SUMMARIES	
	Query				
Score	Match		В	ID	Description
	72.3		9	AI770311	AI770311 42 Mycoba
43.4	20.9	877	17	AQ687771	A0687771 nhxh00751
42.2	20.3	568	<u>1</u> 3	BI995346	BI995346 1031026F0
39	18.8	326	10	BE359066	BE359066 DG1 38 F0
39	18.8	444	12	BE918452	BE918452 OVI 4 AOA
39	18,8	520	13	BI246073	BI246073 [P1_68_D0

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45	44	43	42	41	40	9	8	۷.	6	, ,	4	. W	32	ω	30	29	22	27	26	25	24	N W	22	21	20	19	18	17	16	15	14	13	12		10	ع د	· œ	7
7.	38.2	œ	œ	39	39	39	39	39	39	9	39	39	39	39	39	39	39	39	39	9	<u>.</u>	9	39	39	39	9	39	39	39	39	39	39	39	9	39		39	39
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D F	1074667 TD1 14 E	STROOM BYELS	G047785 OV1 27 C	G605028 B1772 B3	G048108 OV1 27 G	E917821 OV1 7	E356124 DG1 122	G412409 OV2 33 F	G412523 OV2 35 D	G356764 OV2 9 F	G048276 OV1 16 B	G605900 RHIZ2 8	E918690 FM1 1 D	918704 FM1 1 F	G048093 OV1 27	G049396 OV1 19	E918695 FM1 1 D	M317840 OV1	7926 OV1 7	G411895 OV2	18122 OV1	49324 OV1	18149 OVI	18608 OV1	18234 OV1	936 OV1	18401 OV1 3 BO	18202 041	18353 OV1 2 F1	05810 BHT7	918453 OV1	22583 DG1 45 F	17902 OV1	G649762 RHIZ2 83	G412695 OV2 33 F	E918899 FM1 1 E1	187 DG1_26	1074353 IP1_14_E

REFERENCE AUTHORS TITLE ACCESSION VERSION KEYWORDS SOURCE FEATURES LOCUS DEFINITION RESULT 1 A1770311/c COMMENT JOURNAL MEDLINE ORGANISM Mycobacterium Laboratory
Institute of Molecular and Cell Biology
30 Medical Drive, Singapore 117609, Republ
Tel: 65 874 3011
Fax: 65 779 1117
Email: mcbbom@fancb.nus.edu.sg
Insert Length: 1282 Std Error: 0.00
Seq primer: T3 Forward; T7 Backward. Mycobacterium smegmatis.

Mycobacterium smegmatis
Bacteria; Actinobacteria; Actinobacteria; Actinobacteria;
Bacteria; Actinobacteria;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.

1 (bases 1 to 1282)
Murugasu-Oel,B., Tay,A. and Dick,T.
Upregulation of stress response genes and ABC transporters in anaerobic stationary-phase Mycobacterium smegmatis

Mol. Gen. Genet. 262 (4-5), 677-682 (1999) A1770311 1282 bp mRNA linear EST 24-JAN-2000 42 Mycobacterium anaerobic stationary phase library Mycobacterium smegmatis cDNA, mRNA sequence.
A1770311 Contact: Murugasu-Oei, B. EST AI770311.1 GI:6742680 Location/Qualifiers
1. .1282 Republic of Singapore

ALIGNMENTS

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REFERENCE
AUTHORS
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                                                                                                                    Clemson University Genomics Institute Clemson University 100 Jordan Hall, Clemson, SC 29634, US Tel: 864 656 7288 Fax: 864 656 4293
                                                                                                                                                                                                                                                          Wing,R.A. and Dean,R.A.
A BAC End Sequencing Framework to Sequence the Rice Genome Unpublished (1998)
                                             Email: rwing@clemson.edu
Seq primer: TAATACGACTCACTATAGGG
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                    Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AQ687771 877 bp DNA linear GSS 01-JUL-1999 nbxb0075L01f CUGI Rice BAC Library Oryza sativa genomic clone nbxb0075L01f, DNA sequence.
                                                                                                                                                                                                                                             Contact: Wing RA
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DNASE I was heat-inactivated at 750c for 5 min and removed by using RNeasy columns followed by phenol extraction and ethanol precipitation. The RNA preparations were confirmed to be free of genomic DNA contamination by carrying out PCR and RT-PCR using the Access kit (Promega) and primers specific for the histone-like protein gene hip (Lee et al., 1989). CDNA was synthesized using random hexamer primers (Promega) and Stratagene's CDNA synthesis kit. CDNA fragments were ligated into lambda ZAP II vector and packaged in vitro using Stratagene reagents. "
                         quality sequence stop: 85
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/strain="mc2155"
/db_xref="taxon:1772"
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82.7%;
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Pred. No. 2e-29;
D; Mismatches 36;
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Duke University
Durham, NC 27708-1000
Tel: 919 613 8159
Fax: 919 613 8177
                                                                                                                                                                               1 (bases 1 to 568)
Grossman,A., Chang,C.-W., Davies,J., Harris,E., Hauser,C., Lefeb,
.P., McDermott,J.P., Shrager,J., Silflow,C. and Stern,D.
Analyses of the Chlamydomonas reinhardtii Genome: A Model,
Unicellular System for Analyzing Gene Function and Regulation in
                                                                                                                                                                                                                                                                                                   Chlamydomonas reinhardtii.
Chlamydomonas reinhardtii
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B1995346 bp mRNA linear EST 25-C 1031026E07.y2 C. reinhardtii CC-1690, Stress II (normalized) Lambda Zap II Chlamydomonas reinhardtii cDNA, mRNA sequence.
                                                                                                 Contact: Charles Hauser
DCMB Box 91000
                                                                                                                                               Unpublished (2001)
                                                                                                                                                                Vascular Plants. Project: 1031
                                                                                                                                                                                                                                                                                                                                                                                                            BI995346.1 GI:16430136
EST.
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/tissue_type="Leaf"
/lab_host="E. coli DH10B"
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/cu_tivar="Nipponbare"
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAAGGAGAGCGGCTTCGAGGTGGTGCACGGCCTGTTGAACAGGGTCATGGAGGTGCTGGG 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CGACAAGCCCGTGGGCGTGTTCGGCAT 457
                  Unpublished (2000)
Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
                                                                                                                                                                  An EST database from Sorghum:
                                                                                                                                                                                                                                             sorghum bicolor
Sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoldeae; Andropogoneae; Sorghum.
                                                                                                                                                                                                           Cordonnier-Pratt, M.-M., Gingle, A., Marsala, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                      BE359066 326 bp
DG1_38_E06.g1_A002 Dark Grown 1
                                                                                                                                                                                                                                                                                                                                                                                             BE359066.1
                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence.
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                                                                                                                                                                                                                                        (bases 1 to 326)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Anol: Stress condition II library, constructed by John Davies and Jeffrey McDermott, combines cDNAs from CC-1690 cells grown to mid-log phase in TAP (NH4+ - containing) and shifted to TAP - NO3- (24hrs); H2 production conditions (0, 12hr, 24hr) see Melis et al.,(2000) Plant Phys. 122: 127-135; TAP + H202 (1, 12, 24 hr); TAP + sorbitol (1, 2, 6, 24 hr); TAP + Cd (1, 2, 6, 24 hr). PolyA mRNA was purified from each sample, pooled and cDNA synthesized. The cDNA was directionally cloned into lambda ZaP II (Stratagene) in the EcoRI (5') and XhoRI (3') sites. PBluescript II SK- plasmids were excised from the lambda ZAP clones by superinfection with ExAssist (Stratagene) phage. The library was normalized using method 4 described in Bonaldo et al., (1996) Genome Research 6: 791-806."
mmpratt@uga.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                chauser@duke.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Research 6:
206 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism-"Chlamydomonas reinhardtii"
/strain="CC-1690 wild type mt+ 21gr"
/db_xref-"taxon:3055"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="C. reinhardtii CC-1690, Stress II (normalized), Lambda Zap II"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Vector:
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Pred. No. 0.4;
0; Mismatches 103;
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                                                                                                                                                                    dark-grown seedlings
                                                                                                                                                                                                                                                                                                                                                                                                                                                    mRNA linear EST 20-
(DG1) Sorghum bicolor cDNA,
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RESULT 5
BE918452
LOCUS
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AUTHORS
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ORGANISM
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GATCACGCTGAAGGTGGCCAAGGCGGCGGCGGCGGAGGGCGAGGGTGAGGCCGGCGCCGT 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCTGCATGTCGGCGAGCCCATCACGTCGACGCTGACGCGAAGAAGACGTCGTGGCCAC 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAAGGAGACCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CGTCAACTGGTCCATGGAGTTCGACAAGGCCAACGACCAGGTGCCCGACCCGGACGTCAT 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                  An EST database from Sorghum:
Unpublished (2000)
Contact: Cordonnier-Pratt MM
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BE918452
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                                                      High quality sequence start: High quality sequence stop:
                                                                                                                                                                                                                                                                                                                                      Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BE918452 444 bp mrNA linear E. OV1_4_A04.gl_A002 Ovary 1 (OV1) Sorghum bicolor cDNA,
                                                                                                                             Seq primer: PolyTMix
                                                                                                                                                                                                                            Sequences have been
                                                                                                                                                                                                                                                                                          Plant Sciences Bui
Tel: 706 542 1860
Fax: 706 583 0210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Sorghum.
                                                                                                                                                                                          below Phred quality 16.
                                                                                                                                                                                                                                                        Email: mmpratt@uga.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cordonnier-Pratt, M.-M.,
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                                                                                                                                                                   is 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sorghum bicolor
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Seq.primer: PolyTMix
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nilarity 50.3%;
Conservative
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//db_xref="taxon:4558"
/clone_lib="Dark Grown 1 (DG1)"
/clone_lib="Dark Grown 1 (DG1)"
/note="Organ: 5-day-old dark-grown seedlings; Vector:
/note="Organ: 5-day-old dark-grown seedlings; Vector: 1 |
/note: 5-day-old dark-grown seedlin
Location/Qualifiers
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                                                                                                                                                                         trimmed to exclude PolyA, vector and regions 16. The threshold for highest quality sequence
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Pred. No. 2.5;
0; Mismatches
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                                                         : 90
427
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ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GATCACGCTGAAGGTGGCCAAGGCGGCGGCGGCGGAGGGCGAGGGTGAGGCCGGCGCGT 28:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CGTCAACTGGTCCATGGAGTTCGACAAGGCCAACGACCAGGTGCCCGACCCGGACGTCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCTGCATGTCGGCGAGCCCATCACGTCGTCGACGCTGACCGAAGAAGACGTCGTGGCCAC 121
                                                                                                                                                                           Email: mmprattleya.edu

Email: mmprattleya.edu

Sequences have been trimmed to exclude PolyA, vector and regions

below Phred quality 16. The threshold for high quality sequence pelow Phred quality 16. The threshold for high quality sequence 20. Three-prime sequences, which are obtained with PolyTWix or Townsoning primer, are presented as the reverse complement.
                                                                                                                                                                                                                                                                                   Unpublished (2001)
Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271,
Tel: 706 542 1860
Fax: 706 583 0210
                                                                                                                                              POLYA-NO.
                                                                                                                                                                                                                                                                                                                                                                                                     An EST database from Sorghum: developing preanthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                Klein, R.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Sorghum.
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                                                                                                                                                             quality sequence stop: 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
/db_xref="taxon:4558"
/clone_lib="Immature pannicle 1 (IP1)"
/note="Organ: Developing preanthesis pannicles; Vector:
pBluescript II SK(-) from Lambda Zap II; Site_1: xhoI;
                                                                        /organism="Sorghum bicolor"
/cultivar="BTx623"
                                                                                                                             Location/Qualifiers
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/clone_lib="Ovary I (OVI)"
/note="Organ: Mix of ovaries of varying immature stages from 8 week-old plants; Vector: pBluescript II from Lambda Zap II; Site_1: XhoI; Site_2: EcoRI; The library was made from poly-A RNA in the cloning vector lambda Zap II.
Clones to be sequenced were prepared by mass excision."

131 c 142 g 69 t
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/db_xref="taxon:4558"
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n bicolor cDNA,
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122 CATCGAATATCTGGTCCGCTTGCACGAGGGTCAGACCACGATGATCGTTCCGGGCGGCGT 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62 GCTGCATGTCGGCGAGCCCATCACGTCGTCGACGCTGACCGAAGAAGAAGACGTCGTGGCCAC 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271,
Tel: 706 542 1860
Fax: 706 583 0210
                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: mmpratt@uga.edu
Sequences have been trimmed to exclude PolyA, vector and regions
below Phred quality 16. The threshold for high quality sequence is
20. Three-prime sequences, which are obtained with PolyTMix or T7
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                                                                                                                                                                                                                                                                                                                                         High quality sequence start: 13 High quality sequence stop: 528
                                                                                                                                                                                                                                                                                                                                                                                               sequencing primer, are presented as the reverse complement. Seq primer: T7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (2001)
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mRNA sequence.
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/Clone_lib="Immature pannicle 1 (IP1)"
//note="Organ: Developing preanthesis pannicles; Vector:
pBluescript II SK(-) from Lambda Zap II; Site_1: XhoI;
Site_2: EcoRI; The library was made from poly-A RNA in the
cloning vector lambda Zap II. Clones to be sequenced were
prepared by mass excision."

147 c 164 g 114 t
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a 153 c 178 g 76 t
                                                                                                                                                                                       /db_xref="taxon:4558"
                                                                                                                                                                                                                                      /organism="Sorghum bicolor"
                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                   /cultivar="BTx623"
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h bicolor cDNA,
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                                                                                                             Local
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                    CAAGGTGGTGTCGTACAGCGTGGTGGACGGCGAGCTGGTTGACTTCTACAAGAACTTCAA 37:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CGAGGTGCCGG 192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAAGGAGACCG
                                                                                                                                                                                                                                                                                                                                                                                                                        Email: mmpratt@uga.edu
Sequences have been trimmed
below Phred quality 16. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukāryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoldeae; Andropogoneae; Sorghum.

1 (bases 1 to 529)
Cordonnier-Pratt, M.-M., Gingle, A., Marsala, C., Sudman, M. and Pratt
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EST.
                                                                                                                                                                                                                                                                                                                                                          High quality sequence stop: 388 POLYA=No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271,
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                                                                                                            Similarity
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                                                                                                                                                                   /notes Torgan: 5-day-old dark-grown seedlings; Vector: /notes Torgan: 5-day-old dark-grown seedlings; Vector: Lambda Zap; Site_1: XhoI; Site_2: EcoRI; The library was made from poly-A RNA in the cloning vector lambda Zap II. Clones to be sequenced were prepared by mass excision." a 156 c 182 g 75 t
                                                                                                                                                                                                                                                                /clone_lib="Dark Grown 1 (DG1)"
                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                 /organism="Sorghum bicolor"
/db_xref="taxon:4558"
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Sorghum.

1 (bases 1 to 535)

Cordonnier-Pratt, M.-M., Gingle, A., Sudman, M., Marsala, C. and Pratt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271,
Tel: 706 542 1860
Fax: 706 583 0210
                                                                                                                                                                                                                        Similarity
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Sequences have been tr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           An EST database from Sorghum: floral-induced meristems Unpublished (2000) Contact: Cordonnier-Pratt MM
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/db_xref="taxon:132711"
/clone_1lb="Floral-induced Meristem 1 (FM1)"
/clone_1lb="Floral-induced meristems; Vector:
pBluescript II from Lambda Zap II; Site_1: XhoI; Site_2:
pBluescript II from Lambda Zap II; Site_1: XhoI; Site_2:
pBluescript II from Lambda Zap II; Site_1: Above Individual Site of the street of the street
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The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
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Sorghum bicolor
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primer: JEN REV
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/db_xref="taxon:4558"
/db_xref="taxon:4558"
/clone_lib="ovary 2 (oV2)"
/note="Organ: Mix of ovaries of varying immature stages from 8-week-old plants; Vector: pBluescript II from Lambda Zap II; Site_1: XhoI; Site_2: EcoRI; The library was made from poly-A RNA in the cloning vector lambda ZAP II.
Clones to be sequenced were prepared by mass excision."
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RESULT 12
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                                                                                                      sequence.
BE917902
BE917902.1
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OV1_7_E07.
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Sorghum.
                                                    Sorghum bicolor
                                                                       sorghum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271,
Tel: 706 542 1860
Fax: 706 583 0210
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: mmpratt@uga.edu
Seq primer: JEN REV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             An EST database from Sorghum: Sorghum propinguum rhizomes Unpublished (2000)
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RHIZ2_83_C10.b1_A003 Rhizome2
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Panicoideae; Andropogoneae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /Organism="Sorghum propinquum"
/db_xref="taxon:132711"
/db_xref="taxon:132711"
/clone_lib="Rhizome2 (RHIZ2)"
/note="Organ: Rhizomes; Vector: pBluescript II from Lambda Zap II; Site_1: XhoI; Site_2: EcoRI; The library was made from poly-A RNA in the cloning vector lambda ZAP II.
Clones to be sequenced were prepared by mass excision."
a 158 c 181 g 79 t
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50.3%;
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(RHIZ2) Sorghum
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Sorghum bicolor
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propinguum cDNA, mRNA
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An EST database from Sorghum: dark-grown suppublished (2000)
Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of P.
                                                                                                Cordonnier-Pratt, M.-M., Gingle, A., Marsala, C.,
                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Sorghum.

1 (bases 1 to 552)
                                                                                                                                                                                                                                                                                AW922583 552 | DG1_45_E10.g1_A002 Dark Grown
                                                                                                                                                                                     sorghum bicolor
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AW922583.1
                                                                                                                                                                                                                                                                     sequence.
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The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
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Sequences have been trimmed
below Phred quality 16. The
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Contact: Cordonnier-Pratt MM
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Cordonnier-Pratt, M.-M.,
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/note="Organ: Mix of ovaries of varying immature stages from 8 week-old plants; Vector: pBluescript II from Lambda Zap II; Site_1: XhoI; Site_2: EcoRI; The library was made from poly-A RNA in the cloning vector lambda Zap II. Clones to be sequenced were prepared by mass excision."

a 164 c 183 g 80 t
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/db_xref="taxon:4558"
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50.3%;
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31) Sorghum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: 706 542 1860
Fax: 706 583 0210
Email: mmpratt@uga.edu
Sequences have been trimmed the below Phred quality 16. The t
                                                                                                                                                                                                                                                 Sorghum bicolor Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Sorghum.

1 (bases 1 to 555)

1 (bases 1 to 555)
                                                                                      Plant Sciences Building,
Tel: 706 542 1860
Fax: 706 583 0210
                                                                                                                    Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant
Plant Sciences Building, Rm. 2502, Athens, GA 2
                                                                                                                                                                          Unpublished (2000)
Contact: Cordonnier-Pratt MM
                               below Phred quality 16.
                                                    Email: mmpratt@uga.edu
Sequences have been tr
                                                                                                                                                                                                                                            Cordonnier-Pratt, M.-M., Gingle, A., Marsala, C.,
                    is 20.
                                                                                                                                                                                                          An EST database from Sorghum: ovaries of varying
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EST.
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OV1_4_A05.g1_A002 Ovary 1 (OV1)
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primer: PolyTMix
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/db_xref="taxon:4558"
/clone_1lb="bark Grown 1 (DG1)"
/clones to be sequenced were prepared by mass excision."

a 154 c 173 g 117 t
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Sorghum bicolor cDNA,
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30602-7271,
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VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CATCGAATATCTGGTCCGCTTGCACGAGGGTCAGACCACGATGATCGTTCCGGGCGGCGT 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Sorghum propinguum.
Sorghum propinguum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Epermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Sorghum.

1 (bases 1 to 557)
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                                                                                                                                                                                High quality sequence start: 15 High quality sequence stop: 548
                                                                                                                                                                                                                       Email: mmpratt@uga.edu
Seq primer: PolyTMix
                                                                                                                                                                                                                                                            Plant Sciences Building,
Tel: 706 542 1860
Fax: 706 583 0210
                                                                                                                                                                                                                                                                                             Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
                                                                                                                                                                                                                                                                                                                                                           Unpublished (2000)
Contact: Cordonnier-Pratt MM
                                                                                                                                                                                                                                                                                                                                                                                                                                   Cordonnier-Pratt, M.-M., Gingle, A., Paterson, A., Sudman, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BG605810 557 bp mRNA linear EST 17-APR-2001 RHIZ2_81_G04.g1_A003 Rhizome2 (RHIZ2) Sorghum propinguum cDNA, mRNA
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/organisma"Sorghum propinquum"
/db_xref="taxon:132711"
/db_xref="taxon:132711"
/clone_lib="Rhizome2 (RHIZ2)"
/notce="Organ: Rhizomes; Vector: pBluescript II from Lambda Zap II; Site_1: XhoI; Site_2: EcoRI; The library was made from poly-A RNA in the cloning vector lambda ZAP II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Sorghum bicolor"
//db_xrefe"taxon;4558"
/clone_lib="ovary 1 (OV1)"
/notce="Organ: Mix of ovaries of varying immature stages
/rom 8-week-old plants; Vector: pBluescript II from Lambda
Zap II; Site_1: XhoI; Site_2: ECORI; The library was made
from poly-A RNA in the cloning vector lambda Zap II.
Clones to be sequenced were prepared by mass excision."
a 154 c 179 g 114 t
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Database :
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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208
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/cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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15 15 16 17 18	1121 1121 1121 1132 1133 1134 1135 1135 1135 1135 1135 1135	No.
31.2 31.2 31.2 31.2 31.2	88 88 88 88 88 88 88 35.6 34 32.4 31.4	Score
15.0 15.0 15.0 15.0 14.9	42.3 42.3 42.3 116.3 115.4 115.4	Query
278 704 752 936 8673 1287	5096 5099 5099 5099 5099 3756 252 680 271 11164 111220 36778	Query Match Length
12 12 10 12	10 10 10 10 10 10 10 10	DВ
US-09-294-093B-1392 US-10-062-254-109 US-10-062-254-111 US-09-815-242-7776 US-09-815-242-7474 US-09-815-242-7474 US-10-029-715-3	US-99-984-711-5 US-10-075-460-5 US-09-887-052-1 US-99-887-052-3 US-09-881-132-425 US-99-881-132-267 US-99-881-132-267 US-99-815-242-7738 US-99-815-242-7738 US-99-815-242-7738 US-99-815-242-77696 US-09-815-242-77696 US-09-861-289-32 US-09-861-289-3	ID
377111	Sequence 5, Appli Sequence 5, Appli Sequence 1, Appli Sequence 3, Appli Sequence 425, Appli Sequence 425, Appli Sequence 8901, App Sequence 7607, App Sequence 7738, App Sequence 7738, App Sequence 7738, Appli Sequence 7738, Appli	Description

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14.2 14.2 14.2	14.3 14.3 14.3	1144	14.5	14.8 14.8 14.7 14.7	14.9 14.9 14.8
914 914 1115	1305 2430 13613 897	14272 1455 2329 4863 592	1298 2109 6252	1440 1534 264 953 1266	3084 8673 337 1293
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US-09-964-824A-553 US-09-880-107-2357 US-09-981-353-126	US-09-815-242-7730 US-09-861-289-23 US-09-861-289-3 US-09-861-289-3 US-09-815-242-4001	US-09-87/0-162A-23 US-09-887-576-782 US-09-816-828-9 US-09-815-242-4071 US-09-894-467-6	US-09-925-300-682 US-09-915-242-7761 US-09-964-824A-313	US-09-796-858-7 US-09-765-231A-20 US-09-765-231A-20 US-09-823-876-4989 US-09-452-239-45 US-09-815-242-7920	US-09-881-752A-79 US-09-815-242-7313 US-09-960-352-10223 US-09-815-242-7978 US-09-815-242-7978
	Sequence 7730, Ap Sequence 7730, Appl Sequence 23, Appl Sequence 3, Appli Sequence 4001, Ap	Sequence 23, Appl Sequence 782, Appl Sequence 9, Appli Sequence 4071, Ap	Sequence 10, Appl Sequence 682, App Sequence 7761, Ap Sequence 313, App	7, 20, 498 45,	

ALIGNMENTS

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APPLICANT: MECKEL, Betting
APPLICANT: BATHE, Brigitte
APPLICANT: STEPHAN, Hans
APPLICANT: STEPHAN, Hans
APPLICANT: KREUTZER, Caroline
APPLICANT: HERMANN, Thomas
APPLICANT: HERMANN, Thomas
APPLICANT: BINDER, Michael
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE IPSL GENE
FILE REFERENCE: 204209US0
CURRENT APPLICATION NUMBER: US/09/984,711
CURRENT APPLICATION NUMBER: DE10108230.9
PRIOR APPLICATION NUMBER: DE10108230.9
PRIOR FILTMG DATE: 2001-0-16
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin version 3.1
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FEATURE:
HAME/KEY: CDS
LOCATION: (702)..(4196)
OTHER INFORMATION:
US-09-984-711-5
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                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 5
LENGTH: 5096
TYPE: DNA
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                                                                                                                                                           Query Match 42.3%;
Best Local Similarity 68.5%;
Matches 137; Conservative
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                                                                          1635 GGTGGCGACCACGATGGTTTGATGACTCTTACTGAAGAGGACATCGCAACCACCATCGAG 1694
                      0; Mismatches 60; Indels
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CURRENT APPLICATION NUMBER: US/10/075,460
CURRENT FILING DATE: 2002-02-15
PRIOR APPLICATION NUMBER: DE 10107230.9
PRIOR FILING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: DE 10162386.0
PRIOR FILING DATE: 2001-12-19
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin version 3.1
SEQ ID NO 5
LENGTH: 5099
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                                                                                                                               Sequence 1, Application US/09887052 Patent No. US20020119537A1 GENERAL INFORMATION:
                                                    APPLICANT:
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Best Local Similarity 68.5%;
Matches 137; Conservative
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                                                                                          APPLICANT: MOECKEL, Bettina APPLICANT: BATHE, Brigitte
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APPLICANT: BATHE, BRIGIT
APPLICANT: HANS, STEFAN
APPLICANT: KREUTZER, CAN
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APPLICANT: PFEFFERLE, WALTER
APPLICANT: BINDER, MICHAEL
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE TPSL GENE
FILE REFERENCE: 218472USOX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: CDS
LOCATION: (702)...
OTHER INFORMATION:
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CANT: BINDER, Michael
OF INVENTION: NUCLEOTIDE SEEQUENCES WHICH CODE FOR THE rpoB GENE
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                                                                         HERMANN, Thomas
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HERMANN, THOMAS
PFEFFERLE, WALTER
                                                      PFEFFERLE, Walter
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0; Mismatches
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; NAME/KEY: CDS
; LOCATION: (702)..(4196)
US-09-887-052-1
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SEQ ID NO 1
LENGTH: 5099
TYPE: DNA
ORGANISM: Corynebacterium glutamicum
                                                                                      Matches
                                                                                                  Query Match 42.3%;
Best Local Similarity 68.5%;
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Matches 137; Conservation
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APPLICANT: BINDER, Michael
TITLE OF INVENTION: NUCLEOTIDE SEEQUENCES WHICH CODE FOR THE rpoB GENE
FILE REFERENCE: 204212USOX
CURRENT APPLICATION NUMBER: US/09/887,052
CURRENT FILING DATE: 2001-06-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: MOECKEL, Bettina
APPLICANT: BATHE, Brigitte
APPLICANT: HERMANN, Thomas
APPLICANT: PFEFFERLE, Walto
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PRIOR APPLICATION NUMBER: DE10107229.5
PRIOR FILING DATE: 2001-02-16
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CURRENT FILING DATE: 2001-06-25
PRIOR APPLICATION NUMBER: DE10107229.5
PRIOR FILING DATE: 2C01-02-16
NUMBER OF SED ID NOS: 8
                                                                                                                                                                                                                       LENGTH: 5099
TYPE: DNA
ORGANISM: Corynebacterium glutamicum
FEATURE:
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1578 AAGCGCTACGACCTGGCTCGCGTTGGTCGTTACAAGATCAACCGCAAGCTCGGCCT---T 1634
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                                                                                Conservative
                                                                              Score 88; DB 10;
Pred. No. 3.5e-17;
0; Mismatches 60
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Pred. No. 3.
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3.5e-17;
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69 GTCGGCGAGCCCATCACGTCGTCGACGCTGACCGAAGAAGACGTCGTGGCCACCATCGAA 128

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RESULT 6
US-09-841-132-425
US-09-841-132-425
: Sequence 425, Application US/09841132
: Patent No. US20020061848A1
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; NAME/KEY: CDS
; LOCATION: (702)..(4196)
US-09-887-052-5
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US-09-887-052-5
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GENERAL INFORMATION:
APPLICANT: Bhatia, Ajay
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Probst, Peter
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT,
TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
FILE REFERENCE: 210121.469C8
CURRENT APPLICATION NUMBER: US/09/841,132
CURRENT FILING DATE: 2001-04-23
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CURRENT FILING DATE: 2001-06-25
PRIOR APPLICATION NUMBER: DE10107229.5
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PALENTIN VERSION 3.0
SEQ ID NO 5
LENGTH: 5099
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Best Local :
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APPLICANT: BATHE, Brigitte
APPLICANT: HERMANN, Thomas
APPLICANT: HERMANN, Thomas
APPLICANT: PFEFFERLE, Walter
APPLICANT: BINDER, Michael
TITLE OF INVENTION: NUCLEGOTIDE SEEQUENCES WHICH CODE FOR THE rpob GENE
FILE REFERENCE: 204212USOX
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Local Similarity 68.5%;
les 137; Conservation
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Pred. No. 3.5e-17;
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RESULT 8
US-09-841-132-267
; Sequence 267, Application US/09841132
; Patent No. US20020061848A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                        ; LENGTH: 252
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: 701101828H1
US-09-878-574-8901
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US-09-878-574-8901
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: La Rosa, Thomas J.
APPLICANT: Thompson, Michael D.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(15401)B
CURRENT APPLICATION NUMBER: US/09/878,574
CURRENT FILING DATE: 2001-12-21
PRIOR FILING DATE: 1999-06-14
NUMBER OF SEQ ID NOS: 15775
SEQ ID NO 8901
APPLICANT: Bhatia, Ajay
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Probst, Peter
                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                Matches
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SOFTWARE: FASTSEQ for Windows Version 3.0/4.0
SEQ ID NO 425

LENGTH: 3756

TYPE: DNA
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Best Local Similarity
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APPLICANT: La Ro
APPLICANT: Thomp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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                                                                                                                                                                202 CGGCATCGACTACGTCGACGCGCGCGAGGTCCTCACCCTCGCCGACGACG
                                                                                                                                                                                           137 CCGCTTGCACGAGGGTCAGACCACGATGATCGTTCCGGGCGGCGGCGTCGAGG 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           118 CCACCATCGAATATCTGGTCCGCTTGCACGAGGG 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    77 GCCCATCACGTCGTCGACGCTGACCGAAGAAGACGTCGTGGCCACCATCGAATATCTGGT 136
                                                                                                                                                                                                                                                                                                              82
                                                                                                                                                                                                                                                                                                                                                17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 GGCTGC---ATGTCGGCGAGCCCATCACGTCGTCGACGCTGACCGAAGAAGACGTCGTGG 117
                                                                                                                                                                                                                                  CCCCGTCATGGCCACGGCCCATCGGCCACTTCGTCGAGGCCCAGATCCTCGAGGCCCT
                                                                                                                                                                                                                                                                                                    CGGCGTGGCCCGCATGAGCGACCCGCAGCTCATCAAGGCCATCACGCGGGCCGTCACCAT 141
                                                                                                                                                                                                                                                                                                                                    CGACCTGGCCCGCGTCGGTCGCTATAAGGTCAACAAGAAGCTCGGGCTGCATGTCGGCGA 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GATTCCCATTAGACGACGAAACATTATCTCAAGTGACTTTGAGAAAAGAAGATGTTATCG
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50.0%;
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 Mismatches

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Pred. No. 0.16;
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                                                                                                                                                                                                                                                                                                                                                                                                         DB 10;
                                                                                                                                                                                                                                                                                                                                                                         85;
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                                                                                                                                                                                                                                                                                                                                                                                                      Length 252;
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TITLE OF INVENTION: IDentification of Essential Genes in TITLE OF INVENTION: Prokaryotes FILE REFERENCE: ELITRA.011A

CURRENT APPLICATION UNMBER: US/09/815,242

CURRENT FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR FILING DATE: 2000-05-23

PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR APPLICATION NUMBER: 60/247,593

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR APPLICATION NUMBER: 60/257,931
  US-09
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; TYPE: DNA
; ORGANISM: Chlamydia
US-09-841-132-267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-815-242-7738
                                                                                                                             SOFTWARE: FastSEQ for Windows Version SEQ ID NO 7738 LENGTH: 1437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 7738, Application US/09815242 Patent No. US20020061569A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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NAME/KEY: CDS
LOCATION: (1)...
09-815-242-7738
                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/269,308 PRIOR FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                        PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/
PRIOR FILING DATE: 2000-12-22
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SOFTWARE: FastSEQ for Windows Version 3.0/4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/841,132 CURRENT FILING DATE: 2001-04-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION FILE REFERENCE: 210121.469C8
                                                                               ORGANISM: Pseudomonas aeruginosa
                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               562 GCGCGTTGAAATATTTGATTCGTTTGCGAATGGG 595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    502 GCTTCCCATTAGACGACGAAACATTATCTCAAGTGACTTTGAGAAAAAGAAGATGTTATCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 GGCTGC---ATGTCGGCGAGCCCATCACGTCGTCGACGCTGACCGAAGAAGAAGACGTCGTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Carr, Grant J.
Yamamoto, Robert T.
Xu, H. Howard
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Trawick, John D.
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55.8%;
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Pred. No. 0.2;
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ORGANISM: Pseudomonas aeruginosa; FEATURE:
NAME/KEY: CDS
LCCATION: (1)...(711)
US-09-815-242-7723
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                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 7723
                                                                                                                                                               Query Match
Best Local Similarity
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Best Local S
                                                                                                                                                  Matches
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CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA 011A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                           TYPE: DNA
                                                                                                                                                                                                                                                                                                                              LENGTH:
                               152 TCAGACCACGATGATCGTTCCGGGCGGCGTCGAGGTGCCGGTGGAAACCGAC 203
           231
                                                                 171 GATGCTGCCGGGCGAGGACGGCCTGTCCATCTGCCGCCAGGTGCGCCCGCAGTTCGACGG
                                                                                                                                                                                                                                                                                                                                                                                                                              OR APPLICATION NUMBER: 60/207,727
OR FILING DATE: 2000-05-26
OR APPLICATION NUMBER: 60/242,578
OR APPLICATION NUMBER: 60/253,625
OR APPLICATION NUMBER: 60/253,625
OR APPLICATION NUMBER: 60/257,931
OR APPLICATION NUMBER: 60/257,931
OR APPLICATION NUMBER: 60/257,931
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             106 AAGACGTCGTGGCCACCATCGAATATCTGGTCCGCTTGCACGAGGGTCAGACCACGATGA 165
                                                                                        92 GACGCTGACCGAAGAAGACGTCGTGGCCACCATCGAATATCTGGTCCGCTTTGCACGAGGG 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            929 GCGTTCCGGGCGTCTTCG 946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 809 TCGACAAGCTGATCGTCGCGGTCGCCGTCGCCCGGTGACCACCGACCTGCTGGCCGCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46 TCAACAAGAAGCTCGGGCTGCATGTCGGCGAGCCCATCACGTCGTCGACGCTGACCGAAG 105
TCCGATCCTGATGCTCACCGCGCGCACCGACGATATGGACGAGGTACTCGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7723, Application US/09815242
o. US20020061569A1
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72; Conservative
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                                                                                                                                              Conservative
                                                                                                                                                             15.4%;
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52.2%;
                                                                                                                                              0;
                                                                                                                                                           Score 32; DB 10; Length 711; Pred. No. 0.78;
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                                                                                                                                              Mismatches
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                                                                                                                                          Indels
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 282
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                                                                                                                                          Gaps
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APPLICANT: XU, H. HOWARD

TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITA, 011A
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 05/19/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/21/078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-3
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR PRICING DATE: 2000-10-23
PRIOR PRICING DATE: 2000-11-27
PRIOR PRICING DATE: 2000-11-27
PRIOR PRICING DATE: 2000-12-72
                                                                     US-09-861-289-32/c
Sequence 32, Application US/09861289
Patent No. US20020110897A1
GENERAL INFORMATION:
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: LOCATION: (1)...(1164)
US-09-815-242-7696
                                                                                                                                                          RESULT 12
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US-09-815-242-7696
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                                                      APPLICANT: Sherman, D.H.
                                     APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 10110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ENGTH:
                                                                                                                                                                                                                   738
                                                                                                                                                                                                                                                                                                678
                                                                                                                                                                                                                                                                                                                                      143
                                                                                                                                                                                                                                                                                                                                                                 618 CATCTGCGACCAACTGATCGTCGGCGGCGGCATCGCCAACACCTTCCTCGCCGCGGCCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                               558 GGCGATCGTCGCCGGCTCCAAGGTTTCCACCAAGCTCGACGTGCTGAACAGCCTGGCCGG 617
                                                                                                                                                                                                                                                      203 CGACA 207
                                                                                                                                                                                                                                                                                                                                                                                          83 CACGTCGTCGACCGAACAAGAAGACGTCGTGGCCACCATCGAATATCTGGTCCGCTT 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23 GGCCCGCGTCGGTCATAAAGGTCAACAAGAAGCTCGGGCTGCATGTCGGCGAGCCCAT 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
                                                                                                                                                                                                                 CGCCA 742
                                                                                                                                                                                                                                                                                        ACACAAGGTCGGCAAGTCACTGTACGAGGCCGACCTGGTCGAGACCGCCAAGGCCATCGC 737
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              Liu, H.
Xue, Y.
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2yskind, Judith W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Trawick, John D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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Pred. No. 1.3;
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Sequence 5, Application US/09861289
Patent No. US20020110897A1
GENERAL INFORMATION:
APPLICANT: Sherman, D.H.
APPLICANT: Liu, H.
APPLICANT: Liu, H.
APPLICANT: Liu, H.
APPLICANT: Liu, Y.
APPLICANT: Liu, Y.
APPLICANT: Shao, L.
FILLE OF INVENTION: DNA encoding methymycin and FILE REFERENCE: 600.438US1
CURRENT APPLICATION NUMBER: US/09/861,289
CURRENT FILING DATE: 2001-05-18
PRIOR APPLICATION NUMBER: 09/105,537
PRIOR APPLICATION NUMBER: 09/105,537
PRIOR FILING DATE: 1998-06-26
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; TYPE: DNA
; ORGANISM: Streptomyces venezuelae
US-09-861-289-5
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; ORGANISM: Streptomyces venezuelae
US-09-861-289-32
                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: DNA encoding methymycin and pikromycin FILE REFERENCE: 600.438US1 CURRENT APPLICATION NUMBER: US/09/861,289 CURRENT FILING DATE: 2001-05-18 PRIOR APPLICATION NUMBER: 09/105,537 PRIOR FILING DATE: 1998-06-26 NUMBER OF SEQ ID NOS: 43 SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 32 LENGTH: 11220
                                                                                                                                                                                                                                                                 Query Match
Best Local (
                                                                                                                                                                                                                                               Matches
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                                                                                                                                                     NUMBER OF SEQ ID NOS: 43
                                    132 CTGGTCCGCTTGCACGAGGGTCAGACCACGATGATCGTTCCGGGCGGCGTCGAGGTGCCG 191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5475 GCGCTGCTGCGAGGGCCCGTTCGGGGCGGTCAGGCCGTTGCTCGCGCCGTCCTGGTTGAC 5416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 192 GTGGA 196
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                                                                                                                                                                           12 CGCTACGACCTGGCCCGCGTCGCTCGCTATAAGGTCAACAAGAAGCTCGGGCTGCATGTC 71
                                                                                                                                                                                                                                       y Match 15.1%;
Local Similarity 48.1%;
hes 89; Conservative
                                                                                                                              72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           72 GGCGAGCCCATCACGTCGACGCTGACCGAAGAAGACGTCGTGGCCACCATCGAATAT 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12 CGCTACGACCTGGCCCGCGTCGGTCGCTATAAGGTCAACAAGAAGCTCGGGCTGCATGTC 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
CGCCCTGCCGCGCACGACCGCCAGCACACGGTGTCCGTTGCGGCGGGGCGTCCGACAGGCG 2104:
                                                                                                              GGCGAGCCCATCACGTCGTCGACGCTGACCGAAGAAGACGTCGTGGCCACCATCGAATAT 131
                                                                         GCGCTGCTGCGAGGGCCCGTTCGGGGCCGTCAGGCCGTTGCTCGCGCCGTCCTGGTTGAC 21103
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48.1%;
                                                                                                                                                                                                                                       Score 31.4; DB 10;
Pred. No. 2.6;
0; Mismatches 96;
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Pred. No. 2.1;
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                                                                                                                                                                                                                                       Indels
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192 GTGGA 196

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RESULT 15
US-10-062-254-109
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    NAME/KEY: misc_feature
    OTHER INFORMATION: Incyte ID No. US20010051335A1 700344235H1
    NAME/KEY: unsure
    LOCATION: 158
    OTHER INFORMATION: a, t, c, g, or other
    US-09-294-093B-1392
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US-09-294-093B-1392
Sequence 1392, Application US/09294093B
Patent No. US20010051335A1
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Patent No. US20020138882A1
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APPLICANT:
APPLICANT:
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APPLICANT:
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SEQ ID NO 1392
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APPLICANT: Lal
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CURRENT APPLICATION NUMBER: US/10/062,254
CURRENT FILING DATE: 2002-02-01
PRIOR APPLICATION NUMBER: 09/630,346
PRIOR FILING DATE: 2000-07-28
                                                                        APPLICANT: Zhu, Qun
TITLE OF INVENTION: Polynucleotides Encoding Proteins Involved In Plant Metabolism
                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Cahoon, Edgar B
APPLICANT: Cahoon, Rebecca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Ito, Laura, Y.
APPLICANT: Sherman, Bradley, K.
APPLICANT: Sherman, Bradley, K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN TASSEL
FILE REFERENCE: PL-0009 US
CURRENT APPLICATION NUMBER: US/09/294,093B
CURRENT FILING DATE: 1999-04-16
PRIOR APPLICATION NUMBER: 60/082,567
PRIOR FILING DATE: April 21, 1998
NUMBER OF SED ID NOS: 6207
                                                                                                                                                       APPLICANT:
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                                                                                                                                                                                           APPLICANT:
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TYPE: DNA
ORGANISM: Zea mays
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          224 TCGTCTACCAGCTCAACATCGCCCCCAAGAAGATCGGCGTTGATGAGG 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                164 AGCTGATGCGCCAGCACCTGGCCACCGATGCCGGCAAGGAGGTCACCAAGAAGGTCGGCC 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64 TGCATGTCGGCGAGCCCATCACGTCGTCGACGCTGACCGAAGAAGACG 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 AGGAGAAGCGCTACGACCTGGCCCGCGCTCGCTATAAGGTCAACAAGAAGCTCGGGC 63
                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION:
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                                                                                                                            Rafalski, Antoni
Sakai, Hajime
Zheng, Peizhong
                                                                                                                                                                                     Ode11,
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                                                                                                                                                                                                                                                                                                                     Cahoon, Rebecca E
Falco, Saverio Carl
Fang, Yiwen
                                                                                                                                                                                                        Niu, Xiping
                                                                                                                                                                                                                            Morgante, Michele
                                                                                                                                                                                                                                                                           Hantke, Sabine S.
Lee, Jian-Ming
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                                                                                                                                                                                       Joan
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55.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0,
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Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 10;
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; LOCATION: (696)
US-10-062-254-109
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PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: 60/156899
PRIOR FILING DATE: 1999-09-30
PRIOR FILING DATE: 1999-10-01
PRIOR APPLICATION NUMBER: 60/157287
PRIOR FILING DATE: 1999-12-09
PRIOR APPLICATION NUMBER: 60/171054
PRIOR APPLICATION NUMBER: 60/171054
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: 60/172958
PRIOR APPLICATION NUMBER: 60/171515
PRIOR APPLICATION NUMBER: 60/171515
PRIOR APPLICATION NUMBER: 60/173535
PRIOR FILING DATE: 1999-12-29
PRIOR APPLICATION NUMBER: 60/173535
PRIOR FILING DATE: 1999-12-29
PRIOR APPLICATION NUMBER: 60/173535
PRIOR FILING DATE: 1999-12-29
PRIOR FILING DATE: 1999-12-29
PRIOR APPLICATION NUMBER: 60/173535
PRIOR FILING DATE: 1999-12-29
PRIOR PRIOR PRIOR DATE: 1999-12-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 375
SOFTWARE: Microsoft Office 97
SEQ ID NO 109
LENGTH: 704
TYPE: DNA
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Best Local Similarity
                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Zea mays
FEATURE:
NAME/KEY: unsure
LOCATION: (640)
                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: unsure
LOCATION: (692)
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LOCATION: (688)
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                                                                                              275 AGCTGATGCGCCAGCACCTGGCCACCGATGCCGGCAAGGAGGTCACCAAGAAGGTCGGCC 334
                                                             64
                                                                                                                                            4 AGGAGAAGCGCTACGACCTGGCCCGCGTCGGTCGCTATAAGGTCAACAAGAAGCTCGGGC 63
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TCGTCTACCAGCTCAACATCGCCCCCAAGAAGATCGGCGTTGATGAGG
                                                TGCATGTCGGCGAGCCCATCACGTCGTCGACGCTGACCGAAGAAGACG 111
                                                                                                                                                                                                         60;
                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                        15.0%;
55.6%;
                                                                                                                                                                                               Score 31.2; DB Pred. No. 1.3; 0; Mismatches
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Search completed: November 12, 2002, 16:59:27 Job time: 51.1607 secs

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Maximum Match 100%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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              US-08-250-030-1
PCT-US95-06790-1
US-08-313-185-57
US-08-097-831-1
US-09-029-633-4
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US-08-722-001-29
US-08-34-698-1
US-08-28-932-1
US-08-468-939-1
US-08-468-939-1
US-08-468-939-1
US-08-468-939-1
US-08-46-855A-1
US-09-266-899-1
US-09-463-702B-251
US-09-453-702B-50
US-08-474-933-1
US-09-453-702B-50
US-09-453-702B-50
US-09-453-702B-50
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(without alignments)
2286.857 Million cell updates/sec
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Sequence 1, Appli Sequence 57, Appli Sequence 57, Appli Sequence 4, Appli Sequence 4, Appli Sequence 13, Appli Sequence 13, Appli Sequence 11, Appli Sequence 1, Appli Sequence 257, Appli Sequence 267, Appli Sequence 50, Appli Sequence 50, Appli Sequence 50, Appli Sequence 1070, Ap
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Db Qy	3 W O	US.	
1 26	Query Ma Best Loc Matches	RESULT 1 Sequence 1, Patent NO. 5 GENERAL INF APPLICANT TITLE OF TITLE OF TITLE OF TITLE OF CORRESPON ADDRESS STREET: CITY: STATE: COUNTRY ZIP: STATE: COMPUTER MEDIUM COMPUTER OPERATI SOFTWARE CURRENT ARPLICAN FILING I CLASSIF ATTORNEY/ NAME: REFEREN REFEREN REFEREN TELEPAN INFORMATION SEQUENCE LENGTH: TYPE: TY	444443333310322 444443333310321032103210331033103310331033103
TCAAGG! TCAAGG!	/ Match Local Simi nes 207;	T 1 -250-030-1 uence 1, Appl: ent No. 56437: NERAL INFORMAT APPLICANT: PRITITLE OF INVENTITLE OF INV	32 32 32 33 31 31 31 31 31 31 31 31 31 31 31 31
TCAAGGAGAAGCGCTACGACCTGGCCCCGCGTCGGTCGCTATAAGGTCAACAAGAAGCTCG	99.2 Similarity 99.5 7; Conservative	THE CONTRACT ON THE STATE OF TH	15.11 15.12 15.12 15.13 15.13 15.13 15.13 15.13 15.13
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CGT	205.4 No. 4 match	& Woessner Wersion Wersion	8-911-853 9-479-409 9-479-453 9-479-453 9-479-409 9-479-453 9-479-453 9-479-453 9-4713-569 8-713-569 9-031-606 8-461-775 9-031-606 8-461-759 9-031-606
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PCT-US95-06790-1
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Best Local Similarity
                                                                                                                                                                                                                                                   Matches 207;
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                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 35,651
REFERENCE/DOCKET NUMBER: 15
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-339-0331
TELEFAX: 612-339-3061
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Raasch, Kevin W.
REGISTRATION NUMBER: 35,6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06790
FILING DATE: 26-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Mayo Foundation for Medical Education and Research APPLICANT: and Hoffmann-La Roche Inc.
TITLE OF INVENTION: Detection of a Genetic Locus Encoding TITLE OF INVENTION: Resistance to Rifampin
         206
                                      181
                                                                    146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                              86
                                                                                                                                                           61
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                                                                                                                                                                                                                                                                                                                                                                                      LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 3500 IDS (CITY: Minneapolis
                                                                                                                                                                                                 1 TCAAGGAGAAGCGCTACGACCTGGCCCGCGTCGGTCGCTATAAGGTCAACAAGAAGCTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
                                                            CCATCGAATATCTGGTCCGCTTGCACGAGGGTCAGACCACGATGATCGTTCCGGGCGGCG 180
      TCGAGGTGCCGGTGGAAACCGACGACAT 233
                                                                                                                                         GGCTGCATGTCGGCGAGCCCATCACGTCGTCGACGCTGACCGAAGAAGACGTCGTGGCCA 120
                                   TCGAGGTGCCGGTGGAAACCGACGACAT 208
                                                                                                                         GGCTGCATGTCGGCGAGCCCATCACGTCGTCGACGCTGACCGAAGAAGACGTCGTGGCCA
                                                                                                                                                                                   TCAAGGAGAAGCGCTACGACCTGGCCCGCGTCGGTCGCTATAAGGTCAACAAGAAGCTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCGAGGTGCCGGTGGAAACCGACGACAT 208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGCTGCATGTCGGCGAGCCCATCACGTCGTCGACGCTGACCGAAGAAGACGTCGTGGCCA
                                                                                                                                                                                                                                                                                                                                                                     nucleic acid
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26-маү-1995
                                                                                                                                                                                                                                                                99.2%;
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                                                                                                                                                                                                                                                              Score 206.4; DB 5
Pred. No. 4.5e-48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .50.105WO1
                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                         DB 5; Length 970;
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US-09-082-614A-57
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LENGTH: 3447 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-313-185-57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 3
US-08-313-185-57
; Sequence 57, A
                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 25,146
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 0235
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 401-4000
TELEPAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 3447 base pairs
                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                  Query Match
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, V
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Honore, Nadine
APPLICANT: Telenti, Amalio
APPLICANT: Bodmer, Thomas
TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
TITLE OF INVENTION: in Mycobacterium Tuberculosis
NUMBER OF SEQUENCE: 66
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                            869
       989
                                181 TCGAGGTGCCGGTGGAAACCGACGACAT 208
                                                                                  121 CCATCGAATATCTGGTCCGCTTGCACGAGGGTCAGACCACGATGATCGTTCCGGGGGGCGC 180
                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
FILING DATE: 12-OC
CLASSIFICATION: 43
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CITY: W
STATE:
                                                                                                                                                     61 GGCTGCATGTCGGCGAGGCCCATCACGTCGTCGACGCTGACCGAAGAAGACGTCGTGGCCA 120
                                                                                                                                                                                                                                                                            Local Similarity 81.7 es 170; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                       1 TCAAGGAGAAGCGCTACGACCTGGCCCGCGTCGGTCGCTATAAGGTCAACAAGAAGCTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Finnegan, Henderson, Farabow, Garrett ADDRESSEE: Dunner
TAGAAGTGCCAGTGGAAACTGACGATAT 1016
                                                               CCATAGAGTACCTGGTTCGTCTGCATGAGGGTCAGTCGACAATGACTGTCCCAGGTGGGG
                                                                                                                                 GTTGCACGCCGGTGAGTTGATCACGTCGTCCACGCTGACCGAAGAGGATGTCGTCGCCA
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Zhang, Ying
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Cole, Stewart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-OCT-1994
                                                                                                                                                                                                                                                                      70.8%; Score 147.2; DB 2; 81.7%; Pred. No. 9.2e-32; O. Mismatches 38;
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                                      RESULT 5
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Best Local :
Sequence 1, Application US/08097831
                                                                                                                                                                                                                                                                                                                                                                                        Matches 170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EILING DESCRIPTION:
CLASSIFICATION:
PRIOR APPLICATION NUMBER: US 08/
APPLICATION NUMBER: 12-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 12-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Meyers Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 02356.0068-00000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 3447 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Young, Douglas
APPLICANT: Zhang, Ying
APPLICANT: Honore, Nadine
APPLICANT: Honore, Nadine
APPLICANT: Telenti, Amalio
APPLICANT: Bodmer, Thomas
TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
TITLE OF INVENTION: in Mycobacterium Tuberculosis
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                          869
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                                                                                                                                                                                                                                                     61 GGCTGCATGTCGGCGAGGCCCATCACGTCGTCGTCGACGCTGACCGAAGAAGACGTCGTGGCCA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & ADDRESSEE: Dunner STREET: 1300 I Street, N.W.
                                                                                                                                                                                                                                                                                                                              1 TCAAGGAGAAGCGCTACGACCTGGCCCGCGCTCGCTATAAGGTCAACAAGAAGCTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                        TAGAAGTGCCAGTGGAAACTGACGATAT 1016
                                                                                                                          TCGAGGTGCCGGTGGAAACCGACGACAT 208
                                                                                                                                                           CCATAGAGTACCTGGTTCGTCTGCATGAGGGTCAGTCGACAATGACTGTCCCAGGTGGGG
                                                                                                                                                                              CCATCGAATATCTGGTCCGCTTGCACGAGGGTCAGACCACGATGATCGTTCCGGGCGGCG 180
                                                                                                                                                                                                                                    GGTTGCACGCCGGTGAGTTGATCACGTCGTCCACGCTGACCGAAGAGGATGTCGTCGCCA
                                                                                                                                                                                                                                                                                                         TCAAGGAGAAACGCTACGACCTGGCCAGGGTTGGTCGTTACAAGGTCAACAAGAAGCTCG 868
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                                                                                                                                                                                                                                                                                                                                                                                                  h 70.8%; Score 147.2; DB 3; Length 3447; Similarity 81.7%; Pred. No. 9.2e-32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nucleic acid
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Cole, Stewart
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linear
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RESULT 6
US-09-029-603-4
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; LOCATION:
US-08-097-831-1
GENERAL INFORMATION:
APPLICANT: Schupp, Thomas
APPLICANT: Engel, Natalie
APPLICANT: Betechhader, Jurg
APPLICANT: Toupet, Christine
APPLICANT: Pospiech, Andreas
TITLE OF INVENTION: Staurosporin Biosynthesis Gene Clusters
                                                                                                                               Sequence 4, Application US/09029603 Patent No. 6210935
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E.
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: NIHO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 714,760-0404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 714-760-9502 INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Camerini-Otero, Rafael D.
APPLICANT: Angov, Evangelina
TITLE OF INVENTION: Cloning and Expression of Tag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HYPOTHETICAL:
ANTI-SENSE: NO
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                          490 TTCGGTGGCCGCTTTGGTGCCCAAGG 515
                                                                                                                                                                                                                                                         170 TCCGGGCGGCGTCGAGGTGCCGGTGG 195
                                                                                                                                                                                                                                                                                       110 CGTCGTGGCCACCATCGAATATCTGGTCCGCTTGCACGAGGGTCAGACCACGATGATCGT 169
                                                                                                                                                                                                                                                                                                                                                      370 CAAGAAGCTCGGGGTGGACGTGCAGGAGCTTCTGGTCTCCCAGCCGGACACCGGGGAGCA 429
                                                                                                                                                                                                                                                                                                                                                                         50 CAAGAAGCTCGGGCTGCATGTCGGCGAGCCCATCACGTCGTCGACGCTGACCGAAGAAGA 109
                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: 714-70-9502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: FILING DATE: 199307 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Newport Beach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                               79;
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54.1%;
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Pred. No. 0.039;
0; Mismatches 67; Indels 0
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CURRENT APPLICATION NUMBER: US/09/029,603
CURRENT FILING DATE: 1998-03-20
EARLIER APPLICATION NUMBER: PCT/EP96/03643
EARLIER FILING DATE: 1996-08-19
NUMBER OF SEO ID NOS: 11
SOFTWARE: PATENTIN VEY: 2.0
SEO ID NO 4
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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LOCATION: (5071)..(6085)
OTHER INFORMATION: ORF
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OTHER INFORMATION: ORF
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LOCATION: (378)..(1665)
OTHER INFORMATION: ORF
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LOCATION: (1747)..(2553)
OTHER INFORMATION: ORF
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                                                                                 APPLICANT: Elovainio, Minna
APPLICANT: Joutsjoki, Vesa
APPLICANT: Paloheimo, Marja
APPLICANT: Suominen, Pirkko
TITLE OF INVENTION: NOVEL CELLULASES,
TITLE OF INVENTION: USES THEREOF
NUMBER OF SEQUENCES: 45
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                                                                      CORRESPONDENCE ADDRESS
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                                  STREET:
                                                     ADDRESSEE:
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Local Similarity 51.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CGCTTGCACGAGGGTCAGACCACGATGATCGTTCCGGGCGGCGTC 182
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Washington
D.C.
                                                                                                                                                                                                                                                                                                                                                              Application US/09329350
                                E: Sterne, Kessler, Goldstein & Fox P.L.L.C 1100 New York Avenue, N.W., Suite 600
                                                                                                                                                                                                            M ntyl , Arja
Lantto, Raija
                                                                                                                                                                                                                                                                                                     Miettinen-Oinonen, Arja
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                                                                                                                       THE GENES ENCODING THEM AND
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RESULT 8
US-08-722-001-13
; Sequence 13, Application US/08722001
; Patent No. 5760034
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                                                                                                                                            1152 GCCCTTCACCGTGGTGACGCAGTTCCCGGCCGACGCCGAGGGGCCGGCTCGAGAGCATCCA 1211
                                                                                   APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 60/007,926
APPLICATION NUMBER: US 60/007,926
APPLICATION NUMBER: 04-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 17
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/005,335
FILING DATE: 17-OCT-1995
                                                                                                                                                                                                                                                                                                                                FEATURE:
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 17-OCT-1996
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Diskett
                                                                                                               SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: US
FILING DATE: 30-APR-19
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                                                                                                                                                                       77 GCCCATCACGTCGTCGACGCTGACCGAAGAAGACGTCGTGGCCACCATCGAATATCTGGT 136
                                                                                                                                                                                                                                                                                 NAME/KEY: exon
LOCATION: 916..159
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                           NAME/KEY: exon
LOCATION: 233..838
OTHER INFORMATION:
                                                                                                                                                                                                                           Local
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                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH:
                                                                                                                                                                                                                          17.3%;
Similarity 56.9%;
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916..1596
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                                                                                                                                                                                                                     Score 36; DB 4,
Pred. No. 0.24;
                                                                                                                                                                                                         Mismatches
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                                                                                                                                                                                                                                    DB 4; Length 1894;
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RESULT 9
US-08-722-001-29
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US-08-722-001-13
                                                                Sequence 29, Application US/08722001 Patent No. 5760054 GENERAL INFORMATION:
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APPLICATION NUMBER: 08/229,271
FILING DATE: 14-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: APPOLLINA, Mary A.
REGISTRATION NUMBER: 34,087
REFERENCE_DOCKET NUMBER: 1916
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908)594-3462
 APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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TELEX: 138825
INFORMATION FOR SEQ ID NO: 13:
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APPLICANT:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: CI
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ADDRESSEE: Merck & Co.,
                                                                                                                                                                             432 TCTGCGACGTATGGGCCGCCGTGGACGTGCTGCTGCTGCACGGCCCTCCAT 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                            372 CCGTACTGCCCTTCTCGGCCACCATGGAGGTTCTGGGCTTCTGGGCCTTTGGCCGCGCCCT 431
                                                                                                                                                                                                                                                                 100 CCGAAGAAGACGTCGTGGCCACCATCGAATATCTGGTCCGCTTGCACGAGGGTCAGACCA 159
                                                                                                                                                                                                                                                                                                         312 AGACCGTCACCAACTATTTCATCGTGAACCTGGCCGTGGCCGACCTGCTGCTGAGCGCCA 371
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                                                                                                                                                                                                                                                                                                                                          40 ATAAGGTCAACAAGAAGCTCGGGGTGCATGTCGGCGAGCCCATCACGTCGTCGACGCTGA 99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: doub
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Thompson, Wayne J.
Huff, Joel R.
Nerenberg, Jennie B
Lee, Hee-Yoon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Thompson, Wayne J. Huff, Joel R.
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50.3%;
                 Jennie B
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RESULT 10
US-08-334-698-1
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                                                                                                                                                                           Sequence 1, Application US/08334698 Patent No. 5556753
GENERAL INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/22
FILING DATE: 14-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: APPOIllina, Mary A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: CDN
                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                 APPLICANT: Jonathan A. Bard et al. TITLE OF INVENTION: DNA Encoding FTITLE OF INVENTION: Receptors and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 1776 base pair:
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: APPOILING, MATY A.
REGISTRATION NUMBER: 34,087
REFERENCE_DOCKET NUMBER: 19:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908)594-3462
                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                 560
                                                                                                                                                                                                                                                                                                           160 CGATGATCGTTCCGGGCGCGTCGAGGTGCCGGTGGAAACCGACGACAT 208
                                                                                                                                                                                                                                                                                                                                                                                  100 CCGAAGAAGACGTCGTGGCCACCATCGAATATCTGGTCCGCTTGCACGAGGGTCAGACCA 159
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TELLEFAX: 138825
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                                  CITY: New York
STATE: New Yor
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                   COUNTRY:
                                                                 STREET:
                                                                               ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                      TCTGCGACGTATGGGCCGCCGTGGACGTGCTGCTGCTGCACGGCCTCCAT 608
10112
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                                                            30 Rockefeller Plaza
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                 U.S.A.
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                                                                             COOPER & DUNHAM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Floppy disk
                                                                                                                          DNA Encoding Human Alpha 1
Receptors and Uses Thereof
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Pred. No. 0.58;
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RESULT 11
US-08-228-932-1
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Best Local S
Matches 85
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                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: COOPER & DUNHAM
                                                                                                                                                                                                  APPLICANT: Charles Gluchowski, Carlos C. Forray, George Chiu,
APPLICANT: Theresa A. Branchek, John M. Wetzel and Paul R. Hartig
TITLE OF INVENTION: USE OF ALPHA-1C SPECIFIC COMPOUNDS TO TREAT BENIGN
TITLE OF INVENTION: PROSTATIC HYPERPLASIA
                                                                                                                                                                                         NUMBER OF SEQUENCES:
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LENGTH: 2140 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 374
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/952,798
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CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                            160 CGATGATCGTTCCGGGCGGCGTCGAGGTGCCGGTGGAAACCGACGACAT 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100 CCGAAGAAGACGTCGTGGCCACCATCGATATCTGGTCCGCTTGCACGAGGGTCAGACCA 159
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC OPERATING SYSTEM:
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                                                                ZIP: 10112
                                                                                                                                       STREET:
                                                                                    COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                  T: 30 Rockefeller Plaza
New York
: New York
RY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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(212) 664-050
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178..1893
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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422523 COOP UI
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Pred. No. 0.6;
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RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/08468939
Patent No. 5714381
GENERAL INFORMATION:
APPLICANT: Jonathan A. Bard et a
                                                                               COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,939
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TELEX: (212) 422523 COOI
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
ATTORNEY/AGENT INFORMATION:
NAME: White, John P
REGISTRATION NUMBER: 28,
                                                                                                                                                                                                                                                                                                                                            APPLICANT: Jonathan A. Bard et al.
TITLE OF INVENTION: DNA Encoding Human Alpha 1 Adrenergic
TITLE OF INVENTION: Receptors and Uses Thereof
                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: (CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 41878-B/JPW/TEP TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 977-9550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/228,93:
FILING DATE: 13-APR-1994
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ANTI-SENSE:
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        620
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                                              FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                           COUNTRY: U.S.A. ZIP: 10036
                                                                                                                                                                                                                                                STREET: 1185 AVCITY: New York
STATE: New Yorl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40 ATAAGGTCAACAAGAAGCTCGGGCTGCATGTCGGCGAGCCCCATCACGTCGTCGACGCTGA 99
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LOCATION: 178..1893
OTHER INFORMATION:
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DEDNESS: single
                                                                                                                                                                                                                                                New York
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EQ ID NO: 1:
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                                                                                                 SOFTWARE: Patentin Release #1.
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/406,
FILING DATE: 21-AUG-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 4133;
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1013, 201-0526
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                                                                     TELEFAX: (212) 391-0526 INFORMATION FOR SEQ ID NO:
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2140 base pairs
                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Jonathan A. Bard et al.
TITLE OF INVENTION: DNA Encoding Human Alpha 1
TITLE OF INVENTION: Receptors and Uses Thereof
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TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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LOCATION: 178..1893
OTHER INFORMATION:
STRANDEDNESS:
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                                 LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                             New York
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                               2140 base pairs
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Pred. No. 0.6;
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US-08-722-190-1
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Patent No. 5990128
GENERAL INFORMATION:
APPLICANT: Charles Gluchowski, Carlos C. Forray, George
APPLICANT: Chiu, Theresa A. Branchek, John M. Wetzel and Paul R. Hartig
TITLE OF INVENTION: USE OF ALPHA-1C SPECIFIC COMPOUNDS TO
TITLE OF INVENTION: TREAT BENIGN PROSTATIC HYPERPLASIA
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Best Local Similarity
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                                                                                                                                          INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 2140 base pairs
                                                                                                                                                                                                                          ATTORNEY AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 4187
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
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MOLECULE TYPE:
HYPOTHETICAL: N
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                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                MOLECULE TYPE: [
                                    FEATURE:
                                                ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                             TOPOLOGY:
                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                               FILING DATE: 4-APR-1995
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: New York
                                                                                                                              TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: FILING DATE: 4-APR-
                   NAME/KEY:
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LOCATION: 178..1893
OTHER INFORMATION:
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1185 Avenue of the Americas
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CDS
178..1893
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                                                                               DNA (genomic)
                                                                                                               single
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LOCATION: 178..1893
OTHER INFORMATION:
US-08-244-354-1
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2140 base pairs
LENGTH: 2140 base pairs
TYPE: nucleic acid
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US-08-244-354-1
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                                        Query Match 16.6%;
Best Local Similarity 50.3%;
Matches 85; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/244,354
FILING DATE: APTI1 1, 1997
CLASSIFICATION: 514
ATTORNEY/ACENT INFORMATION:
NAME: White, John P.
REFERENCE/DOCKET NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 41878-D-PCT-US/JPW
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/08244354 Patent No. 6015819 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 50.3%; Matches 85; Conservative
                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                  MOLECULE TYPE: I
                                                                                                                                                                                                                ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Charles Gluchowski, et al.

TITLE OF INVENTION: USE OF ALPHA-1C SPECIFIC COMPOUNDS TO TITLE OF INVENTION: TREAT BENIGN PROSTATIC HYPERPLASIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 1185 AV
CITY: New York
STATE: New York
40 ATAAGGTCAACAAGAAGCTCGGGCTGCATGTCGGCGAGCCCATCACGTCGTCGACGCTGA 99
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                                                                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (212) 391-0525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40 ATAAGGTCAACAAGAAGCTCGGGCTGCATGTCGGCGAGCCCATCACGTCGTCGACGCTGA 99
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                                                                                                                                                                                                                                                                    unknown
                                                                                                                                                                                                                                                  DNA (genomic)
                                      Score 34.6; DB 3;
Pred. No. 0.6;
0; Mismatches 84;
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Pred. No. 0.6;
0; Mismatches 84; Indels 0
                                    84; Indels
                                                                        Length 2140;
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                                    Gaps
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Search completed: November 12, 2002, 21:03:40 Job time: 39.8936 secs

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Title:
Perfect score:
Sequence:
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4: /SIDS2/gcgdata/ge
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Gapop 10.0 , Gapext 1.0
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208
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Listing first 45 summaries
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SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001.DAT:

SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001.DAT:

SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001.DAT:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT:*
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                   AAS05216
AAT09676
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AAH02079
AAA74651
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AAS05205
AAS05206
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17.3			18.0	•	•			•		18.7			w		•		•	•	•	•	٠	•		•	٠	•	٠	•	•		•	•	•	81.5	•
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AAT66542	AAT70153	AAZ51698	AA251714	AAZ51713	AA251712	AAZ51710	AAZ51704	AAF28350	AAZ51715	AAT26989	AAZ51711	AAS59541	AAH68525	AAH65512	AAS05213	AAS05207	AAS05218	AAS05221	AAS05209	AAS05214	AAS05220	AAQ51532	AAS05224	AAS05212	AAS05204	AAS05217	AAS05202	AAS05223	AAS05219	AAS05208	AAS05201	AAS05215	AAS05211	052	AAS05210
50K-cellulase gene	S.longisporoflavus			-		Burkholderia cepac	Burkholderia vietn	Streptomyces ambof	Burkholderia cepac	Thermus aquaticus	Burkholderia cepac	Propionibacterium	C glutamicum codin				Mycobacterium flav	Mycobacterium absc		-	rium				-	-	_	-	_	_	Mycobacterium gord	_		gor	Mycobacterium ulce

ALIGNMENTS

RESULT 1
AAS05222
ID AASC

AAS05222 standard; DNA; 208 BP

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New DNA fragments from the rpoB gene of mycobacteria, useful for diagnosis and identification of many mycobacterial species by restriction fragment length polymorphism \,
                                          WPI;
                                                                                                                                          03-MAY-2001.
                                                                                                                                                            WO200131061-A1
                                                              Lee
                                                                                                   27-OCT-1999;
                                                                                                                     27-OCT-2000; 2000WO-KR01223.
                                                                                                                                                                               Mycobacterium africanum.
                                                                                                                                                                                                 Non-tuberculous mycobacteria; rpoB gene fragment; NTM; PCR-restriction fragment length polymorphism analysis;
                                                                                                                                                                                                                              Mycobacterium africanum rpoB gene fragment.
                                                                                                                                                                                                                                                  07-SEP-2001
                                                                                                                                                                                                                                                                       AAS05222;
                                                                               (ERUM-) ERUME BIOTECH CO LTD.
                                                            Ή,
                                        2001-300520/31.
                                                           Park YK,
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                                                                                                   99KR-0046795.
                                                           Bai G,
                                                            Xin
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                                                           Cho
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                                                            КÍП
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                                                            Park HJ;
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RESULT 2
AAS05205
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   Lee н,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence for Mycobacterium africanum rpoB gene fragment is 1 of 24 rpoB gene fragments (AASO5201-AASO5224) from various Mycobacterial species. These rpoB gene fragments can be used in the diagnosis and identification of Mycobacterium species using a novel PCR-restriction fragment length polymorphism analysis (PRA)
                               (ERUM-) ERUME BIOTECH CO LTD
                                                             27-OCT-1999;
                                                                                            27-OCT-2000; 2000WO-KR01223
                                                                                                                           03-MAY-2001.
                                                                                                                                                                                        Mycobacterium tuberculosis
                                                                                                                                                           WO200131061-A1
                                                                                                                                                                                                                        PCR-restriction
                                                                                                                                                                                                                                      Non-tuberculous
                                                                                                                                                                                                                                                                  Mycobacterium tuberculosis rpoB gene fragment.
                                                                                                                                                                                                                                                                                                       07-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                AAS05205 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 208 BP; 46 A; 61 C; 67 G; 34 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCATCGAATATCTGGTCCGCTTGCACGAGGGTCAGACCACGATGATCGTTCCGGGCGGCG 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               h 100.0%;
Similarity 100.0%;
   Park YK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                  (first entry)
                                                             99KR-0046795
                                                                                                                                                                                                                    mycobacteria; rpoB gene fragment; NTM;
fragment length polymorphism analysis;
 Bai G,
 Kim S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 208; DB 22,
Pred. No. 6.2e-46;
 Cho
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Kim
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Park HJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 208;
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The present sequence for Mycobacterium tuberculosis rpoB gene (C fragment is 1 of 24 rpoB gene fragments (AAS05201-AAS05224) from CC various Mycobacterial species. These rpoB gene fragments can be used C in the diagnosis and identification of Mycobacterium species using a CC novel PCR restriction fragment length polymorphism analysis (PRA) CC method. The method comprises obtaining a restriction fragment length CC polymorphism (RFLP) pattern of the 24 rpoB gene fragments; isolating, CC amplifying and digesting the DNA fragment from the microorganism to Cc are useful to identify a wide range of Mycobacterium species, e.g. for C arguments with the unidentified fragment. The rpoB gene fragments CC are useful to identify a wide range of Mycobacterium species, e.g. for C diagnosis or to obtain epidemiological and pathogenesis information for CC selection of appropriate therapies, including M. tuberculosis, M. leprae CC with human immunodeficiency virus (HIV). Analysis of the rpoB gene CC fragments is rapid, precise, simple and cost effective (only 1 PCR crequired), and can differentiate between many species in a single CC experiment, including those difficult to distinguish by usual biochemical tests. Also described are oligonucleotide probes (AAS05227-AAS05242) for CC detecting specific Mycobacterial species.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 41; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New DNA fragments from the rpoB gene of mycobacteria, useful for diagnosis and identification of many mycobacterial species by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tragment length polymorphism
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Sequence 208 BP; 46 A; 62 C; 67 G; 33 T; 0 other;

Ş B Q В Qγ 밁 δÃ Query Match
Best Local Simi
Matches 207; 181 181 121 121 61 61 Local Similarity 1 TCAAGGAGAAGCGCTACGACCTGGCCCGCGCTCGGTCGCTATAAGGTCAACAAGAAGCTCG 60 CCATCGAATATCTGGTCCGCTTGCACGAGGGTCAGACCACGATGATCGTTCCGGGCGGCG 180 TCGAGGTGCCGGTGGAAACCGACGACAT TCAAGGAGAAGCGCTACGACCTGGCCCGCGTCGGTCGCTATAAGGTCAACAAGAAGCTCG 60 GCTGCATGTCGGCGAGCCCATCACGTCGTCGACGCTGACCGAAGAAGACGTCGTGGCCA 120 GECTGCATGTCGGCGAGCCCATCACGTCGTCGACGCTGACCGAAGAAGACGTCGTGGCCA 120 TCGAGGTGCCGGTGGAAACCGACGACAT Conservative 99.2%; 99.5%; 0; Score 206.4; DB 22; Pred. No. 1.6e-45; Mismatches μ, Length 0; Gaps 0

RESULT 3 AAS05206

AAS05206 standard; DNA; 208

ВP

208

07-SEP-2001

(first entry)

Mycobacterium terrae rpoB gene fragment.

Non-tuberculous mycobacteria; rpoB gene fragment; NTM; PCR-restriction fragment length polymorphism analysis;

Mycobacterium terrae

03-MAY-2001.

27-OCT-2000; 2000WO-KR01223

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RESULT 4
AASO5216
AASO5216
AASO
XX
AAC
AASO
XX
DT 07-S
XX
DE Mycc
XX
KW PCR-X
XX
OS Mycc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CC The present sequence for Mycobacterium terrae rpoB gene
CC fragment is 1 of 24 rpoB gene fragments (AASO5201-AASO524) from
CC various Mycobacterial species. These rpoB gene fragments can be used
CC in the diagnosis and identification of Mycobacterium species using a
CC novel PCR-restriction fragment length polymorphism analysis (PRA)
CC method. The method comprises obtaining a restriction fragment length
CC polymorphism (RFLP) pattern of the 24 rpoB gene fragments; isolating,
CC amplifying and digesting the DNA fragment from the microorganism to
CC be identified and comparing the RFLP patterns from the known rpoB gene
CC fragments with the unidentified fragment. The rpoB gene fragments
CC are useful to identify a wide range of Mycobacterium species, e.g. for
CC diagnosis or to obtain epidemiological and pathogenesis information for
CC selection of appropriate therapies, including M. tuberculosis, M. leprae
CC and non-tuberculous mycobacteria (NTM) encountered in subjects infected
CC with human immunodeficiency virus (HIV). Analysis of the rpoB gene
CC fragments is rapid, precise, simple and cost effective (only 1 PCR
CC required), and can differentiate between many species in a single
CC experiment, including those difficult to distinguish by usual biochemical
CC tests. Also described are oligonucleotide probes (AASO5227-AASO5242) for
CXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
 Mycobacterium bovis
                         Non-tuberculous mycobacteria; rpoB gene fragment; NTM; HIV; pRA; RFLP; PCR-restriction fragment length polymorphism analysis; ds.
                                                                               Mycobacterium
                                                                                                             07-SEP-2001
                                                                                                                                                                            AAS05216 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New DNA fragments from the rpoB gene of mycobacteria, useful for diagnosis and identification of many mycobacterial species by restriction fragment length polymorphism \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 208 BP; 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 42; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-OCT-1999;
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                                                                                                            (first entry)
                                                                            bovis rpoB gene fragment.
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                                                                                                                                                                            DNA;
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99.5%;
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Pred. No. 1.6
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AAT09676 standard; DNA; 970

ВP

15-OCT-1996

(first entry)

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comovel por restriction fragment length polymorphism analysis (PRA) comparison the method. The method comprises obtaining a restriction fragment length CC polymorphism (RFLP) pattern of the 24 rpoB gene fragments; isolating, CC amplifying and digesting the DNA fragment from the microorganism to CC be identified and comparing the RFLP patterns from the known rpoB gene fragments with the unidentified fragment. The rpoB gene fragments CC are useful to identify a wide range of Mycobacterium species, e.g. for CC diagnosis or to obtain epidemiological and pathogenesis information for Selection of appropriate therapies, including M. tuberculosis, M. leprae CC and non-tuberculous mycobacteria (NTM) encountered in subjects infected CC with human immunodeficiency virus (HIV). Analysis of the rpoB gene CC fragments is rapid, precise, simple and cost effective (only 1 PCR CC required), and can differentiate between many species in a single experiment, including those difficult to distinguish by usual blochemical CC tests. Also described are oligonucleotide probes (AASO5227-AASO5242) for detecting specific Mycobacterial smariae
                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Sim
Matches 207;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 208 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence for Mycobacterium bovis rpoB gene fragment is 1 of 24 rpoB gene fragments (AAS05201-AAS05224) from various Mycobacterial species. These rpoB gene fragments can be used in the diagnosis and identification of Mycobacterium species using a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 45; 50pp; English.
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                                                    TCGAGGTGCCGGTGGAAACCGACGACAT 208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        specific Mycobacterial species.
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99.58;
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 Mismatches

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Pred. No. 1.6e-45;
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/note= "primer /
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RESULT 6
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This oligonucleotide DNA primer is specific for Mycobacterium tuberculosis, and may be used to amplify a sample DNA by targeting a portion of the gene encoding rpoB. The 1st several bases comprise a nonhybridizing tail consisting of filler bases followed by a restriction site incorporated to facilitate cloning using the amplicon at a later date, if desired. The remaining bases hybridize to bacterial rpoB DNA. The method provides for the detection of M. tuberculosis and the concurrent determination of its drug susceptibility, particularly to rifamycin. The method can provide often greater than 95% sensitivity and 100% specificity. The biological sample is a fluid or tissue sample from a human.
                                                                                                                                          Mycobacterium tuberculosis potential drug target gene SEQ ID
13-NOV-2000; 2000WO-US31152
                                 17-MAY-2001
                                                             WO200135317-A1
                                                                                      Mycobacterium tuberculosis
                                                                                                                   Drug target;
                                                                                                                                                                               04-SEP-2001
                                                                                                                                                                                                           AAH51976;
                                                                                                                                                                                                                                     AAH51976 standard; DNA; 3519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 970 BP; 182 A; 302 C; 330 G; 156 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig.3; 54pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Detection of Mycobacterium tuberculosis - by amplifying sample DNA with a primer set that targets portions of the gene encoding rpoB.
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Young KKY;
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milarity 99.5%;
Conservative
                                                                                                             growth; organism viability; characterisation; ds
                                                                                                                                                                          (first entry)
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RESULT 7
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                                                        Species specific; genus specific; family specific; probe; detection; identification; algal; archaeal; bacterial; fungal; parasitical; microorganism; diagnosis; translation elongation factor Tu; toxin; translation elongation factor G; RecA recombinase; resistance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This invention relates to a method for identifying a nucleotide or polypeptide sequence that may be a drug target, or essential for growth or viability of an organism. Polynucleotide sequences AAH51947 - AAH52092 represent DNA encoding proteins AAG81096 - AAG81241, Mycobacterium tuberculosis proteins which are potential drug targets. The DNA and protein sequences are used to illustrate the method of the invention. The method involves providing an unknown nucleotide or polypeptide sequences, and comparing it to a number of sequences along with at least one nucleotide and polypeptide sequences. The method is useful for characterising the function of nucleic acids and polypeptides that may be useful as a target for a drug or essential for the growth or viability of
                                                                                                                                                                                                                                                                                                                                         1004
                                            catalytic subunit of proton-translocating
                                                                                                                             Mycobacterium tuberculosis nucleotide sequence
                                                                                                                                                                                                               AAH02079 standard; DNA; 3534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3519 BP; 675 A; 1081 C; 1183 G; 580 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Identifying nucleotide or polypeptide sequence for use as drug target, involves providing algorithm that analyzes a functional relationship between nucleotide or polypeptide sequences, and comparing the
                                                                                                                                                                                                                                                                                                              181
                                                                                                                                                                                                                                                                                                                                                                   121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-NOV-1999;
01-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                               944
                                                                                                                                                                                                                                                                                                                                                                                                                                                    884
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                                                                                                                                                                                                                                                                                                                                                                                                                       61
                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                    GGCTGCATGTCGGCGAGCCCATCACGTCGTCGACGCTGACCGAAGAAGACGTCGTGGCCA 120
                                                                                                                                                                                                                                                                                                TCGAGGTGCCGGTGGAAACCGACGACAT 208
                                                                                                                                                                                                                                                                                                                                  CCATCGAATATCTGGTCCGCTTGCACGAGGGTCAGACCACGATGACCGTTCCGGGCGGCG
                                                                                                                                                                                                                                                                                                                                              TCGAGGTGCCGGTGGAAACCGACGACAT 1091
                                                                                                                                                                                                                                                                                                                                                                                       2001-329193/34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      al Similarity
207; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ) UNIV
                                     primer; ds.
                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Page 68-69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CALIFORNIA.
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2000US-0179531
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99.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 206.4; DB 2
Pred. No. 2.3e-45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Marcotte
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                                            ATPase; antimicrobial;
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Mycobacterium

tuberculosis

RESULT 8 AAA74651

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                                                                                                                                                                                                                                                                                                                                                                               cc nucleic acids of tut, fus, atpD and/or recA genes from which probes cc and/or primers are derived. The method comprises amplifying the nucleic acids of determined algal, archaeal, bacterial, fungal and parasitical cc species with a combination of defined primer pairs. The method can be cused for producing probes and/or primers for detecting one or more cc used for producing probes and/or primers for detecting one or more cc parasites, for universal detection and for specific and ubiquitous cd detection and identification of an algal, archaeal, bacterial, fungal and cc detection and identification fan algal, archaeal, bacterial, fungal co detection of any bacterium, fungus or parasite and ubiquitous cd detection of any bacterium, fungus or parasite in a sample and for the cleast one toxin gene, hexa nucleic acids are used for the specific and ubiquitous detection and for identification of Streptococcus pneumoniae. Cc defection seed to design a therapeutic agent which is effective against which can be detected include Abiotrophia adlacens, Bordetella sp., cc which can be detected include Abiotrophia adlacens, Bordetella sp., cc Mycobacterium sp. Enterobacteriaceae group, Escherichia coli, cc Mycobacterium sp. Enterobacteriaceae group, Escherichia coli, cc Mycobacterium sp. Enterobacteriaceae group, Escherichia coli, cc Mycobacteriaceae family, Pseudomonads group, Escherichia coli, cc Mycobacteriaceae family prophacterium sp. Streptococcus sp. Using DNA based tests color determined in an hour and improved accuracy is also achieved.

Cc Which are given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                             Best Loc
Matches
                                                                                                                                                                                                                                                                                                                               Query Match
     1082
                                                                                                                                                                                                                                                                                                                                                    Sequence 3534 BP; 679 A; 1081 C; 1188 G; 586 T; 0 other;
                                                                            1022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acid sequences are used to generate universal probes and primers which can be used to identify and detect the presence of algal, archaeal, bacterial, fungal and parasitical species in a test sample -
                                      181
                                                                                                              121
                                                                                                                                                  962
                                                                                                                                                                                                                       902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes a method for generating a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bergeron MG,
Picard FJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (INFE-) INFECTIO DIAGNOSTIC (IDI) INC.
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19-MAY-2000;
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                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                         TCAAGGAGAAGCGCTACGACCTGGCCCGCGTCGGTCGCTATAAGGTCAACAAGAAGCTCG
                   TCGAGGTGCCGGTGGAAACCGACGACAT
                                                                                 GGCTGCATGTCGGCGAGCCCATCACGTCGTCGACGCTGACCGAAGAAGACGTCGTGGCCA 120
TCGAGGTGCCGGTGGAAACCGACGACAT
                                                              CCATCGAATATCTGGTCCGCTTGCACGAGGGTCAGACCACGATGACCGTTCCGGGCGGCG
                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Page 1478-1479; 1580pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Roy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000CA-2307010
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99CA-2283458
                                                                                                                                                                                                                                                                                                     99.2%;
99.5%;
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                                                                                                                                                                                                                                                                                Score 206.4; DB 22; Length Pred. No. 2.3e-45; O; Mismatches 1; Indels
                                  208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouellette
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RESULT 9
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Best Local
 AAA89994;
                       AAA89994 standard;
                                                                                     1657
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                                                                                                                                                                                     1537
                                                                                                                                                                                                                                       1477
                                                                                                                                                                                                                                                                                                                                                                   The present sequence is the rpoB gene from Mycobacterium tuberculosis. Rifampin resistance is largely associated with point mutations localised in a small core region of 81 base pairs in the rpoB gene, which encodes the RNA polymerase beta subunit. To detect a mutation, a complex is formed comprising a first sequence representing the predetermined region of the gene of the organism and a second sequence representing the corresponding region of the gene of the wild type organism in double stranded form. Each member of at least one pair of non-complementary strands within the complex has a label. The association of the labels in the complex is related to the presence of the mutation. The presence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Method for detecting drug resistance in a strain of an organism, particularly for detecting rifampin resistance in Mycobacterium
                                                                                                            181
                                                                                                                                                              121
                                                                                                                                                                                                                                                                                                                                        Sequence 3853 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 1; Fig 4; 86pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Liu YP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19-JAN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mycobacterium tuberculosis; rpoB; RNA polymerase beta subunit; rifampin resistance; mutation detection; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (DADE-) DADE BEHRING INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAA74651 standard;
                                                                                                                                                                                                              61
                                                                                                                                                                                                                               mutation is related to the drug resistance of the strain.
                                                                                 TCGAGGTGCCGGTGGAAACCGACGACAT 208
                                                                                                                                                                                               GGCTGCATGTCGGCGAGCCCATCACGTCGTCGACGCTGACCGAAGAAGACGTCGTGGCCA 120
                                                                                                                                               GGCTGCATGTCGGCGAGCCCATCACGTCGTCGACGCTGACCGAAGAAGACGTCGTGGCCA
                                                                                                                                  CCATCGAATATCTGGTCCGCTTGCACGAGGGTCAGACCACGATGACCGTTCCGGGCGGCG
                                                                                                                                                                                                                                                                                         207;
                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kurn N;
                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tuberculosis
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                                                                                                                                                                                                                                                                                                                                  723 A; 1173 C; 1293 G; 664 T; 0 other;
                       DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA;
                                                                                                                                                                                                                                                                                                99.2%;
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                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rpoB gene
                                                                                                                                                                                                                                                                                             Score 206.4; DB 21;
Pred. No. 2.3e-45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          detection;
                                                                                                                                                                                                                                                                                   Mismatches
                                                                                   1684
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                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                           Length 3853;
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                                                                                                                                 1656
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RESULT 10
AAS05210
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                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                             Matches 207;
                                                                                                                                                                                                                                                                                                                                                             This invention relates to a method for detecting drug resistance in a strain of an organism. The method comprises detecting the presence of a least 1 mutation in a first sequence and relating the presence of the mutation to drug resistance. Included in the invention are a kit for carrying out the method and a method for detecting the presence of a difference between two related nucleic acid sequences in an organism. The methods are useful for detecting resistance to drugs such rifampin and pyrazinamide in Mycobacterium. The present sequence represents the Mycobacterium tuberculosis rpoB gene (which encodes the RNA polymerase beta subunit). The sequence is used in an example of the method of the invention for the detection of rifampin resistance in M. tuberculosis.
                                                                                        1657
AAS05210;
                       AAS05210
                                                                                                                                                                                            1537
                                                                                                                                                                                                                                             1477
                                                                                                                                                                                                                                                                                                                                         Sequence 3853 BP; 723 A; 1173 C; 1293 G; 664 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Detecting resistance of drugs such as rifampicin in strains Mycobacterium, comprising detecting mutations in a gene and them to drug resistance \cdot
                                                                                                               181
                                                                                                                                                                  121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 1; Fig 4; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-499235/44
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22-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drug resistance; rifampin; rifampicin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Liu YP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200043545-A2
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                                                                                                                                                                                                                   61
                                                                                                                                                                                                                                   tuberculosis rpoB gene encoding RNA
                                                                                                                             CCATCGAATATCTGGTCCGCTTGCACGAGGGTCAGACCACGATGACCGTTCCGGGCGGCG
                                                                                                                                                                                                 GGCTGCATGTCGGCGAGCCCATCACGTCGTCGACGCTGACGAAGAAGAAGACGTCGTGGCCA 120
                                                                                   TCGAGGTGCCGGTGGAAACCGACGACAT
                                                                                                           TCGAGGTGCCGGTGGAAACCGACGACAT
                                                                                                                                                       GGCTGCATGTCGGCGAGCCCATCACGTCGTCGACGCTGACCGAAGAAGACGTCGTGGCCA
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                     standard;
                                                                                                                                                                                                                                                                                            Conservative
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99US-0296894
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                     DNA;
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99.5%;
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                     208
                     ВP
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relating
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07-SEP-2001

(first entry)

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The present sequence for Mycobacterium ulcerans rpoB gene
CC fragment is 1 of 24 rpoB gene fragments (AAS05201-AAS05224) from
CC various Mycobacterial species. These rpoB gene fragments can be used
CC in the diagnosis and identification of Mycobacterium species using a
CC movel PCR restriction fragment length polymorphism analysis (PRA)
CC method. The method comprises obtaining a restriction fragment length
CC polymorphism (RFLP) pattern of the 24 rpoB gene fragments; isolating,
CC amplifying and digesting the DNA fragment from the microorganism to
CC diagnosis and comparing the RFLP patterns from the known rpoB gene
CC fragments with the unidentified fragment. The rpoB gene fragments
CC are useful to identify a wide range of Mycobacterium species, e.g. for
CC diagnosis or to obtain epidemiological and pathogenesis information for
CC selection of appropriate therapies, including M. tuberculosis, M. leprae
CC and non-tuberculous mycobacteria (NTM) encountered in subjects infected
CC with human immunodeficiency virus (HIV). Analysis of the rpoB gene
CC required), and can differentiate between many species in a single
CC experiment, including those difficult to distinguish by usual biochemical
CC detecting specific Mycobacterial species
                                                                                                                                                                                                                                                                                         Query Match
Best Local 9
                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New DNA fragments from the rpoB gene of mycobacteria, useful for diagnosis and identification of many mycobacterial species by restriction fragment length polymorphism \,
 181
                                  181
                                                                    121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mycobacterium ulcerans rpoB
                                                                                                                                    61
                                                                                                                                                                    61
                                                                                                                                                                                                                   1 TCAAGGAGAAGCGCTACGACCTGGCCCGCGTCGGTCGCTATAAGGTCAACAACAAGAAGCTCG
                                                                                                                                                                                                        <u>.</u>
                                                                                                                                                                                                                                                                                         Local Similarity
                 TCGAGGTGCCGGTGGAAACCGACGACAT 208
                                                           CCATCGAATATCTGGTCCGCTTGCACGAGGGTCAGACCACGATGATCGTTCCGGGCGGCG 180
                                                                                                                                               GGCTGCATGTCGGCGAGCCCATCACGTCGTCGACGCTGACCGAAGAAGACGTCGTGGCCA 120
TCGAGGTGCCGGTCGAGACCGACGACAT
                                                                                                                           GCCTGAACGCCGGCCAGCCCATCACCAGCTCGACGCTGACCGAGGAAGACGTCGTCGCCA 120
                                                                                                                                                                                               TCAAGGAGAAGCGCTACGACCTGGCTCGCGTGGGTCGGTACAAGGTCAACAAGAAGCTCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Park YK, Bai G,
                                                                                                                                                                                                                                                                                                                                           208 BP;
                                                                                                                                                                                                                                                                                                                                                                         specific Mycobacterial species.
                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99KR-0046795
                                                                                                                                                                                                                                                                                                                                         45 A; 68 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mycobacteria; rpoB gene fragment; NTM; HIV; PRA; RFLP; fragment length polymorphism analysis; ds.
                                                                                                                                                                                                                                                                                     82.3%;
88.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kin
                                                                                                                                                                                                                                                                Score 171.2; DB 22;
Pred. No. 3.4e-36;
"""matches 23;
                                                                                                                                                                                                                                                                                                                                    67 G; 28 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'n
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                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                    Length 208;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Park HJ;
                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                Gaps
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RESULT 11

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Best Local
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                                                                                                                                                                                                                                                                             and non-tuberculous mycobacteria (NTM) encountered in subjects infected with human immunodeficiency virus (HIV). Analysis of the rpoB gene fragments is rapid, precise, simple and cost effective (only 1 PCR required), and can differentiate between many species in a single experiment, including those difficult to distinguish by usual blochemical tests. Also described are oligonucleotide probes (AAS05227-AAS05242) for detecting specific Mycobacterial species.
                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 41; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New DNA fragments from the rpoB gene of mycobacteria, useful for diagnosis and identification of many mycobacterial species by restriction fragment length polymorphism .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-300520/31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mycobacterium gordonae type III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mycobacterium gordonae type III rpoB gene fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lee H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (ERUM-) ERUME BIOTECH CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-OCT-2000; 2000WO-KR01223.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Non-tuberculous
PCR-restriction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAS05203 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAS05203;
                                                                                                                      GGCTGCATGTCGGCGAGGCCCATCACGTCGACGTCGACGCTGACCGAAGAAGACGTCGTGGCCA 120
                          CCATCGAATATCTGGTCCGCTTGCACGAGGGTCAGACCACGATGATCGTTCCGGGCGGCG 180
CCATCGAGTACCTGGTCCGTCTGCACGAGGGTCAGCACACGATGACCGTTCCGGGCGGCA
                                                                                                                                                                                                184;
                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                             208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Park YK, Bai G, Kim S,
                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                           BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99KR-0046795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mycobacteria; rpoB gene fragment; NTM; HIV; PRA; RFLP; fragment length polymorphism analysis; ds.
                                                                                                                                                                                                                                                        46 A; 69 C;
                                                                                                                                                                                                      81.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              208 BP
                                                                                                                                                                                           0,
                                                                                                                                                                                                                                                     63 G; 30 T; 0 other;
                                                                                                                                                                                                     Score 169.6; DB 2
Pred. No. 8.9e-36;
                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cho s,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kim
                                                                                                                                                                                                                       DB 22;
                                                                                                                                                                                    24; Indels
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AAS05211
                                                                                                                                                                                                    The present sequence for Mycobacterium marinum rpoB gene CC fragment is 1 of 24 rpoB gene fragments (AAS05201-AAS05224) from CC various Mycobacterial species. These rpoB gene fragments can be used CC in the diagnosis and identification of Mycobacterium species using a covel PCR-restriction fragment length polymorphism analysis (PRA) CC method. The method comprises obtaining a restriction fragment length polymorphism analysis (PRA) CC mplifying and digesting the DNA fragment from the microorganism to be identified and comparing the RFLP patterns from the known rpoB gene CC fragments with the unidentified fragment. The rpoB gene fragments comparing the RFLP patterns from the known rpoB gene CC are useful to identify a wide range of Mycobacterium species, e.g. for CC diagnosis or to obtain epidemiological and pathogenesis information for CC selection of appropriate therapies, including M. tuberculosis, M. leprae CC and non-tuberculous mycobacteria (NTM) encountered in subjects infected fragments is rapid, precise, simple and cost effective (only 1 PCR crequired), and can differentiate between many species in a single cappending those difficult to distinguish by usual biochemical tests. Also described are oligonucleotide probes (AAS05227-AAS05242) for CX detecting specific Mycobacterial species.
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                                                                                                                   Matches
                                                                                                                                   Query Match
Best Local
                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New DNA fragments from the rpoB gene of mycobacteria, useful diagnosis and identification of many mycobacterial species by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 43; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        restriction fragment length polymorphism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lee H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ERUM-) ERUME BIOTECH CO LTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Non-tuberculous mycobacteria; rpoB gene fragment; NTM; HIV; PRA; RFLP; PCR-restriction fragment length polymorphism analysis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W0200131061-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mycobacterium marinum rpoB gene fragment.
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                       61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181
                                                     -
                                                                                                                                  Local
GGCTGCATGTCGGCGAGCCCATCACGTCGTCGACGCTGACCGAAGAAGACGTCGTGGCCA 120
                                                             TCAAGGAGAAGCGCTACGACCTGGCCCGCGTCGGTCGCTATAAGGTCAACAAGAAGCTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCGAGGTGCCGGTGGAAACCGACGACAT 208
                                                                                                                              Similarity
                                                                                                                                                                             208 BP;
                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99KR-0046795
                                                                                                                                                                           45 A; 69 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bai G,
                                                                                                                              81.5%;
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                                                                                                              0;
                                                                                                          Score 169.6; DB 22;
Pred. No. 8.9e-36;
0; Mismatches 24;
                                                                                                                                                                      68 G; 26 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cho s,
                                                                                                                                        DB 22;
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                                                                                                              Indels
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                                                                                                                                          Length
                                                                                                                                          208;
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                                                                                                         Gaps
                                              60
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The present sequence for Mycobacterium avium rpoB gene
C fragment is 1 of 24 rpoB gene fragments (AASO5201-AASO5224) from
CC various Mycobacterial species. These rpoB gene fragments can be used
CC in the diagnosis and identification of Mycobacterium species using a
CC method. The method comprises obtaining a restriction fragment length
CC polymorphism (RFLP) pattern of the 24 rpoB gene fragments; isolating,
CC amplifying and digesting the DNA fragment from the known rpoB gene
CC are useful to identify a wide range of Mycobacterium species, e.g. for
CC are useful to obtain epidemiological and pathogenesis information for
CC selection of appropriate therapies, including M. tuberculosis, M. leprae
CC and non-tuberculous mycobacteria (NTM) encountered in subjects infected
CC fragments is rapid, precise, simple and cost effective (only 1 PCR
CC experiment, including those difficult to distinguish by usual blochemical
CC tests. Also described are oligonuclectide probes (AASO5227-AASO5242) for
XX
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AAS05215
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                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 44; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                      New DNA fragments from the rpoB gene of mycobacteria, useful for diagnosis and identification of many mycobacterial species by restriction fragment length polymorphism -
                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-300520/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lee н,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Non-tuberculous mycobacteria; rpoB gene fragment; NTM; HIV; PRA; PCR-restriction fragment length polymorphism analysis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mycobacterium avium rpoB gene fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ERUM-) ERUME BIOTECH CO LTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCATCGAATATCTGGTCCGCTTGCACGAGGGTCAGACCACGATGATCGTTCCGGGCGGCG 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kim Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Park HJ;
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Matches 183; Conserv

Conservative

0,:

Score 168; Pred. No. 2.

DB 22;

Length 208; Indels

0

Gaps

0

Query Match Best Local Sequence

208 BP;

44

A; 69 80.8%;

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69

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26 T; 0 other;

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The present sequence for Mycobacterium gordonae type I rpoB gene CC fragment is 1 of 24 rpoB gene fragments (AASO5201-AASO5224) from CC various Mycobacterial species. These rpoB gene fragments can be used CC in the diagnosis and identification of Mycobacterium species using a CC method. The method comprises obtaining a restriction fragment length cC method. The method comprises obtaining a restriction fragment length CC polymorphism (RFLP) pattern of the 24 rpoB gene fragments; isolating, CC amplifying and digesting the DNA fragment from the microorganism to be identified and comparing the RFLP patterns from the known rpoB gene CC fragments with the unidentified fragment. The rpoB gene fragments comparing the RFLP patterns from the known rpoB gene CC are useful to identify a wide range of Mycobacterium species, e.g. for CC diagnosis or to obtain epidemiological and pathogenesis information for CC selection of appropriate therapies, including M. tuberculosis, M. leprae CC and non-tuberculous mycobacteria (NTM) encountered in subjects infected CC with human immunodeficiency virus (HIV). Analysis of the rpoB gene CC fragments is rapid, precise, simple and cost effective (only 1 pCR CC experiment, including those difficult to distinguish by usual biochemical CC tests. Also described are oligonucleotide probes (AASO5227-AASO5242) for XX
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AAS05201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          restriction fragment length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-300520/31.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ERUM-) ERUME BIOTECH CO LTD
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novel PCR restriction fragment length polymorphism analysis (PRA) method. The method comprises obtaining a restriction fragment length polymorphism (RFLP) pattern of the 24 rpoB gene fragments; isolating polymorphism (RFLP) pattern of the 24 rpoB gene fragments; isolating, amplifying and digesting the DNA fragment from the microorganism to be identified and comparing the RFLP patterns from the known rpoB gene fragments with the unidentified fragment. The rpoB gene fragments diagnosis or to obtain epidemiological and pathogenesis information for selection of appropriate therapies, including M. tuberculosis, M. leprae and non-tuberculous mycobacteria (NTM) encountered in subjects infected with human immunodeficiency virus (HIV). Analysis of the rpoB gene
                                                                                                                                                             The present sequence for Mycobacterium kansasii rpoB gene fragment is 1 of 24 rpoB gene fragments (AAS05201-AAS05224) from various Mycobacterial species. These rpoB gene fragments can be used in the diagnosis and identification of Mycobacterium species using a
                                                                                                                                                                                                                                            Claim 1; Page 42; 50pp; English.
                                                                                                                                                                                                                                                                                  New DNA fragments from the rpoB gene of mycobacteria, useful for diagnosis and identification of many mycobacterial species by
                                                                                                                                                                                                                                                                                                                                                                     Lee
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                                                                                                                                                                                                                                                                                        fragments is rapid, precise, simple and cost effective (only 1 PCR required), and can differentiate between many species in a single experiment, including those difficult to distinguish by usual biochemical tests. Also described are oligonucleotide probes (AAS05227-AAS05242) for detecting specific Mycobacterial species.
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SUMMARIES

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ALIGNMENTS

REFERENCE AUTHORS		ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION		DEFINITION	LOCUS	MTU318818	RESULT 1
1 Herrera,L., Jimenez,M.S. and Saez,J.A.	Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium tuberculosis complex.	Mycobacterium tuberculosis	Mycobacterium tuberculosis.	RNA polymerase beta subunit: rpoB gene	AJ318818.1 GI:22208412	АJ318818	beta subunit, isolate 1415-97.	l rpoB ger	MTU318818 610 bp DNA circular RCT 09-AUG-2002		

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207; Conserv
                                             Herrera, L., Jimenez, M.S. and Saez, J.A. Molecular analysis of rifampin-resistant Mycobacterium tuberculosis isolated in Spain (1996–2001). Description of new alleles into rpoB
                                                                                                                Mycobacterium tuberculosis
Mycobacterium tuberculosis
Bacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobact
                        Unpublished
                                                                                                                                                                          RNA polymerase beta subunit;
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Submitted (07-AUG-2001) Herrera L., Servicio Bacteriologia,
Nacional Microbiologia, Ctra. Majadahonda-Pozuelo, Km 2.5,
Majadahonda. Madrid. 28220, SPAIN
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/product="RNA polymerase beta subunit"
/protein_id="CAC87035_1"
/db_xref="GI:22208413"
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/isolate="1415-97"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       207;
            Submitted (07-AUG-2001) Herrera L., Servicio Bacter Nacional Microbiología., Ctra. Majadahonda-Pozuelo, Majadahonda. Madrid. 28220, SPAIN
                                                                                                                                   Herrera,L., Jimenez,M.S. and Saez,J.A.
Molecular analysis of ritampin-resistant Mycobacterium tuberculosis
isolated in Spain (1996-2001). Description of new alleles into rpoB
gene and review
                                                                                                                                                                                                                          Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterium; Mycobacterium
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                                                                     Direct Submission
                                                                                   Herrera, L.
                                                                                                                     Unpublished
                                                                                                                                                                                                                     tuberculosis complex.
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Submitted (07-AUG-2001) Herrera L.,
Nacional Microbiologia., Ctra. Majac
Majadahonda. Madrid. 28220, SPAIN
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Location/Qualifiers
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(protein_id="CAC87036.1"

/protein_id="CAC87036.1"

/db_xref="Gi:22208415"

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RLRTVGELIQNQIRVGMSAMERVVRERWTTQUVEAITPQTLINIRPVVAAIKEFFGTS

QPSQFMQQNNPLSGLTHKRRLSALGGGLSRERAGLEVRDVHP"

a 191 c 202 g 95 t
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/codon_start=1
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/isolate="1417-97"
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                            Servicio Bacteriologia,
dahonda-Pozuelo, Km 2.5,
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                                                                                                                  Direct Submission
Submitted (07-AUG-2001) Herrera L., Servicio Bacteri
Nacional Microbiologia., Ctra. Majadahonda-Pozuelo,
Majadahonda. Madrid. 28220, SPAIN
                                                                                                                                                                                                                                            Herrera,L., Jimenez,M.S. and Saez,J.A.
Molecular analysis of rifampin-resistant Mycobacterium tuberculosis
isolated in Spain (1996-2001). Description of new alleles into rpoB
                                                                                                                                                                                                                                                                                                                    Mycobacterium tuberculosis.
Mycobacterium tuberculosis
Mycobacterium tuberculosis
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium
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                                                                                                                                                                                                                                       gene and review
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Mycobacterium tuberculosis partial beta subunit, isolate 2540-97.
                                                                                                                                                                                                                        Unpublished
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/gene="rpoB"
<1. .>618
                              /db_xref="taxon:1773"
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/isolate="2540-97"
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QLSQFIFMDQNNPLSGLTHKRRLSALGPGGLSRERAGLEVRDVHP"
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/transl_table=11
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/isolate="1763-97"
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                                                                                                                                                                                       Submitted (07-AUG-2001) Herrera L., Servicio Bacteriologia, Centro Nacional Microbiologia., Ctra. Majadahonda-Pozuelo, Km 2.5, Majadahonda. Madrid. 28220, SPAIN Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                             RNA polymerase beta subunit;
Mycobacterium tuberculosis
Mycobacterium tuberculosis
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Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium
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190 c 207 g 97 t
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                                                                                                                                                                                                                                                                                                                           Submitted (07-AUG-2001) Herrera L., Servicio Bacteriologia, Centro Nacional Microbiologia, Ctra. Majadahonda-Pozuelo, Km 2.5, Majadahonda. Madrid. 28220, SPAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Herrera,L., Jimenez,M.S. and Saez,J.A. Molecular analysis of rifampin-resistant Mycobacterium tuberculosis isolated in Spain (1996–2001). Description of new alleles into rpob gene and review
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RNA polymerase beta subunit; rpoB
Mycobacterium tuberculosis.
Mycobacterium tuberculosis
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AAIKEFFGTSQLSQFMDQNNPLSGLTYKRRLSALGPGGLSRERAGLEVRDV"
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Majadahonda. Madrid. 28220, SPAIN
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/translation="VGTDEALLDIYRKLRPGEPPTKESAQTLLENLFFKEKRYDLARV
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                                                                                                                                                                                                                             /gene="rpoB"
<1. .>637
                                                                                                                                                                                                                                                                                     /organism="Mycobacterium
/isolate="1255-98"
                                                                                                                                                                                                               /gene="rpoB"
                                                                                                                                                                                                                                                                     db_xref="taxon:1773"
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                 99.2%;
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  Score 206.4; DB 1;
Pred. No. 1.5e-33;
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                                                                   TCAAGGAGAAGCGCTACGACCTGGCCCGCGTCGGTCGCTATAAGGTCAACAAGAAGAAGCTCG 60
                                                     TCAAGGAGAAGCGCTACGACCTGGCCCGCGTCGCTATAAGGTCAACAAGAAGCTCG 160
      GGCTGCATGTCGGCGAGCCCATCACGTCGTCGACGCTGACCGAAGAAGACGTCGTGGCCA
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Submitted (07-AUG-2001) Herrera L., Servicio Bacteriologia, Nacional Microbiologia., Ctra. Majadahonda-Pozuelo, Km 2.5, Majadahonda. Madrid. 28220, SPAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     beta subunit, isolate 1071-98
AJ318821
AJ318931.1 GI:22208418
RNA polymerase beta subunit;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished
2 (bases 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Herrera, L., Jimenez, M.S. and Saez, J.A. Molecular analysis of rifampin-resistant Mycobacterium tuberculosis isolated in Spain (1996-2001). Description of new alleles into rpoB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium
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Mycobacterium tuberculosis partial
beta subunit, isolate 1071-98.
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/protein_id-"CACB7038.1"
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IDHFGNRRLRTVGELIONQIRVGMSRMERVVRERMTTQDVEAITPQTLINIRPAVAAI
KEFFGTSOLSOFMVQNNPLSGLTQKRRLSALGPGGLSRERAGLEVRDVHPSHS"
a 202 c 212 g 99 t
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<1. .>639
                                                                                                                                                                                                                                                                            /codon_start=1
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                     /organism="Mycobacterium
/isolate="1071-98"
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CCATCGAATATCTGGTCCGCTTGCACGAGGGTCAGACCACGATGACCGTTCCGGGCGGCG
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                                                                   Mycobacterium tuberculosis.

Mycobacterium tuberculosis

Bacteria, Firmicutes, Actinobacteria, Actinobacteridae;

Bacteria, Firmicutes, Actinobacterineae;

Mycobacterium, Mycobacterium tuberculosis complex.

I (bases 1 to 3534)

Bergeron, M.G., Boissinot, M., Huletsky, A., m Nard, C., Ou Plcard, F.J. and Roy, P.H.
                                                                                                                                                                                                                                                          Sequence 207
AX111339
AX111339.1
Highly conserved genes and their use to for detection of microorganisms Patent: WO 0123604-A 2072 05-APR-2001; Infectio Diagnostic (I.D.I.) INC. (CA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  l (bases 1 to 970)
Persing,D.H., Hunt,J.J., Young,K.K.Y., Felmlee,T.A., Roberts,G.D. and Whelan,A.Christian.
Detection of a genetic locus encoding resistance to rifampin in mycobacterial cultures and in clinical specimens patent: US 5643723-A 1 01-JUL-1997;
Patent: US 5643723-A 1 01-JUL-1997;
1. . 970
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Mycobacterium tuberculosis H37Rv
gene, partial cds.
U12205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (11-JUL-1994) Paul Imboden, Institute for Medical Microbiology, University of Berne, Friedbuehlstrasse 51, Be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 3853)
Imboden, P., Troller, R., Marchesi, F.,
Cole, S., Schopfer, K. and Burkart, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The rpoB gene of Mycobacterium tuberculosis
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                                                                                                                                                                                                                                                                   /organism="Mycobacterium
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576. .>3853
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TEKGTFIINGTERVVVSQLVRSPGVYDETIDKSTDKTLHSVKVIPSRGAWLEFDVDK
RDTVVVRIDKKRQPVTVLLKALGWTSEQIVERFGSSEIMRSTLEKNNTVGTDEALLD
IYRKLRPGEPPTKESAQTLLENLFFKEKRYDLARVGRYKVNKKLGLHVGEPITSSTLT
EEDVVATIEYLVRLHEGQTTMTVPGGVEVPVETDDIDHFGNRRLRTVGELIQNQIRVG
                                                                                                                                                                           /codon_start=1
/transl_table=11

    .3534
/organism="Mycobacterium tuberculosis"
/strain="Rv"

                                                                                                                                                                                                                /gene="rpoB"
                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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1081 c 1188 g
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Pred. No. 1.
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RNA-polymerase beta
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REFERENCE
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ORGANISM
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DEFINITION
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                                                                                                                                                                                                                                                                                                                                                     Corynebacter....
tuberculosis complex.
1 (bases 1 to 5084)
Miller, L.P., Crawford, J.T. and Shinnick, T.M.
Miller, Department of Mycobacterium tuberculosis
The rpoB gene of Mycobacterium tuberculosis
1 and 3 (4), 805-81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RNA polymerase beta-subunit; rpoB gene. Mycobacterium tuberculosis (strain Rv) DNA. Mycobacterium tuberculosis
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Mycobacterium tuberculosis RNA polymerase beta-subunit (rpoB)

gene, complete cds and RNA polymerase beta'-subunit rpoC gene,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Actinobacteria; Actinobacte
Corynebacterineae; Mycobacteriaceae;
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/gene="rpoB"
1065. .4598
/gene="rpoB"
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DILVGKVTPKGETELTPEERLLAAIFGEKAREVRDTSLKVPHGESGKVIGIRVESRED
EDELPAGVNELVRVYAQKKKISDGDKLAGRHGNKGVIGKILPVEDMPFLADGTPDI
ILNTHGVPRRMNIGQILETHLGWCAHSGWKVDDAAKGVPDWAARLPDELLEAQPNAIVS
TPVFDGAQEAELQGLLSCTLPNRDGDVLVDADGKAMLFDGRSGEPFPYPVTVGYMYIM
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EVEYVPSSEVDYMDVSPRQMVSVATAM1PFLEHDDANRALMGANMQRQAVPLVRSSAP
LVGTGMELRAA1DAATSSQESGV1EEVSADY TIVMHUNGTRRTYRMRKEARSNHGE
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/protein_id="AAA21416.1"
/db_xref="GI:448334"
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HKRRLSALGPGGLSRERAGLEVRDVHPSHYGRWCPIETPEGPNIGLIGSLSVYARVNP
                                                                                      /evidence=experimental
/transl_table=11
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TIKS "
                                                                                                                                    /codon_start=1
                                                                                                                                                                                                                                                                                                                            Cocation/Qualifiers
                                                                                                                                                                                                                                        db_xref="taxon:1773"
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99.5%;
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 Mismatches

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Pred. No. 1.3e-33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Actinobacteridae; Actinomycetales; cteriaceae; Mycobacterium; Mycobact
                                                                                                                                                                                                                                                                                                                                                                                        38 (4), 805-811
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                                                                                                                                                                                                                                                                                  tuberculosis"
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Best Local
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Fleischmann,R.D., Alland,D., Eisen,J.A., Car
Peterson,J., DeBoy,R., Dodson,R., Gwinn,M.,
Kolonay,J.F., Nelson,W.C., Umayam,L.A., Ermc
                                                                                                                    Mycobacterium: Mycobacterium tuberculosis (bases 1 to 19352)
                                                                                                                                                                                                                     Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                   Mycobacterium tuberculosis CDC1551.
Mycobacterium tuberculosis CDC1551
                                                                                                                                                                                                                                                                                                                                                                                                               complete genome. AE006964 AE000516
                                                                                                                                                                                          Actinomycetales; Corynebacterineae; Mycobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                        AE006964.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AE006964
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MSRMERVYRERMTTODVEA I TPOTT LI NI RPVVAA I KEFFGT SOLSOFMDONRPLSGIT
HKRRLSALGFGGLSRERAGLEVROVHBSHYGRWCP I ETPEGEN IGLIGSLSVYARVNP
FGFT ETPYRRVVDGVVSDEIVYLTADEEDRHVVAQANS PIDADGRFVEPRVLYRRKAG
EVEYVPSSEVDYMVSPROMVSVATAMI PFLEHIDDANRALMGANMOROAVPLVRSEAP
LVGTGMELRAA IDAATSSSOESGVI EEVSADY I TVMHDNGTRRT YRMRKFARSNHGTC
ANOCPT IVDAGDRVEAGQVV ADGRFCTDDGEMALGKNLLVA I NPEWEGHNYEDA I I LSNRL
VEEDVLTSI HI EEHEI DARDTKLGAEEI TROI PN I SDEVLADLDERGI VRIGAEVRDG
DI LVGKVTPKGETELTPEERLLRAI FGEKAREVRDTSIK VPHGESGKVIGI RVFSRED
EDELPAGVNELVRYVYAQOKRK I SDGDKLAGRHGNKGVIGK ILPVEDMPFLADGTPVDI
ILNTHGVPRRMNIGOI LETHLGWCAHSGWKVDAAKGVDDWARALDDEELLERHANAIVS
TROUTTON OF TOTT OT TOTT OT TOTT OT TOTT OT TOTT OTT.
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KLHHLVDDKHARSTGPYSMITQQPLGGKAQFGGQRFGEMECWAMQAYGAAYTLQELL
TIKSDDTVGRVKVYEAIVKGENIPEPGIPESFKVLLKELQSLCLNVEVLSSDGAAIEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
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4641. .>5084
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                                                                                                                                                                                                                                                                                                                                                                                    GI:13880217
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99.5%;
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Pred. No. 1.3e-33;
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|sis CDC1551,
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           Ermolaeva, M.,
                                      M., Haft,D., Hickey,E.,
                                                                                                                                                   complex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear BCT 27-APR-2001 on 50 of 280 of the
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                                                                         White, O.,
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REFERENCE AUTHORS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished
2 (bases 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (25-APR-2001) The Institute for Genomic Research, 9712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
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LEDIWSTFTKLAPKOLIVDENLYRELVDRYGEYFTGAMGAESIQKLIENFWQLDGGR
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LEKPFVMKRLVDLNHAQNIKSAKRMVERQRPQVWDVLEEVIAEHPVLLNRAPTLHRLG
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3744...7694
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                                                                                                                                                                                                                                                                                                                                                                            /note="similar to SP:
similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STPVFDGAQEAELQGLLSCTLPNRDGDVLVDADGKAMLFDGRSGEPFPYPVTVGYMYI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LREGEDEDLERAAANLGINLSRNESASVEDLA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="similar to GB:L27989 GB:L05910 GB:U12205 SP:P47766 PID:149992; identified by sequence similarity; putative"
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                                                                                                                                                                                                                                                                                                                                                                                                         SP:P37871; identified by sequence
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11859. 1740-
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10957
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sequence similarity; putative"
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YLETSAYARTLGTDAVDEAGNVIVERGGDLGDEIDALLAAGTTQYKWRSVLTGATST
GYCATCYGRSMATGKLUDIGEANGIVAAQS ISEEPGTQLIRMTEHQGGVGEDITGGLPR
VQELFEARVPRGKAPIADVTGRVRLEDGERFYKLTIVPDDGGEEVVYDKISKRGRLRV
YRHEDGSERVLSDGDHVEVGQQLMEGSADPHEVLRVQGPREVQLILVREVYGEVYRAQG
VSIHDKHLEVIVRQMLRRAVTIDSGTEFLFGSLIDRAFERADRRVVAEGGEPAAGR
PVLMGITKASLATDSWLSAASFQETTRVLTDAAINCRSDKLNGLKENVIIGKLIPAGT
GINRYRNIAVQPEEARAAAYTIPSYEDQYYSPDFGAATGAAVPLDDYGYSDYR"
                                                                                                                                                                                                                              AFWREVNRCGALDTTTEGPVTTSGATCADNRRVVLLTVDDAGHRWPSFATQTLWRFF#
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LDTCHTWAAGEALTDAVDRIKAITGRIDLVHCNDSRDEAGSGRDRHANLGSGQIDPDLLVAAVKAAGAPVICETADQGRKDDIAFLRERTGS"
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Alkaatlpiyvhapylinlasannrripsrkilqetcaaaadigaaavivhgghvad
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10167. .10925
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note-"This region contains an authentic frame shift and is not the result of a sequencing artifact; identified by Glimmer2; putative; conserved hypothetical protein, authentic frameshift"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(7691..8065)
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complement(7691..8065)
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                                                                                       /gene="MT0701"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPASGRPLAMPRLDMVTGLYYLTTEVPEDTGEYQPASGDHPETGVYSSDAEAIMAADR
GVLSVAAKIKVRLTQLRPPVEIEAELFGHSGWQPGDAWMAETTLGRVMFNELLPLGYP
FVNKQMHKKVQAAIINDLAERYPMIVVAQTVDKLKDAGFYWATRSGVTVSMADVLYPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /transl_table=11
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IITIVDSGATGNFTORTLAGMKGLVTNPKGEFIPRPVKSSFREGLTVLEYFINTHGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="hypothetical
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/transl_table=11
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                                                                                                                                                                                                                                                                                                       TCGAGGTGCCGGTGGAAACCGACGACAT 208
                                                                                                                                                                                                                                                                                                                                                        CCATCGAATATCTGGTCCGCTTGCACGAGGGTCAGACCACGATGATCGTTCCGGGCGGCG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                     GGCTGCATGTCGGCGAGCCCATCACGTCGTCGACGCTGACCGGAAGAAGAAGACGTCGTGGCCA 1183
                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGCTGCATGTCGGCGAGCCCATCACGTCGTCGACGCTGACCGAAGAAGACGTCGTGGCCA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCAAGGAGAAGCGCTACGACCTGGCCCGCGTCGGTCGCTATAAGGTCAACAAGAAGCTCG 1123
                                                                                                                                                                                                                                                                                    TCGAGGTGCCGGTGGAAACCGACGACAT 1271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            207;
Mycobacterium tuberculosis H37Rv.
Mycobacterium tuberculosis H37Rv
Bacteria; Pirmicutes; Actinobacteria; Actinobacteridae
Actinomycetales; Corynebacterineae; Mycobacteriaceae;
Mycobacterium; Mycobacterium tuberculosis complex.
                                                                                                                                     Mycobacterium tuberculosis H37Rv Z95972 AL123456
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                                                                                                                          GI:3261790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product-"enoyl-OoA hydratase/isomerase family protein "
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VIAAADAKIGYPPTRVWGVPAAGLWAHRLGDCRAKKLLFTGDCITGAQAAEWGLAVEA
PEPAADLDERTERLVARIAALPVNQLINVKLALNSALLOGGVATSRMVSTVFDGAARHT
14439...15161
14439...15161
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/codon codon codon
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VLADLAVEAEAAT I VAMRMAGATDNAVRGNETEALLRR I GLAAAKYMVCKRSTAHAAE
ALECLAGNGY VEDSGMPRLY REAPLMG I WEGSGNVSALDTLRAMATREACVEVLFDEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="MSDTHVVTNQVPPLENYNPASSPVLIEALIQEGGGWGLDEVNEVGAISASCQAQRWGELADRNRPILHTHDAYGYRVDEVBYDPAYHELMRTAITHGMHAAPWADDRPCAHVYRAAKTSVYMTVEPGHICPISMTYAVPALKTNSELAAVYEPLLTSREYDPELKPATTKAGITAGMSMTEKQGGSDVRAGTTQATPAADGSYSLTGHKWFTSAPMCDIFLVLAQAPDGLSCFLLPRVLPDGTRNRMFLQRLKDKLGNHANASSEYEYDGAVAWLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="MT0703"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="MT0703"
14439. .15161
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13498. .14436
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/transl_table=11
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99.5%;
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Pred. No. 1.2
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                                                                                                                                                           complete genome; segment 32/162.
                                                                                                                                                                                  DNA
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                                         Actinobacteridae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   available on the World Wide Web.

(URL, http://www.sanger.ac.uk/Projects/M_tuberculosis/) CDS have been renumbered from the original cosmid submissions but the old gene designations are in brackets after the new gene numbers.

Gene prediction was based on a Hidden Markov Model of TB genes implemented in TBparse (Krogh) supplemented with visual inspection of postitional base preference in codons, especially where there is an increase in the observed/expected third postition G + C.

CAUTION: In some cases we may not have predicted the correct initiation codon. Where possible we choose an initiation codon (atg, grg, or ttg) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most upstream codon).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (11-JUN-1998) Submitted on behalf of the Mycobacterium tuberculosis sequencing and mapping teams, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA Unite de Genetique Moleculaire Bacterienne, Institut Pasteur, 28 rue du Docteur Roux, 75724 Paris Cedex 15, France E-mail: parkhill@sanger.ac.uk On Jun 27, 1998 this sequence version replaced gi:2143285.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Details of M. tuberculosis sequencing at the Sanger Centre are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 3 98295987
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cole, S.T., Brosch, R., Parkhill, J., Garnier, T., Churcher, C., Harris, D., Gordon, S.V., Eiglmeier, K., Gas, S., Barry III, C.E., Tekaia, F., Badcock, K., Basham, D., Brown, D., Chillingworth, T., Connor, R., Davies, R., Deviin, K., Feltwell, T., Gentles, S., Hamlin, N., Holroyd, S., Hornsby, T., Jagels, K., Krogh, A., McLean, J., Moule, S., Murphy, L., Oliver, S., Osborne, J., Quail, M.A., Rajandream, M.A., Rogers, J., Rutter, S., Seger, K., Skelton, S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 (bases 1 to 19770)
Parkhill, J.
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                                                                               RYSRMFDRDRRGPGGDSRPSLDRWTINLATGAVTAECRDDRAQEFPRINETLVGGPHR
FAYTVGIEGGFLVGAGAALSTPLYKQDCVTGSSTVASLDPDLLIGEMVFVPNPSARAE
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Lrugpnpvaevdpat' hhetgaamyhqvalrogkarmyrnrwyrpavcallgepisa
RPHPRTGIIEGGPNTWLTHAGRTLALVEAGVVNYELTDELDTVGPCDFDGTLHGGYT
AHPQRDPHTGELHAVSYSFARGHRVQYSVIGTDGHARRTVDLEVAGSPMMHSFSLTDN
YVYIYDLPVTFDPMQVVPASVPRWLQRPARLVIQSVLGRVRIPDPIAALGNRMQGHSD
RLPYAMNPSYFARVGYMPREGGNEDVRWFDLEPCYVVHPLNAYSECRNGAEYLVLDVV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Rv0654, (MTC1376.22), len: 501. unknown, FASTA score: Q53353 LIGNOSTILBENE-ALPHA, BETA-DIOXYGENASE (485 aa) opt:280 z-score: 30.1 E(): 2.3e-11, (28.5% identity in 523 aaoverlap). Also similar to M. tuberculosis protein MTCY2IC12.07c (29.5% identity in 522 aa overlap)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="Rv0654"
68. .1573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="agga, possible 68. .1573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="I376"
57. .61
                                                                                                                                                                                                                                                                                                                                                                                                                                          /trans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:83332"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /strain-"H37Rv"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Rv0654"
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                                                                                              complement(3691..369
/note="possible RBS u
complement(3761..447
/gene="Rv0658c"
                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Rv0657c, (MTC1376.19),unknown, len: 51 aa; similar to several other M. tuberculosis hypothetical proteins eg. YW08_MYCTU Q10848 hypothetical 8.9 kd protein cr39.08c (80 aa), fasta scores; opt: 107 z-score: 182.3 E(): 0.0038, 45.8% identity in 48 aa overlap. Also similar to MTCY48_5 andAL020958|SC4H8_7 Streptomyces coelicolor cosmid 4H8 (66 aa), 41.0% identity in 39 aa overlap."
                                          complement(3761. .4477)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(3530. .3685)
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/note="PS00017 ATP/GTP-binding site motif
2074. .2118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(3530. .3685)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(3052. .3435)
/gene="Rv0656c"
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                                                                                                                                                                                                                                 translation - "MSVTQIDLDDEALADVMRIAAVHTKKEAVNLAMRDYVERFRRIE
                                                                                                                                                                                                                                                                   db_xref="SPTREMBL:006782"
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IVTHNINIATAYVPDNMGMLFRKHLVMFGPREVLLTSDEPVVRQFLNGRRIGPIGMSEE
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1585. .2664
(MTCI376.18), len: 238, unknown,
                                                                                                                      RBS upstream .4477)
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Query Match
Best Local Similarity
Matches 207; Conserva
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Sequence 57 from patent
AR067447
AR067447.1
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/gene="Rv0660c"
complement(5048. .5293)
/gene="Rv0660c"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="SPTREMBL.006781"
/translation="MEAGRADIYAPSHRWGLGAFLVVELVFLVASTSLAVVLTGHGPV
SAGVLALALAAPTVVAAGLAILITRIRGNURTBLRUVELWVVFVABLCEEZIYRGLLWG
IPASLVYTAIVGPEANSAVVRIEGGVRASWPWALVVFLVVVFVAPLCEEZIYRGLLWG
AVDRRWGRWAALVVTTVVFALAHLEFARAPLLVVVAIPIALAREYSGGLLASIVTHQV
TNLLPGIVLLGITGAISLP"
Complement(4480. 14483)
/note="possible RBS upstream of Rv0658c"
complement(4753. 5061)
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LVSELELTAVENRVPSDCVVNFDNIHTLPRTAFRRRITRLSPARLHEACQTLRASTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Rv0660c, (MTCI376.16), len: 81, some similarity | AF016485_130 Halobacterium sp; NRC-1 plasm (100 aa), 32.48identity in 74 aa overlap"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="hypothetical protein Rv0659c"
/protein_id="CAB09387.1"
/db_xref="GI:2143302"
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/db_xref="GI:2143303"
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DEFINITION
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Search completed: November 13, Job time: 660.723 secs
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                                                                                                                                                                                                                                                                                                                                                                                        TITLE
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                                                                                                929
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                                                        TCGAGGTGCCGGTGGAAACCGACGACAT 208
                                                                                                        GGTTGCACGCCGGTGAGTTGATCACGTCGTCCACGCTGACCGAAGAGGATGTCGTCGCCA
                                           TAGAAGTGCCAGTGGAAACTGACGATAT 1016
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                                                                                                                                                                                                                                                                                                                                                           tuberculosis Patent: US 5851763-A 57 22-DEC-1998;
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Heym,B., Cole,S., Young,D., Zhang,Y., Honore,N., Telenti,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unknown
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         2002, 01:27:59
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Post-processing: Minimum Match 0%
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20.6	20.6	20.8	21.5	22.1	64.3	Query Match Length DB
635	585	569	417	925	1282	Length
13	13	17	14	17	9	BG
в1065677	BM489075	вн897054	BM865094	CNS0091P	AI770311	ID
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BM698942	AA211560	BF221644	AA112975	AA180706	F25575	F21475	F36189	R86510	F00050	F27471	R86566	R86588	BQ294664	BQ743581	BF177122	BE429399	BE442717	AY103647	BG933256	BE358685	W17149	AW564128	BG159643	AA178937	CNS03VB3	B0824742	AI856228	AV635603	R86542	BE754521	AY109418	BG321153	B1995346	BF864011	3	1686	BM485879	627
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ALIGNMENTS

JOURNAL MEDLINE COMMENT REFERENCE AUTHORS TITLE ACCESSION VERSION KEYWORDS SOURCE ORGANISM FEATURES RESULT 1 A1770311/c DEFINITION Locus Mycobacterium smegmatis.
Mycobacterium smegmatis
Mycobacteriam smegmatis
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium. Mycobacterium Laboratory
Institute of Molecular and Cell Biology
30 Medical Drive, Singapore 117609, Republic of Singapore
Tel: 65 874 3011
Fax: 65 779 1117
Email: mcbbom@imcb.nus.edu.sg
Insert Length: 1282 Std Error: 0.00
Seq primer: T3 Forward; T7 Backward. 1 (bases 1 to 1282)
Murugasu-Oei,B., Tay,A. and Dick,T.
Upregulation of stress response genes and ABC transporters in anaerobic stationary-phase Mycobacterium smegmatis
MOl. Gen. Genet. 262 (4-5), 677-682 (1999) 20092472 Contact: Murugasu-Oei, smegmatis cDNA, mRNA sequence. AI770311 AI770311.1 GI:6742680 AI770311 1282 bp mRNA linear EST 24-JAN-2000 42 Mycobacterium anaerobic stationary phase library Mycobacterium Location/Qualifiers
1. .1282

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BASE COUNT
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Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BBGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
                                                                                                                                                                                                                                                                                                      Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fj
                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 925)
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                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                    Genoscope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster.
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//lab_host="E. coli XL1-Blue MRF/"
//note="vector: Lambda ZAP II; Bacilli were disrupted using the Rheasy protocol (Olagen). RNA was isolated using the Rheasy protocol (Olagen). Purified RNA was subjected to 2 rounds of digestion with RNase-free DNase I (Promega).

DNase I was heat-inactivated at 750C for 5 min. and removed by using RNeasy columns followed by phenol extraction and ethanol precipitation. The RNA preparations were confirmed to be free of genomic DNA contamination by carrying out PCR and RT-PCR using the Access kit (Promega) and primers specific for the histone-like protein gene hlp (Lee et al., 1998). CDNA was synthesized using random hexamer primers (Promega) and Stratagene's CDNA synthesis kit. CDNA fragments were ligated into lambda ZAP II vector and packaged in vitro using Stratagene reagents. "
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/strain="mc2155"
/db_xref="taxon:1772"
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Pred. No. 4.2e-20;
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REFERENCE AUTHORS

JOURNAL TITLE SOURCE ORGANISM

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COMMENT

/organism="Magnaporthe grisea"

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                                                                                                       Chromatogram file of this sequence is available, Best nr hit (Nov. 11, 2001) pir|T49413 probable monooxygenase (lovA) [impor. . . 78 5e-14
                                                                                                                                                                                   Texas A&M University
Peterson Bldg, MS2132,
Peter 979 845 4831
Fax: 979 845 6483
                                                                                                                                                                                                                                                                                                                                   Magnaporthe grisea.
Magnaporthe grisea
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
1 (bases 1 to 417)
Ebbole,D.J., Yuan,J., Thomas,T.L., Bobrowicz,P. and Dean,R.A.
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                        Plate: mgap008 row:
Seq primer: T3.
                                                                FORWARD: T3 primer BACKWARD: T7 prime
                                                                                                                                                                                                                                                Department of Plant Pathology & Microbiology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mgap008xJ06f.b Magnaporthe grisea grisea cDNA clone mgap008xJ06 5',
                                                                                                 PCR PRimers
                                                                                                                                                                                                                                                                         Contact: Ebbole DJ
                                                                                                                                                                                                                                                                                            Unpublished (2002)
                                                                                                                                                                  Email: d-ebbole@tamu.edu
                                                                                                                                                                                                                                                                                                                           Expressed sequence tags
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BM865094.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NY. The library is named RPCI-98 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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/clone_lib="RPCI-98"
/note="end : TET3"
a 61 c 61 g
           Location/Qualifiers
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/db_xref="taxon:7227"
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                                                                                                                                                                                                                                                                                                                    Yuan,J., Thomas,T.L., Bobrowicz,P. and Dean,R.A. quence tags from the rice blast fungus, Magnaporthe
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                                                                                                                                                                                                                College Station, TX 77843-2132, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 733 2227
Fax: 650 725 8221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zea mays.
Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Very probable ligation site of ends cut by single endonuclease. Reverse complemented post-ligation sequence from source sequence. plate: 3526_1_6_1 row: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Maize genomic sequences found using engineered RescueMu transposon 
Unpublished (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Class: transposon-tagged.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: walbot@stanford.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Department of Biological Sciences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Walbot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Walbot, V.
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/note-"Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site_1: BamHI; Site_2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /cell_type-"Appressorium"
/note-"Vector: pBluescriptSK+; Site_1: EcoRI; Site_2: Xho
/note-"Vector: pBluescriptSK+; Site_1 : EcoRI; Site_2: Xho
/note-"Vector: pBluescriptSK+; Site_1 : EcoRI; Site_2: Xho
/note-"Vector: pBluescriptSK+; Site_1 : EcoRI; Site_3: Xho
/note-"Vector: pBluescriptSk+; Site_1 : EcoRI; Site_1 : E
                                                                                                                 /lab_host-"DH10B"
                                                                                                                                                                                         /clone_lib="3526 - RescueMu
/tissue_type="leaf"
                                                                                                                                                                                                                                                             /cultivar="mixed background W23/A188/B73"
/db_xref="taxon:4577"
                                                                                                                                                       /dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                         /organism="Zea mays"
                                                                                                                                                                                                                                                                                                                                                                                                             ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="Magnaporthe grisea Ap Uni-Zap xR Library"
/sex="Matl-2 hermaphrodite"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /strain="70-15"
/db_xref="taxon:148305"
/clone="mgap008xJ06"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GI:22232454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21.5%;
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Pred. No. 2.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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BM489075
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14 CTACGATCTGGCCCGCGTGGGTCGGTACAAGGTGAACAAGAAGCTGGGCCTGGGCCGGCAC 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      74 CAATCCGGCTCAGGTGACCACCACCACCCTCACCGAGGAAGACGTCGTCGCCACCATCGA 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTGCCCCGCCGACCTGCGCGTGGCGGCGTCGACGACGTCCTCCGGCGGCGGCGGCGGCGTGG 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGCCGCTGCCGGGGGGGGAGCTGCGTGCCCACCGGCTGCATGGCGGACCTCAACGGCGC 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BM489075 585 bp mRNA linear EST 07-FEB-2002 pgm2n.pk009.nll Normalized Chicken Breast Muscle, Leg Muscle, and Epiphyseal Growth Plate cDNA library (pgm2n) Gallus gallus cDNA clone pgm2n.pk009.nll 5', similar to splP02588|TPCS_CHICK TROPONIN C, SKELETAL MUSCLE pir|TPCHCS troponin C, skeletal muscle - chicken
                                                                                                                                                                                                                                                                                                                                                                University of Delaware Townsend Hall, Newark, Tel: 302-831-1335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 585)
Cogburn, L.A. and Monsonego-Ornan, E.
ESTs from Normalized Chicken Breast Muscle, Leg Muscle,
Epiphyseal Growth Plate cDNA library, USDA/IFAFS Animal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gallus gallus
Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95;
                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Larry
                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
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                                                                                                                                                                                                                                                                                                cogburn@udel.edu, www.chickest.udel.edu.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                D
                                                                      /tissue_type="Breast muscle,
growth plate"
                                                                                                             and Epiphyseal Growth Plate
/sex="Male and Female"
/dev_stage="Breast,leg:Embryo(d19);post-hatch(1d,1,3,5,7,9
,11 weeks):growth plate(1d,7d,14d post-hatch)"
/lab_host="E. coli EMDH10B"
                                                                                                                                              /clone="pgm2n.pk009.n11"
/clone_1ib="Normalized Chicken Breast Muscle,
                                                                                                                                                                                                                    Strains 90 & 21*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.zmdb.iastate.edu' and follow the links for 'RescueMu.' Grid K was grown at Molokai, Hawaii in Winter 2000-2001. DNA was extracted from leaf punches, double digested using BamHI and BgIII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."
                                                                                                                                                                                            /db_xref="taxon:9031"
                                                                                                                                                                                                                                   /organism="Gallus gallus"
/strain="Commercial broiler
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20.8%;
                                                                                                                                                                                                                                                                                                                                                                                 Newark, DE 19717,
                                                                                                                                                                                                                                                                                                                                                                                                                         Cogburn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 44.6; DE Pred. No. 4.5; 0; Mismatches
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                                                                                                                            cDNA library
                                                                                                                                                                                                                                   and
                                                                                leg muscle and epiphyseal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84;
                                                                                                                                                                                                                                 Ottawa Res.
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                                                                                                                                     Leg Muscle,
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Matches 92
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     218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41 CAAGGTGAACAAGAAGCTGGGCCTGGGCGGCACCAATCCGGCTCAGGTGACCACCACCAC 100
                                                                              CAAGGTGAACAAGAAGCTGGGCCTGGGCGCACCAATCCGGCTCAGGTGACCACCACCAC 100
                 CCTCACCGAGGAAGACGTCGTCGCCACCATCGAGTACCTGGTGCGCCCTGCACGAGGGCCA 160
GGAGGTGGACGAGGAGCAGCGGCACCATCGACTTCGAGGAGTTCCTGGTGATGATGGT
                                                             CACGGTGATGAGGATGCTGGGCCAGAAACCCCCACCAAAGAGGAGCTGGATGCCATCATCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GACCACGATGACCGCCCCCGGCGCGCGTCGAGGTGCCGGTGGATGTGGACGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCGCCAGATGAAAGAGGACGCCAAGGGCAAGTCTGAGGAGGAGCTGGCCAAC 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGAGGTGGACGAGGAGCAGCGGCACCATCGACTTCGAGGAGTTCCTGGTGATGATGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pgfn.pk005.h23 normalized chicken fat cDNA linear EST 15-JUN-201 cDNA clone pgfln.pk005.h23 5' similar to sp|p02588|TPCS_CHICK TROPONIN C, SKELETAL MUSCLE pir|TPCHCS troponin C, skeletal muscle-chickenG, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (2001)
Contact: Larry A. Cogburn
University of Delaware
Townsend Hall, Newark, DE 19717, USA
Tel: 302-831-1335
Fax: 302-831-2822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cogburn,L.A., Morgan,R.W. and Burnside,J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              l Similarity 53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gallus gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         chicken.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BI065677.1 GI:14473199
                                                                                                                                                  Similarity
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                                                                                                                                                                                                               144
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                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                           cogburn@udel.edu, www.chickest.udel.edu
Location/Qualifiers
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                                                                                                                                                                                                            /tissue_type="fat"
/lab_host="E.coli EMDH10B"
/note="Vector: pSPORT1"
162 c 214 g 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pools of total RNA isolated from each tissue (embryonic muscle 33.3%; juvehile muscle 33.3%; and epiphyseal growth plate 33.3% of the final RNA pool). Single pass sequencing from 5'-end" 136 c 202 g 100 t 2 others
                                                                                                                                                                                                                                                                           /clone="pgfln.pk005.h23"
/clone_lib="normalized ch
/sex="Male and Female"
                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:
                                                                                                                                                                                                                                                                                                                                            ∕organism="Gallus gallus"
                                                                                                                                             20.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20.6%;
53.5%;
                                                                                                                              Score 44; DB 1
Pred. No. 6.2;
0; Mismatches
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Pred. No. 6.1;
0; Mismatches
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                                                                                                                                                                                                                                                                                            chicken
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                                                                                                                               80;
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Fax: 302-831-2822
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92; Conserv
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ESTs from Primary Chicken Breast Muscle, Leg Muscle, and Epiphyseal
Growth Plate cDNA library, USDA/IFAFS Animal Genome Project
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C. reinhardtii CC-1690, Stress II (normalized), Lambda Zap II Chlamydomonas reinhardtii cDNA, mRNA sequence.
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Contact: Larry A. Cogburn University of Delaware
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Location/Qualifiers
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/clone="lib="Primary Chicken Breast Muscle, 1
Epiphyseal Growth Plate CDNA library (pgmlc)
/sex="Male and Female"
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/lab_host-"E. coli EMDH10B"
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155 GGGCCAGACCACGATGACCGCCCCCGGCGTGGAGGTGCCGGTGGATGTGGACGACAT 214
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                                                                                     pgmln.pk001.06 Normalized Chicken Breast Muscle, Leg Muscle, and Epiphyseal Growth Plate cDNA library (pgmln) Gallus gallus cDNA clone pgmln.pk001.06 5' similar to sp|P02588|TPCS_CHICK TROPONIN C, SKELETAL MUSCLE pir|TPCHCS troponin C, skeletal muscle - chicken,
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Analyses of the Chlamydomonas reinhardtii Genome: A Model,
Unicellular Sys:em for Analyzing Gene Function and Regulation in
Vascular Plants. Project: 1031
BM485533.1 GI:18606186
                                                                mRNA sequence.
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Eukaryota; Viridiplantae: Chlorophyta; Chlorophyceae; Volvocales;
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EST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   XhoI; Stress condition II library, constructed by John
Davies and Jeffrey McDermott, combines cDNAs from CC-1690
cells grown to mid-log phase in TAP (NH4+ - containing)
and shifted to TAP - NO3 - (24hrs); H2 production
conditions (0, 12hr, 24hr) see Melis et al.,(2000) Plant
Phys. 122: 127-135; TAP + H202 (1, 12, 24 hr); TAP +
sorbitol (1, 2, 6, 24 hr); TAP + Cd (1, 2, 6, 24 hr).
PolyA mRNA was purified from each sample, pooled and cDNA
synthesized. The cDNA was directionally cloned into lambda
synthesized. The cDNA was directionally cloned into lambda
synthesized. The cDNA was directionally cloned into lambda
synthesized. The cDNA was directionally cloned the lambda
synthesized from the EcoRI (5') and XhoRI (3')
sites. pBluescript II SK- plasmids were excised from the
lambda ZAP clones by superinfection with Exassist
(Stratagene) phage. The library was normalized using
method 4 described in Bonaldo et al., (1996) Genome
Research 6: 791-806.*
31 a 207 c 224 g 110 t
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/db_xref="taxon:3055"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ), Lambda Zap II"
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Pred. No. 6.2;
D; Mismatches 85
                                                                                                                                                                                                                                   682 bp
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                                                                                                  ORGANISM
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                                                                                                                                                                                                                                                                                                                                                      161 GACCACGATGACCGCCCCCGGCGCGCGTCGAGGTGCCGGTGGATGTGGACGAC
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   Grossman,A.,
Lefebvre,P.,
                                                                      Chlamydomonas reinhardtii
Eukaryota: Viridiplantae; Chlorophyta;
                                                                                                                                   BF864011.1 GI:12254155
EST.
                                                                                                                                                                                         963048D06.yl C.
, Lambda Zap II
                                                                                                                Chlamydomonas reinhardtii.
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                                                           Chlamydomonadaceae; Chlamydomonas
                                                                                                                                                                                                                                BF864011
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Cogburn,L.A. and Monsonego-Ornan,E.
ESTs from Normalized Chicken Breast Muscle, Leg Muscle,
Epiphyseal Growth Plate cDNA library, USDA/IFAFS Animal
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (2002)
Contact: Larry A. Cogburn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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                                           (bases 1 to 783)
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /Strain="Commercial broiler
Strains 90 & 21"
/db_xref="taxon:9031"
/Clone="pommin" -1.20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Vector: pCMVSPORT6; Library made from equivalent pools of total RNA isolated from each tissue (embryonic muscle 33.3%; juvenile muscle 33.3%; and epiphyseal growth plate 33.3% of the final RNA pool). Single pass sequencing from 5'-end"

179 c 230 g 120 t 2 others
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//sex="Male and Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 growth plate"
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.11 weeks):growth plate(1d,7d,14d post-hatch)"
/lab_host="E. coli EMDH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="Breast muscle, leg muscle and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="pgmln.pk001.o6"
Davies,J., Federspiel,N., Harris,E., Hauser,C. McDermott,J.P., Shrager,J., Silflow,C. and Ste
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20.6%;
                                                                                                                                                                                   783 bp mRNA linear EST 19-JAN reinhardtii CC-1690, Stress condition I, norma Chlamydomonas reinhardtii cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 44; DB;
Pred. No. 6.3;
0; Mismatches
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6.3;
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                                                                        Chlorophyceae;
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on I, normalized
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                                                     Grossman,A., Chang'C.-W., Davies,J., Harris,E., Hauser,C., P., McDermott,J.P., Shrager,J., Silflow,C. and Stern,D. Analyses of the Chlamydomonas reinhardtii Genome: A Model, Unicellular System for Analyzing Gene Function and Regulat Vascular Plants. Project: 1031
Unpublished (2001)
                                                                                                                                                                                                                 Chlamydomonas reinhardtii.
Chlamydomonas reinhardtii
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
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                                                                                                                                                                                                                                                                                                                                                B1995346 bp mRNA linear EST 25-OCT-2001 1031026E07.y2 C. reinhardtii CC-1690, Stress II (normalized), Lambda Zap II Chlamydomonas reinhardtii cDNA, mRNA sequence.
                                        Contact: Charles
                                                                                                                                                                                    Chlamydomonadaceae; Chlamydomonas
1 (bases 1 to 568)
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95; Conserv
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Tel: 919 613 8159
Fax: 919 613 8177
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DCMB Box 91000
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Unicellular System for Analyzing Gene Function and Regulation
Vascular Plants; project phase 3
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Box 91000
University
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/note="Yector: pBluescript II SK-; Site_l: EcoRI; Site_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Chlamydomonas reinhardtii"
/strain="CC-1690 wild type mt+ 21gr"
/db_xref="taxon:3055"
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RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   182 CGGCGTCGAGGTGCCGGTGGATGTGGACGACAT 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             311 CGTG-----CCGTACAGGGACGAGCCCGGCGCCTCCTCCGCGCCCCGTGTCCTACCACTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      251 CAACGAGAGCGCCTTCGAGGTGGTGCACGGCCTGTTGAACAGGGTCATGGAGGTGCTGGG 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTGCGGCGACAAGCCCGTGGGCGTGTTCGGCAT 457
                                                                                                                                                                                                                                                                                                                                  Zm04_05f06_R Zm04_AAFC_ECORC_cold_stressed_maize_seedlings CDNA clone Zm04_05f06, mRNA sequence.
BG321153
BG321153.1 GI:13150831
EST.
Unpublished (2001)
Contact: Singh, J.A.
Eastern Cereal and Oilseed Research Centre
Agriculture and Agri-food Canada
KW Neatby Bidg., Central Experimental Farm,
                                                                                                          Singh, J.A., Wakui, K., Couroux, P., De Moors, A., Harris, L.J., J.I., Ouellet, T., Robert, L.S., Sprott, D. and Tinker, N.A. Expressed Sequence Tags from Cold-Stressed Maize Seedlings
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Tel: 919 613 8159
Fax: 919 613 8177
                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Vector: pBluescript II SK-; Site_1: EcoRI; Site_2: xhoI; Stress condition II library, constructed by John Davies and Jeffrey McDermott, combines cDNAs from CC-1690 cells grown to mid-log phase in TAP (NH4+ - containing) and shifted to TAP - NO3- (24hrs); H2 production (0, 12hr, 24hr) see Melis et al., (2000) plant Phys. 122: 127-135; TAP + H202 (1, 12, 24 hr); TAP + sorbitol (1, 2, 6, 24 hr); TAP + Cd (1, 2, 6, 24 hr). PolyA mRNA was purified from each sample, pooled and cDNA synthesized. The cDNA was directionally cloned into lambda ZAP clones by superinfection with Exhasist (Stratagene) in the EcoRI (5') and XhoRI (3') sites. pBluescript II SK- plasmids were excised from the lambda ZAP clones by superinfection with Exhasist (Stratagene) phage. The library was normalized using method 4 described in Bonaldo et al., (1996) Genome 80 a 206 c 185 g 97 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              chauser@duke.edu
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/strain="CC-1690 wild type mt+ 21gr"
/db_xref-"taxon:3055"
/clone_lib="C._reinhardtii CC-1690, Stress II (normalized
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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Pred. No. 6.7;
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    Ottawa, Ontario,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 78 CCGGCTCAGGTGACCACCACCACCTCACCGAGGAAGACGTCGTCGCCACCATCGAGTAC 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18 GATCTGGCCCGCGTGGGTCGGTACAAGGTGAACAAGAAGCTGGGCCTGGGCGGCACCAAT 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTGGTGCGCCTGCACGAGGGCCAG 161
                                                                                                                                                                                                                         Submitted (25-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA
                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                        Coe, E.C
                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 1856)
Hainey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whitsitt, M.S.,
Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1856 bp
Zea mays CL2386_1 mRNA sequence.
AY109418
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Tel: (613) 759-1662
Fax: (613) 759-1701
Email: singhja@em.agr.ca
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/note-"this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed DuPont contigs; this resource was assembled by DuPont as part of a collaboration for t
                                                                                   /organism="Zea mays"
/db_xref="MaizeDB:630950"
/db_xref="MaizeDB:630950"
/db_xref="taxon:4577"
/clone="CL2386_1"
/clone_lib="Maize Mapping Project/DuPont Cornsensus
                                                                                                                                                                                                               Location/Qualifiers
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/note="Vector: Bluescript SK-/XhoI-EcoRI; Site_1: Eco RI;
Site_2: Xho I; Lower temperature 50 C / hour from 22 to
12oC; bring to 50 in 1 hour from 12oC. Leave at 5oC 2 days
/photoperiod 16 hours. Light intensity was 125 uE-1.
Library prepared by in vivo mass excision from amplified
library."
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/cultivar="C0328"
/db_xref="Laxon:4577"
/clone="Zm04_05f06"
/clone=1ib="Zm04_AAFC_BCORC_cold_stressed_maize_seedlings"
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55.6%;
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                                                                                                                                                                                                                                                                              FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTTCCCAGTCACGACG
Plate: 54 row: M column: 18
Seg primer: ATTTAGGTGACACTATAG.
                                                                                                                                                                                                                                                                                                                                                                  Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -innmatch 12 options.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   CONTACT: Smith TPL USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA Tel: 402 762 4366 Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                               Email: smith@email.marc.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001) 21180013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and Keele, J.W.
                                                                                                                                                                                                                                                                                                                                                         PCR PRimers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BE754521 558 bp mRNA linear 208060 MARC 2BOV Bos taurus cDNA 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bovidae; Bovinae; Bos. 1 (bases 1 to 558)
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                                                           113
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                                                           a
                                                                                                                                               /organism-"Bos taurus"
/db_xref."taxon:9913"
/clone_lib-"MARC 2BOV"
/tissue_type-"pooled"
/lab_host-"DH10B"
                                                   /note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: Sa
Library made from pooled tissue from testis, thymus,
semitendonosus muscle, longissimus muscle, pancreas,
adrenal, and endometrium."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       <sub>D</sub>
                                                                                                                                                                                                                                                              Location/Qualifiers
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a 548 c 585 g 281 t 122 others
   20.1%;
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 Score 43;
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Pred. No. 11;
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DB 12;
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Length 558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   122 others
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                                                                                                                            SalI;
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Search completed: November 13, 2002, 04:00:40 Job time : 1154.63 \ \text{secs}
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                                                                                                                                                                                                                                                Best Local Similarity 54.0%;
Matches 88; Conservative
                                                                                       145 GCCTGCACGAGGGCCAGACCACGATGACCGCCCCCGGCGGCGT 187
                                                                                                                                                                              198 CCATCATGGGCCAGTTCGAGCACCCCAATATCATCCGCCTGGAGGGCGTGGTCACCAACA 257
                                                                                                                             258
                                                                                                                                               85 AGGTGACCACCACCCTCACCGAGGAAGACGTCGTCGCCACCATCGAGTACCTGGTGC 144
                                                                                                                                                                                                 25 CCCGCGTGGGTCGGTACAAGGTGAACAAGGAGGTGGGCCTGGGGCGGCACCAATCCGGCTC 84
                                                                                                                  GGCTGAACGACGGCCAGTTCACCGTGATCCAGCTCGTGGGCAT
                                                                                                                                                                                                                                                 0
                                                                                                                                                                                                                                                           Pred. No. 10;
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                                                             360
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Database :
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq
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Perfect score:
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                                                                                  Published_Applications_NA:*

1: /cgn2_6/ptodata/2/pubpna/US

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3: /cgn2_6/ptodata/2/pubpna/US

4: /cgn2_6/ptodata/2/pubpna/US

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6: /cgn2_6/ptodata/2/pubpna/US

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6: /cgn2_6/ptodata/2/pubpna/US

7: /cgn2_6/ptodata/2/pubpna/US

9: /cgn2_6/ptodata/2/pubpna/US

11: /cgn2_6/ptodata/2/pubpna/US

12: /cgn2_6/ptodata/2/pubpna/US

13: /cgn2_6/ptodata/2/pubpna/US

14: /cgn2_6/ptodata/2/pubpna/US

14: /cgn2_6/ptodata/2/pubpna/US
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length: 2000000000
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Gapop 10.0 , Gapext 1.0
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214
1 tcaaggagaagcgctacgat.....ccggtggatgtggacgacat 214
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10 US-09-984-711-5
9 US-10-075-460-5
10 US-09-887-052-1
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10 US-09-968-242-4133
10 US-09-968-242-4133
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    Sequence 5, Appli
Sequence 1, Appli
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Sequence 3, Appli
Sequence 3598, Appli
Sequence 29, Appli
Sequence 1034, Ap
Sequence 7989, Ap
Sequence 229, Appl
Sequence 217, Appl
Sequence 317, Appl
Sequence 11, Appl
Sequence 11, Appli
Sequence 413, Ap
Sequence 4133, Ap
Sequence 4133, Ap
Sequence 4133, Ap
Sequence 4133, Ap
Sequence 4135, Ap
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US-09-815-242-7949	US-09-810-861B-4	US-10-074-279-10	US-10-033-190-5	US-09-938-956-5	US-10-052-586-367	-09	-09	60-	-09	US-09-822-687-3	US-09-822-830A-105	US-09-815-242-7960	US-09-732-680A-1	US-09-997-664-1	US-09-997-664-99	US-09-815-242-4160	US-09-815-242-7943	US-09-878-574-2105	-815	-09-982-610-	-921	-803	-09-803	-09-748-	US-09-815-242-4131
e 79	Sequence 4. Appli	5 ,	л (ω 5	77:	Sequence 9. Appli	_ ;	_ ,		105	79	- :		99. Ac	Sequence 4160. An		2105		. د	Sequence 4. Appli	۱ س	- :		Sequence 4131 An

ALIGNMENTS

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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: BATHE, Brigitte
APPLICANT: STEPHAN, Hans
APPLICANT: KREUTZER, Caroline
APPLICANT: KREUTZER, Caroline
APPLICANT: HERMANN, Thomas
APPLICANT: BINDER, Michael
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE rpsL GENE
FILE REFERENCE: 204209US0
CURRENT APPLICATION NUMBER: US/09/984,711
CURRENT APPLICATION NUMBER: D31-10-31
PRIOR APPLICATION NUMBER: D510108230.9
PRIOR FILING DATE: 2001-0-16
NUMBER OF SEQ ID NOS: 6
                                            Qy
                                                                                     В
                                                                                                                                                                                                                                    ; 'NAME/KEY: CDS
; LOCATION: (702)..(4196;
; OTHER INFORMATION:
US-09-984-711-5
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US-09-984-711-5
                                                                                                                                                              Query Match
Best Local S
Matches 136
                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn version 3.1
SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5, Application US/09984711
Patent No. US20020119549A1
                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Corynebacterium glutamicum FEATURE:
1638 GGCGACCACGATGGTTTGATGACT-----CTTACTGAAGAGGACATCGCAACCACC 1688
                                                                        LENGTH: 5096
                                                  69
                                                                                                                                                                         Match 37.6%; Local Similarity 66.0%;
                       GGCACCAATCCGGCTCAGGTGACCACCACCACCGAGGAAGAGGTCGTCGCCACC 128
                                                                                                                                                              136;
                                                                                                                                                            Conservative
                                                                                                                                                    Score 80.4; DB 10;
Pred. No. 1.3e-11;
0; Mismatches 61;
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APPLICANT: MOCKEL, BETTINA
APPLICANT: BATHE, BRIGITTE
APPLICANT: HANS, STEFAN
APPLICANT: HANS, STEFAN
APPLICANT: HERMANN, THOMAS
APPLICANT: HERMANN, THOMAS
APPLICANT: HERMANN, THOMAS
APPLICANT: PFEFFERLE, WALTER
APPLICANT: BINDER, MICHAEL
FILLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE rPSL GENE
FILLE REFERENCE: 218472USOX
CURRENT APPLICATION NUMBER: US/10/075,460
CURRENT FILING DATE: 2002-02-15
PRIOR APPLICATION NUMBER: DE 10107230.9
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-12-19
NUMBER OF SEQ ID NOS: 14
                                                                                                                                                                             RESULT 3
US-09-887-052-1
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                                                                                                                     Sequence 1, Application US/09887052 Patent No. US20020119537A1 GENERAL INFORMATION:
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APPLICANT: MOEKEL, Bettina
APPLICANT: MOEKEL, Brigitte
APPLICANT: HERMANN, Thomas
APPLICANT: PEFFERIE, Walter
APPLICANT: BINDER, Michael
TITLE OF INVENTION: NUCLEOTIDE SEEQUENCES WHICH CODE FOR THE rPOB GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn version 3.1
SEQ ID NO 5
LENGTH: 5099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 5, Application US/10075460 Patent No. US20020155557A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
NAME/KEY: CDS
LOCATION: (702)..(4196)
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Corynebacterium glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                       1749 GAGATCCCAGTCGAGACCGATGACAT 1774
                                                                                                                                                                                                                                                                                                                                                                                   1638 GGCGACCACGATGGTTTGATGACT------CTTACTGAAGAGGACATCGCAACCACC 1688
                                                                                                                                                                                                                                                                                                                                   129 ATCGAGTACCTGGTGCGCCTGCACGAGGGCCAGACCACGATGACCGCCCCCGGCGGCGCTC 188
                                                                                                                                                                                                                                                                                         189
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                                                                                                                                                                                                                                                                                                                                                                                                                                     69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        / Match 37.6%;
Local Similarity 66.0%;
les 136; Conservative
                                                                                                                                                                                                                                                                  GAGGTGCCGGTGGATGTGGACGACAT 214
                                                                                                                                                                                                                                                                                                                                                                                                                    GGCACCAATCCGGCTCAGGTGACCACCACCACCTCACCGAGGAAGACGTCGTCGCCACC 128
                                                                                                                                                                                                                                                                                                            ATCGAGTACCTGGTGCGTCTGCACGCAGGTGAGCGCGTCATGACTTCTCCAAATGGTGAA 1748
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Pred. No. 1.
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1.3e-11;
hes 61;
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PRIOR APPLICATION NUMBER: DE10107229.5
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 8
SOFTMARE: Patentin version 3.0
SEQ ID NO 3
SEQ ID NO 3
LENGTH: 5099
TYPE: DNA
ORGANISM: Corynebacterium glutamicum FEATURE:
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                                                                                                                                                                     ; NAME/KEY: CDS
; LOCATION: (702)..(4196)
US-09-887-052-3
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CURRENT APPLICATION NUMBER: US/09/887,052
CURRENT FILING DATE: 2001-06-25
PRIOR APPLICATION NUMBER: DE10107229.5
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1
LENGTH: 5099
TYPE: DNA
ORGANISM: Corynebacterium glutamicum
PEATHIDE:
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; LOCATION: (702)..(4196)
US-09-887-052-1
                                                                                           Best Local Similarity
Matches 136; Conserv
                                                                                                                              Query Match
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Patent No. US20020119537A1
                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: BINDER, Michael
TITLE OF INVENTION: NUCLEOTIDE SEEQUENCES WHICH CODE FOR THE rPOB GENE
FILE REFERENCE: 204210USQX
CURRENT APPLICATION NUMBER: US/09/887,052
CURRENT FILING DATE: 2001-06-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: MOECKEL, Bettina
APPLICANT: BATHE, Brigitte
APPLICANT: HERMANN, Thomas
APPLICANT: PEEFFERLE, Walte
APPLICANT: BINDER, Michael
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Best Local Similarity 66.0%;
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1578 AAGCGCTACGACCTGGCTCGCGTTGGTCGTTACAAGATCAACCGCAAGCTCGGCCTTGGT 1637
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                                                                                                       37.6%;
66.0%;
                                                                              Score 80.4; DB 10;
Pred. No. 1.3e-11;
0; Mismatches 61;
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Pred. No. 1.3e-11;
0; Mismatches 61;
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                                                                                                                    Length 5099;
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69 GGCACCAATCCGGCTCAGGTGACCACCACCACCTCACCGAGGAAGACGTCGTCGCCACC 128

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US-09-878-574-3598

: Sequence 3598, Application US/09878574

: Patent No. US20020110548A1
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; LOCATION: (702)..(4196)
US-09-887-052-5
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APPLICANT: Byrum, Joseph R.
APPLICANT: La ROSA, Thomas J.
APPLICANT: Thompson, Michael D.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated |
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(15401)B
CURRENT APPLICATION NUMBER: US/09/878,574
CURRENT FILING DATE: 2001-12-21
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APPLICANT: BINDER, MICHAEL
TITLE OF INVENTION: NUCLEOTIDE SEEQUENCES WHICH CODE FOR THE rpoB GENE
FILE REFERENCE: 204212USOX
CURRENT APPLICATION NUMBER: US/09/887,052
CURRENT FILING DATE: 2001-06-25
PRIOR APPLICATION NUMBER: DE101107229.5
PRIOR APPLICATION NUMBER: DE101107229.5
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 8
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ORGANISM: Corynebacterium glutamicum
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Pred. No. 1.3e-11;
0; Mismatches 61;
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US-09-861-893-29
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OTHER INFORMATION: Clone ID: LIB3028-008-Q1-B1-C6
US-09-878-574-3598
                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 29
LENGTH: 399
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Patent No. US20020045257A1
GENERAL INFORMATION:
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PRIOR FILING DATE: 1999-06-14
NUMBER OF SEQ ID NOS: 15775
SEQ ID NO 3598
LENGTH: 392
TYPE: DNA
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CURRENT FILING DATE: 2001-05-22
PRIOR APPLICATION NUMBER: 60/206,158
PRIOR FILING DATE: 2000-05-22
PRIOR APPLICATION NUMBER: 60/206,161
PRIOR FILING DATE: 2000-05-22
NUMBER OF SEQ ID NOS: 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Jiang, Shan
TITLE OF INVENTION: METHODS FOR ASSAYING GENE IMPRINTING
TITLE OF INVENTION: METHYLATED CPG ISLANDS
FILE REFERENCE: 01107.00128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
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TYPE: DNA
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52.1%;
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Pred. No. 0.051;
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; Sequence 1034, Application US/09954456
; Patent No. US20020115057A1

GENERAL INFORMATION

APPLICANT: Young, Paul

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APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
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APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
FITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT FILLNG ATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191.078
PRIOR APPLICATION NUMBER: 60/191.078
PRIOR APPLICATION NUMBER: 60/191.078
PRIOR FILING DATE: 2000-03-21
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PRIOR APPLICATION NUMBER: US/60/235,134
PRIOR FILING DATE: 2000-09-25
PRIOR APPLICATION NUMBER: US/60/235,637
PRIOR FILING DATE: 2000-09-26
PRIOR FILING DATE: 2000-09-26
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PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: US/60/234,052
PRIOR FILING DATE: 2000-09-20
PRIOR APPLICATION NUMBER: US/60/234,923
PRIOR APPLICATION NUMBER: US/60/234,923
PRIOR FILING DATE: 2000-09-25
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SOFTWARE: PatentIn version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 431
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          177 CAGACCAACGTGCTCAACATCGCCAACGAGGACTGCATCAAGGTGGCGGGCCGTGCTCAAC 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          156 GGCCAGACCACGATGACCGCCCCCGGCGGCGTCGAGGTGCCGGTG 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57 ATCAAGACCACGACGCCCGAGAGCGACCTGGGGCACGCTGCGGTTG 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96 ACCACCTCACCGAGGAAGACGTCGTCGCCACCATCGAGTACCTGGTGCGCCTGCACGAG 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36 CGGTACAAGGTGAACAAGAAGCTGGGCCTGGGGCGCACCAATCCGGCTCAGGTGACCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 2000-09-26
APPLICATION NUMBER: US/60/235,711
FILING DATE: 2000-09-27
APPLICATION NUMBER: US/60/235,720
FILING DATE: 2000-09-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/60/235,863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 2000-09-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AACGCCTTCTACCTGGAGAACCTGCACTTCACCATCGAGGGCAAGGACACGCACTACTTC
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                                                                                                                                                                                                                           Zyskind, Judith W. Wall, Daniel Trawick, John D.
                                                                                                                                                                                Carr, Grant J.
Yamamoto, Robert T.
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Pred. No. 0.2;
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; ORGANISM: Homo sapiens
US-09-764-853-229
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US-09-764-853-229/c
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; LOCATION: (1).
US-09-815-242-7989
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PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 229, Application US/09764853 Patent No. US20020090672A1 GENERAL INFORMATION:
                                                                                                                                          Matches
                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Ver.
SEQ ID NO 229
LENGTH: 250
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Best Local Similarity
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LENGTH: 1818
                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/764,853
CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and
FILE REFERENCE: PJZ06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 104;
                                                                                                                                                                                                                                                                                              Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 14110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 60/269,308 PRIOR FILING DATE: 2001-02-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
                                                                          125
65 CCAGTTTCCCGAAGACGTCCACCTCGACACCCMCCGTGAAAGGCGTCTCCGCAGCC
                                                                                    13 GCTACGATCTGGCCCGCGTGGGTCGGTACAAGGTGAACAAGAAGCTGGGCCTGGGCGGCA 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       534
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     414 CTGGGTCATCGACCAGATCTTCGACCTGTTCGACAACCTCGGCGCCACCGACGAGCAACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          83 TCAGGTGACCACCACCCTCACCGAG---GAAGACGTCGTCGCCACCATCGAGTACCT 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23 GCCCGCGTGGGTCCGGTACAAGGTGAACAAGAAGCTGGGCCTGGGCCGGCACCAATCCGGC
                                                               GCTCCACACTGAGAGGCTTGGGCTGTTGGAAGGTGAACTTGGACATTGGGAGGCGAACGGC
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                                                                                                                                        66;
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                                                                                                                                    Conservative
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                                                                                                                                                  17.48;
56.98;
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53.3%;
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    Mismatches

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                                                                                                                                               Score 37.2; DB Pred. No. 0.42;
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Pred. No. 0.29;
0; Mismatches 88;
                                                                                                                                                              DB 10;
                                                                                                                                 49;
                                                                                                                                 Indels
                                                                                                                                                              Length 250;
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RESULT 11 US-09-925-302-317

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APPLICANT: Sherman, D.H.

APPLICANT: Liu, H.

APPLICANT: Xue, Y.

APPLICANT: Xue, Y.

APPLICANT: Zhao, L.

APPLICANT: Dhao, I.

ITILE OF INVENTION: DNA encoding methymycin and pikromycin

FILE REFERENCE: 600,438US1

CURRENT APPLICATION NUMBER: US/09/861,289

CURRENT FILING DATE: 2001-05-18

PRIOR APPLICATION NUMBER: 09/105,537

PRIOR APPLICATION NUMBER: 09/105,537

PRIOR FILING DATE: 1998-06-26

NUMBER OF SEQ ID NOS: 43

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 11
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                                                                                                                                       : LENGTH: 879
: TYPE: DNA
: ORGANISM: Streptomyces venezuelae
US-09-861-289-11
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LENGTH: 2383
TYPE: DNA
ORGANISM: Homo saplens
US-09-925-302-317
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Patent No. US20020044941A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA104
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PRIOR APPLICATION NUMBER: PCT/US00/05918
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
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CURRENT FILING DATE: 2001-08-10
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87 GTGACCACCACCACCTCACCGAGGAAGACGTCGTCGCCACCATCGAGTACCTGGTGCGC 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              958 CTTCGAAACCCTGCAGGACAAGTACTATGAGGAGTACAGGATGTCCGACCGTGTGGACCT 1017
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                                                  Local Similarity
nes 70; Conserv
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Local Similarity 49.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96; Conservative
                                                  Conservative
                                                                    17.3%; Score 37; DB 10.56.0%; Pred. No. 0.53;
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                                                Mismatches
                                                                                    DB 10; Length 879
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                                             Indels
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                                         Gaps
                                         0;
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APPLICANT: Xue, Y.

APPLICANT: Zhao, L.

TITLE OF INVENTION: DNA encoding methymycin and pikromycin FILE REFERENCE: 600.438US1

CURRENT APPLICATION NUMBER: US/09/861,289

CURRENT FILING DATE: 2001-05-18

PRIOR APPLICATION NUMBER: 09/105,537

PRIOR FILING DATE: 1998-06-26

NUMBER OF SEO ID NOS: 43

SOFTWARE: FastSEO for Windows Version 3.0

SEQ ID NO 3
  APPLICANT: Carr, Grant J.

APPLICANT: Yamamoto, Robert T.

APPLICANT: Xu, H. Howard

TITLE OF INVENTION: Identification of Essential Genes in

TITLE OF INVENTION: Prokaryotes

FILE REFERENCE: ELITRA, 011A

CURRENT APPLICATION NUMBER: US/09/815,242

CURRENT FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21
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; TYPE: DNA
; ORGANISM: Streptomyces venezuelae
US-09-861-289-3
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Patent No. US20020061569A1
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Best Local :
                                                                                                                                                                                                                                         APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith w
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
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PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Sherman, D.H. APPLICANT: Liu, H.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                147 CTGCACGAGGGCCAGACCACGATGACCGCCCCCGGCGGCGTCGAGGTGCCGGTGGATGTG 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        207 GACGA 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        87 GTGACCACCACCACCACCAGGAAGACGTCGTCGCCACCATCGAGTACCTGGTGCGC 146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 147 CTGCACGAGGGCCAGACCACGATGACCGCCCCGGCGGCGTCGAGGTGCCGGTGGATGTG
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Local Similarity 56.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 70; Conservative
                                                                                                                                                                                            Trawick, John D.
Carr, Grant J.
Yamamoto, Robert T.
                                                                                                                                                                                                                                                           Zyskind, Judith W. Wall, Daniel
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CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR PRIOR PRILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
PRIOR PRILING DATE: 2000-09-09-27
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
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PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
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; LOCATION: (1)...(855)
US-09-815-242-7681
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PRIOR FILING DATE: 2000-10-23
PRIOR PPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-26
PRIOR FILING DATE: 2011-02-16
                                                                                                                                                                                                                                                                                                                          APPLICANT: Rank, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Chen, Mensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY FILE REFERENCE: Acomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
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ORGANISM: Pseudomonas
FEATURE:
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; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.88
; OTHER INFORMATION: EST_HUMAN HIT: AA454168.1, EVALUE 2.20e-01
; OTHER INFORMATION: NT HIT: AF105999.1, EVALUE 1.00e-127
; OTHER INFORMATION: SWISSPROT HIT: Q04844, EVALUE 3.00e-22
US-09-864-761-33210
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Best Local
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SEQ ID NO 33210
LENGTH: 350
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ORGANISM: Homo :
FEATURE:
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PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
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PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
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CGCAGCCGCGGGACATGGCGTGGGTGGTGGGCGTCCGCTGGGACACGTTG
                                                                                                                 CAGGTGACCACCACCCTCACCGAGGAAGACGTCGTCGCCACCATCGAGTACCTGGTG 143
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Pred. No. 0.61;
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  61
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Search completed: November 12, 2002, 16:58:57 Job time: 36.7711 secs

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Result
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1: /cgn2_6/ptodata/1,

2: /cgn2_6/ptodata/1,

3: /cgn2_6/ptodata/1,

4: /cgn2_6/ptodata/1,

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6: /cgn4_6/ptodata/1,
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/cgn2_6/ptodata/1/ina/BCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/backfiles1.seq:*
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first 45 summaries
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              3 US-09-335-409-1

4 US-09-568-102-1

4 US-09-568-480-1

US-09-568-472-1

US-09-568-472-1

US-09-568-472-1

US-09-568-472-1

US-09-567-899-1

US-09-202-768-67

US-09-202-768-67

US-09-202-768-69

US-09-202-768-69

US-09-202-768-69

US-09-202-768-69

US-09-202-768-69

US-09-202-768-69

US-09-105-537-1

US-09-105-537-3

US-09-105-537-3

US-09-103-878-3

US-09-103-878-3

US-09-103-840A-1

US-09-9103-840A-1

US-08-911-853-34
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PCT-US95-06790-1
US-08-313-185-57
US-09-082-614A-57
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Sequence 1, Appli
Sequence 3, Appli
Sequence 67, Appli
Sequence 67, Appli
Sequence 7, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 2, Appli
Sequence 31, Appli
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Sequence 1
Sequence 1
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Sequence 1, Appli
Sequence 57, Appl
Sequence 57, Appl
Sequence 57, Appl
Patent No. 5352575
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TYPE: nucleic acid
STRANDENNESS: single
TOPOLOGY: linear
US-08-250-030-1
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               g
                                                                                                                                                                ATTORNEY AGENT INFORMATION:

NAME: Mueting, Ann M.

REGISTRATION NUMBER: 33,977

REFERENCE/DOCKET NUMBER: 150.

TELECOMMUNICATION: NORMATION:

TELEPHONE: 612-339-0331

TELEPRAX: 612-339-3061

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 970 base pairs
                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.
CURRENT APPLICATION DATA:
APPLICATION UNHER: US/08/250,030
FILING DATE: 26-MAY-1994
ATTORNEY/AGENT ... 435
ATTORNEY/AGENT ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 1
US-08-250-030-1
                                                                   Query Match
Best Local Similarity
                                                             Matches 169;
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                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Schwegman,
STREET: 3500 IDS Cente
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
COMPUTER: IBM PC COMPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Persing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Persing,
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TCAAGGAGAAGCGCTACGATCTGGCCCGCGTGGGTCGGTACAAGGTGAACAAGAAGCTGG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: Schwegman, Lundberg & Woessner
3500 IDS Center
                                                          Conservative
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79
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Defrection of a Genetic Locus Encoding
Resistance to Rifampin in Mycobacterial Cultures
Clinical Specimens
                                                                     .08;
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4 US-09-479-453-34
3 US-08-911-853-29
4 US-09-479-453-29
1 US-07-820-011A-1
5 PCT-US93-00445-1
4 US-09-103-840A-2
4 US-09-103-840A-2
1 US-08-920-827-13
1 US-08-920-827-13
1 US-08-921-77-13
1 US-08-921-77-13
1 US-08-921-77-13
2 US-08-921-77-13
3 US-08-921-77-13
1 US-08-921-77-13
                                                     Score 129.6; DE Pred. No. 7.2e-20; Mismatches
                                                                                                                                                                                                                                            150.105US1
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                                                       39;
                                                   Indels
                                                                            Length
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Sequence 24, Appl
Sequence 29, Appl
Sequence 29, Appl
Sequence 1, Appl
Sequence 1, Appl
Sequence 2, Appl
Sequence 2, Appl
Sequence 1, Appl
Sequence 13, Appl
Sequence 14, Appl
Sequence 17, Appl
Sequence 18, Appl
Sequence 19, Appl
Sequence 19, Appl
Sequence 19, Appl
Sequence 2, Appli
Sequence 2, Appli
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Best Local S
Matches 169
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PCT-US95-06790-1
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                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 612-339-3061
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: RABSCH, Kevin W.
REGISTRATION NUMBER: 35,651
REFERENCE/DOCKET NUMBER: 150.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-339-0331
TELEPAX: 612-339-3061
                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Rel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Mayo Foundation for Medical Education and Research APPLICANT: and Hoftmann-La Roche Inc.
TITLE OF INVENTION: Detection of a Genetic Locus Encoding
TITLE OF INVENTION: Resistance to Rifampin
NUMBER OF SEQUENCES: 15
CORRESSPONDENCE ADDRESS:
    200
                 181 GCGGCGTCGAGGTGCCGGTGGATGTGGACGACAT 214
                                                               140
                                                                         121 TCGCCACCATCGACTACCTGGTGCGCCTGCACGAGGGCCAGACCACGATGACCGCCCCCG 180
                                                                                                                           86
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                                                                                                                                             61 GCCTGGGCGGCACCAATCCGGCTCAGGTGACCACCACCACCTCACCGAGGAAGACGTCG 120
                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: sing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: FILING DATE: 26-MAN CLASSIFICATION:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                  1 TCAAGGAGAAGCGCTACGATCTGGCCCGCGTGGGTCGGTACAAGGTGAACAAGAAGCTGG 60
                                                                                                                                                                                                                                                                                                                                                                                        LENGTH:
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GCGGCGTCGAGGTGCCGGTGGAAACCGACGACAT 233
                                                         TGGCCACCATCGAATATCTGGTCCGCTTGCACGAGGGTCAGACCACGATGACCGTTCCGG
                                                                                                                                                                                TCAAGGAGAAGCGCTACGACCTGGCCCGCGTCGGTCGCTATAAGGTCAACAAGAAGCTCG
                                                                                                                       GGCTGCATGTCGGCGAGCC-----CATCACGTCGTCGACGCTGACCGAAGAAGACGTCG
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                                                                                                                                                                                                                                                                                                                                                                                        970 base pairs
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3500 IDS Center
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                                                                                                                                                                                                                                                                                                                                                             single
                                                                                                                                                                                                                                                            60.6%; Score 129.6; DB 5 79.0%; Pred. No. 7.2e-21;
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    Mismatches

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; MOLECULE TYPE:
US-08-313-185-57
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US-08-313-185-57
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                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Heym, S
APPLICANT: Cole, S
APPLICANT: Young, I
APPLICANT: Zhang,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 57, App. Patent No. 58517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC LOS/MS-DOS
SOFTWARE: PAtentIn Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/313,185
FILING DATE: 12-OCT-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Weyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 02356.0068-
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (202) 408-44
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 3447 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: (202) 408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Honore, Nadine
APPLICANT: Telenti, Amalio
APPLICANT: Bodmer, Thomas
TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
TITLE OF INVENTION: in Mycobacterium Tuberculosis
                             181 GCGGCGTCGAGGTGCCGGTGGATGTGGACGACAT 214
                                                                                                                           869 GGTTGCACGCCGGTGAGTTGA-----TCACGTCGTCCACGCTGACCGAAGAGGATGTCG
      983
                                                                                                                                                                                                        809
                                                                                                                                                                        61
                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (20)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 20005-3315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 1300 I STATE: D.C.
GTGGGGTAGAAGTGCCAGTGGAAACTGACGATAT 1016
                                                          TCGCCACCATAGAGTACCTGGTTCGTCTGCATGAGGGTCAGTCGACAATGACTGTCCCAG
                                                                            TCGCCACCATCGAGTACCTGGTGCGCCCCGCCCGCAGAGGGCCACGACGATGACCGCCCCCG 180
                                                                                                                                               GCCTGGGCGGCACCAATCCGGCTCAGGTGACCACCACCACCCTCACCGAGGAAGACGTCG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Application US/08313185
                                                                                                                                                                                                                                                                     Conservative
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Cole, Stewart
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Zhang, Ying
                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                   DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                  single
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408-4400
NO: 57:
                                                                                                                                                                                                                                                                                50.8%;
72.9%;
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                                                                                                                                                                                                                                                                Score 108.8; DB 2;
Pred. No. 3.1e-16;
0; Mismatches 52;
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                                                                                                                                                                                                                                                                                             Length 3447;
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US-09-082-614A-57

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RESULT 5
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/313
FILING DATE: 12-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: MEYOR'S, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 0235
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 57, Application US/09082614A
Patent No. 6124098
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: 11 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 3447 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/082,614A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Honoré, Nadine
APPLICANT: Telenti, Amalio
APPLICANT: Telenti, Amalio
APPLICANT: Bodmer, Thomas
TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
TITLE OF INVENTION: In Mycobacterium Tuberculosis
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W.
                                                                                       983
                                                                                                 181 GCGGCGTCGAGGTGCCGGTGGATGTGGACGACAT 214
                                                                                                                                                                                            121
                                                                                                                                                                                                                            698
                                                                                                                                                                                                                                                                                                   809
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                                                                                                                                                                                                                                              61 GCCTGGGCGCACCAATCCGGCTCAGGTGACCACCACCACCCTCACCGAGGAAGACGTCG 120
                                                                                                                                                                                                                                                                                                                                                           y Match 50.8%; Score 108.8; DB 3; Local Similarity 72.9%; Pred. No. 3.1e-16; hes 156; Conservative 0; Mismatches 52;
                                                                                                                                                                                                                                                                                                          1 TCAAGGAGAAGCGCTACGATCTGGCCCGCGGTGGGTCGGTACAAGGTGAACGAGGAGCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 1300 I STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 20005-3315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                           GGTTGCACGCCGGTGAGTTGA-----TCACGTCGTCCACGCTGACCGAAGAGGATGTCG
                                                                              GTGGGGTAGAAGTGCCAGTGGAAACTGACGATAT 1016
                                                                                                                                                                                                                                                                                    TCAAGGAGAAACGCTACGACCTGGCCAGGGTTGGTCGTTACAAGGTCAACAAGAAGCTCG
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Cole, Stewart
Young, Douglas
Zhang, Ying
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; ORGANISM: Sorangium cellulosum
US-09-335-409-1
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                                                                                                                                                                                                                                                                                                        SEQ ID NO 1
                                                                                                                                                                                             Query Match
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APPLICANT: Moinar, Istvan
APPLICANT: Moinar, Istvan
APPLICANT: Zirkia, Ross
APPLICANT: Cyr, Devon
APPLICANT: Goerlach, Joern
TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
FILE REFERENCE: 4-30582A
CURRENT STLING DATE: 1999-06-17
CURRENT STLING DATE: 1999-06-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/09335409
Patent No. 6121029
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Best Local :
                                                                    21325 ATCGCGCGAGCGCCGGCGGGCCAGCCGGGGACGGGGACCTGCTCCGCCGCCTCGCCGCTG 21384
21385 CCGAGCCGAGCGCGGAGCGCGCTCCTGGAGCCGCTCCTCCGCGCGCAGATCTCGCAGG 21444
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                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 30
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APPLICATION NUMBER: US/07/51
FILING DATE: 20-APR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 100,817
FILING DATE: 29-JUN-1987
APPLICATION NUMBER: 886,260
FILING DATE: 16-JUL-1986
APPLICATION NUMBER: 784,787
FILING DATE: 04-OCT-1985
APPLICATION NUMBER: 801,799
FILING DATE: 26-NOV-1985
APPLICATION NUMBER: 301,799
FILING DATE: 26-NOV-1985
                                                                                                                                                                                                                                                                                   LENGTH: 68750
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     116 CGTCGTCGCCACCATCGAGTACCTGGTGCGCCTGCACGAGGGCCAGAGCCACGATGACCGC 175
                                                                                                                                                          Local Similarity
les 84; Conserv
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                                    CGGCTCAGGTGACCACCACCACCACCCTCACCGAGGAAGACGTCGTCGCCCACCATCGAGTACC 138
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86; Conserv
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52.5%;
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Pred. No. 1.
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Pred. No. 0.18;
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                                                                                                                                                                                   Length 68750;
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TGGTGCGCCTGCACGAGGGCCAGACCACGATGACCGCCCC 178

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; TYPE: DNA
; ORGANISM: Sorangium cellulosum
US-09-567-969-1
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                                                                                                       SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 68750
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      Query Match
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APPLICANT: Ligon, James
APPLICANT: Ligon, James
APPLICANT: Molnar, Istvan
APPLICANT: Zirkle, Ross
APPLICANT: Cyr, Devon
APPLICANT: Goerlach, Joern
APPLICANT: Geriach, Joern
TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
FILE REFERENCE: 4-30582A
CURRENT APPLICATION NUMBER: US/09/567,969
CURRENT FILING DATE: 2000-05-10
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APPLICANT: Schupp,
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PRIOR FILING DATE: 1999-06-17
NUMBER OF SEQ ID NOS: 30
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APPLICANT: Goerlach, Joern
TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
FILE REFERENCE: 4-30582A
CURRENT APPLICATION NUMBER: US/09/568,102
CURRENT FILING DATE: 2000-05-10
PRIOR APPLICATION NUMBER: 09/335,409
PRIOR FILING DATE: 1999-06-17
NUMBER OF SEQ ID NOS: 30
NUMBER OF SEQ ID NOS: 30
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TYPE: DNA
ORGANISM: Sorangium cellulosum
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Zirkle, Ross
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  17.9%; Score 38.4;
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  DB 4;
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Length 68750;
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CURRENT APPLICATION NUMBER: US/09/568,480
CURRENT FILING DATE: 2000-05-10
PRIOR APPLICATION NUMBER: 09/335,409
PRIOR FILING DATE: 1999-06-17
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 68750
TYPE: DNA
ORGANISM: Sorangium cellulosum
US-09-568-480-1
APPLICANT: Schupp, Thomas

APPLICANT: Ligon, James

APPLICANT: Molnar, Istvan

APPLICANT: Molnar, Istvan

APPLICANT: Zirkle, Ross

APPLICANT: Cyr, Devon

APPLICANT: Goerlach, Joern

TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF

FILE REFERENCE: 4-30.82A

CURRENT APPLICATION NUMBER: US/09/568,486

CURRENT FILING DATE: 2000-05-10
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Best Local Similarity
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APPLICANT: Cyr, Devon
APPLICANT: Goerlach, Joern
TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS
FILE REFERENCE: 4-30582A
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APPLICANT: Ligon, James
APPLICANT: Molnar, Istva
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Zirkle, Ross
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milarity 52.5%;
Conservative
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; Pred. No. 1.5;
0; Mismatches
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                                                         OF EPOTHILONES
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Sequence 1, Application US/09567899 Patent No. 6383787
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SEQ ID NO 1
LENGTH: 68750
                                                                                                                                                                                                                                     21325 ATCGCGCGAGCGCCGGCGGCCAGCCGGGGACGGGGACCTGCTCCGCCGCCTCGCCGCTC 21384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: MoInar, Istvan
APPLICANT: Zirkle, Ross
APPLICANT: Cyr, Devon
APPLICANT: Goerlach, Joern
TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
FILE REFERENCE: 4-30592A
CURRENT APPLICATION NUMBER: US/09/568,472
CURRENT FILING DATE: 2000-05-10
PRIOR APPLICATION NUMBER: 09/335,409
PRIOR APPLICATION NUMBER: 09/335,409
PRIOR FILING DATE: 1999-06-17
NUMBER OF SEC IN MOIS: 20
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                                                                                                                                                                               21385
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APPLICANT: Ligon,
APPLICANT: Molnar,
                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Sorangium cellulosum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 09/335,409
PRIOR FILING DATE: 1999-06-17
NUMBER OF SEQ ID NOS: 30
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ORGANISM: Sorangium cellulosum
                                                                                                                      139 TGGTGCGCCTGCACGAGGGCCAGACGATGACCGCCCC 178
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Local Similarity 52.5%;
hes 84; Conservative
                                                                                                                                                                 CCGAGCCGAGCGCGCGCGCGCGCTCCTGGAGCCGCTCCTCCGCGCGCAGATCTCGCAGG 21444
                                                                                                                                                                                                 CGGCTCAGGTGACCACCACCACCCTCACCGAGGAAGACGTCGTCGCCACCATCGAGTACC 138
                                                                                                   TGCTGCGCCTCCCGAGGGCAAGATCGAGGTGGACGCCCC 21484
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Similarity 52.5%; Pred. No. 1.5;
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0; Mismatches
                                                                                                                                                                                                                                                                                                                  Mismatches
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US-08-881-784-8
; Sequence 8, Application US/08881784
; Patent No. 6083731
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; TYPE: DNA
; ORGANISM: Sorangium cellulosum
US-09-567-899-1
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APPLICANT: Croteau
APPLICANT: Lupien,
APPLICANT: Karp, F
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Best Local
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APPLICANT: Schupp, Thomas
APPLICANT: Ligon, James
APPLICANT: Molnar, Istva
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APPLICANT: Zirkle, Ross
APPLICANT: Zirkle, Ross
APPLICANT: Cyr, Devon
TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
FILE REFERENCE: 4-30582A
CURRENT APPLICATION NUMBER: US/09/567,899
CURRENT FILING DATE: 2000-05-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT FILING DATE: 2000-05-10
PRIOR APPLICATION NUMBER: 09/335,409
PRIOR FILING DATE: 1999-06-17
NUMBER OF SEQ ID NOS: 30
                                                                                                                                                COMPUTER: LBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/881,784
FILING DATE:
CIASCOTTON:
        ATTORNEY/AGENT INFORMATION:
NAME: Shelton, Dennis K.
REGISTRATION NUMBER: 26,997
REFERENCE/DOCKET NUMBER: WSUR19777
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 224-0718
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                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: RECOMBINANT MATERIALS AND METHODS FOR TITLE OF INVENTION: THE PRODUCTION OF LIMONENE HYDROXYLASES 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  139 TGGTGCGCCTGCACGAGGGCCAGACCACGATGACCGCCCC 178
                                                                                                                                      CLASSIFICATION: 435
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(206) 224-0779
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Lupien, Shari L.
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52.5%;
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Pred. No. 1.5;
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INFORMATION FOR SEQ ID NO: 8
SEQUENCE CHARACTERISTICS:
LENGTH: 1665 base pairs

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nucleic acid

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: LOCATION: (19)..(1518)
US-09-292-768-3
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APPLICANT: Lupien, Shari L
APPLICANT: Karp, Frank
TITLE OF INVENTION: RECOMBINANT MATERIALS AN
TITLE OF INVENTION: LIMONENE HYDROXYLASES
FILE REFERENCE: wsur13463
CURRENT APPLICATION NUMBER: US/09/292,768
CURRENT FILING DATE: 1999-04-14
EARLIER APPLICATION NUMBER: 08/881,784
EARLIER FILING DATE: 1997-06-24
NUMBER OF SEQ ID NOS: 70
SOFTWARE: PATENTIN Ver. 2.0
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                                                                                                                                                                                                                   Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3, Application US/09292768 Patent No. 6194185
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Best Local Similarity 51.8

Matches 86; Conservative
                                                                                                                                                                                                                                                                                                                                                           LENGTH: 1665
TYPE: DNA
ORGANISM: Mentha piperita
                                                                                                                                                                                                                                                                                                                                          FEATURE:
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ORIGINAL SOURCE:
ORGANISM: Men
                                                                330 CGAGAGCATCGGGACGAAGATCATGTGGTACGACAACGACGACATCATCTTCAGCCCCTA 389
390 CAGCGTGCACTGGCGCCAGATGCGGAAGATCTGCGTCTCCGAGCTC
                              143 GCGCCTGCACGAGGGCCAGACCACGATGACCGCCCCCGGCGGCGGCGTC 188
                                                                                                                                    270 GTCCCGCGAGGCCACGAAGGAGGCGATGAAGCTGGTGGACCCGGCCTGCGCGCGGACCGGTT 329
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                                                                                                  83 TCAGGTGACCACCACCCTCACCGAGGAAGACGTCGTCGCCACCATCGAGTACCTGGT 142
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Local Similarity 51.8%;
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Pred. No. 1.5;
0; Mismatches 80; Indels
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Search completed: November 12,
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; LOCATION: (19)..(1518)
US-09-292-768-67
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CURRENT APPLICATION NUMBER: US/09/292,768
CURRENT FILING DATE: 1999-04-14
EARLIER APPLICATION NUMBER: 08/881,784
EARLIER FILING DATE: 1997-06-24
NUMBER OF SEQ ID NOS: 70
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SEQ ID NO 67
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Patent No. 6194185
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LOCATION: (1)..(1665)
OTHER INFORMATION: computer-generated nucleic acid sequence encoding
OTHER INFORMATION: limonene-3-hydroxylase variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: computer-generated nucleic acid sequence encoding OTHER INFORMATION: limonene-3-hydroxylase
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TYPE: DNA
ORGANISM: Artificial Sequence
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                                                                                                   390 CAGCGTGCACTGGCGCCAGATGCGGAAGATCTGCGTCTCCGAGCTC
                                                                                                                                   330 CGAGAGCATCGGGACGAAGATCATGTGGTACGACGACGACGACGATCATCTTCAGCCCCTA 389
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                                                                                                                                                                        83 TCAGGTGACCACCACCCTCACCGAGGAAGACGTCGTCGCCACCATCGAGTACCTGGT 142
                                                                                                                                                                                                                                     23 GGCCCGCGTGGGTACAAGGTGAACAAGAAGCTGGGCCTGGGCGGCACCAATCCGGC 82
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Local_Similarity 51.8%;
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           2002,
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Pred. No. 1
           21:03:28
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                                                                                                                                                                                                                                                                                            8O;
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Title:
Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Gapop 10.0 , Gapext 1.0
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214
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2: \SID$2\gcqdata\geneseq\geneseqn\embl\Na1981\daries\
3: \SID$2\gcqdata\geneseq\geneseqn\embl\Na1982\daries\
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6: \SID$2\gcqdata\geneseq\geneseqn\embl\Na1985\daries\
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8: \SID$2\gcqdata\geneseq\geneseqn\embl\Na1980\daries\
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15: \SID$2\gcqdata\geneseq\geneseq\geneseq\embl\Na1990\daries\
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9 14:	8 142	7 142	6 142	5 145	4 145	3 153	2 186.8	1 2	Result No. Score
211	208	208	208	214	208	208	214	214	Query Match Length DB
22	22	22	22	22	22	22	22	22	
AAS05218	AAS05210	AAS05208	AAS05201	AAS05214	AAS05215	AAS05219	AAS05207	AAS05221	ID
Mycobacterium flav	_			_	Mycobacterium aviu	_	Mycobacterium chel	Mycobacterium abso	Description

ABL12631	.8 537 21 AAC56489	40.4 18.9 109519 22 AASO8693	.4 19.3 547 21 AAC03907	42.2 19.7 1734 22 AAF90627	0 42.2 19.7 1734 22 AAS09832	42.2 19.7 1734 15 AAQ73490	8 42.2 19.7 1734 8 AAN70995 S	7 42.8 20.0 77536 21 AAA14651	6 43.2 20.2 1844 12 AAQ12000	5 43.8 20.5 5895 23 ABN87076	43.8 20.5 1734 21 AAA40350	3 55.2 25.8 27426 23 AAS59541	80.4 37.6 349980 22	80.4 37.6 3495 22 AAH65512	103 48.1 223 22 AAS05209	107.8 50.4 223 22 AAS05213	108.8 50.8 3447 14 AAQ51532	119.2 55.7 207 22 AAS05204	120.8 56.4 207 22 AAS05212	121.6 56.8 205 22 AAS05220	128 59.8 208 22 AAS05223	128 59.8 208 22 AAS05222	129.6 60.6 3853 21 AAA89994	129.6 60.6 3853 21 AAA74651	129.6 60.6 3534 22 AAH02079	129.6 60.6 3519 22 AAH51976	.6 60.6 970 17 AAT09676	129.6 60.6 208 22 AAS05216	129.6 60.6 208 22 AAS05206	129.6 60.6 208 22 AAS05205	136 63.6 208 22 AAS05224	136 63.6 208 22 AAS05203	.6 64.3 208 22 AAS05202	140:8 65:8 208 22 AAS05217	
Drosophila melanog	Eucalyptus grandis	Micromonospora DNA	Human secreted pro	PRV glycoprotein q	Pseudorabies virus	DNA encoding al of	Sequence encoding	Nucleotide sequenc	Maize nitrite redu	Pseudorabies virus	Swine psudorables	Propionibacterium		Ω.								a	-	_			_		-	_	_	_	_	_	

ALIGNMENTS

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Mycobacterium abscessus rpoB gene fragment.
                                                                                                                                             07-SEP-2001 (first entry)
Non-tuberculous mycobacteria; rpoB gene fragment; NTM; HIV; PRA; PCR-restriction fragment length polymorphism analysis; ds.
                                                                                                                                                                                                                     AAS05221;
                                                                                                                                                                                                                                                                      AAS05221 standard; DNA; 214 BP
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RFLP;

WPI; 2001-300520/31. Lee H, 27-OCT-1999; 27-OCT-2000; 2000WO-KR01223 03-MAY-2001. WO200131061-A1. Mycobacterium abscessus. (ERUM-) ERUME BIOTECH CO LTD. Park YK, Bai G, Kim S, 99KR-0046795. Cho ß Kim Y, Park HJ;

New DNA fragments from the rpoB gene of mycobacteria, useful for diagnosis and identification of many mycobacterial species by restriction fragment length polymorphism $\,\cdot\,$

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Best Local :
         Lee H,
                                                                                                                                                                                                                                                                                                           Non-tuberculous mycobacteria; rpoB gene fragment; NTM; HIV; PRA; RFLP; PCR-restriction fragment length polymorphism analysis; ds.
                                             (ERUM-) ERUME BIOTECH CO LTD
                                                                                                27-OCT-1999;
                                                                                                                                         27-OCT-2000; 2000WO-KR01223
                                                                                                                                                                                         03-MAY-2001
                                                                                                                                                                                                                                WO200131061-A1
                                                                                                                                                                                                                                                                              Mycobacterium chelonae
                                                                                                                                                                                                                                                                                                                                                                                           Mycobacterium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAS05207 standard; DNA; 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence for Mycobacterium abscessus rpoB gene fragment is 1 of 24 rpoB gene fragments (AASO5201-AASO5224) from various Mycobacterial species. These rpoB gene fragments can be used in the diagnosis and identification of Mycobacterium species using a novel PCR-restriction fragment length polymorphism analysis (PRA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 214 BP; 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        method. The method comprises obtaining a restriction fragment length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          y Match 100.0%; Score 214; DB 22;
Local Similarity 100.0%; Pred. No. 5.4e-38;
hes 214; Conservative 0; Mismatches 0;
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         Park YK,
                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                           99KR-0046795
                                                                                                                                                                                                                                                                                                                                                                                   chelonae rpoB gene fragment.
    Baí G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; 69 C; 72 G; 28 T; 0 other;
    Kim S,
  Cho
  'n
  Kin
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Park
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The present sequence for Mycobacterium chelonae rpoB gene C fragment is 1 of 24 rpoB gene fragments (AASO5201-AASO5224) from CC various Mycobacterial species. These rpoB gene fragments can be used CC in the diagnosis and identification of Mycobacterium species using a CC method. The method comprises obtaining a restriction fragment length polymorphism analysis (PRA) CC polymorphism (RFLP) pattern of the 24 rpoB gene fragments; isolating, CC amplifying and digesting the DNA fragment from the microorganism to CC digenors with the unidentified fragment from the known rpoB gene fragments with the unidentified fragment. The rpoB gene fragments CC are useful to identify a wide range of Mycobacterium species, e.g. for CC diagnosis or to obtain epidemiological and pathogenesis information for Selection of appropriate therapies, including M. tuberculosis, M. leprae CC and non-tuberculous mycobacteria (NTM) encountered in subjects infected fragments is rapid, precise, simple and cost effective (only 1 PCR CC experiment, including those difficult to distinguish by usual blochemical CC detecting specific Mycobacterial species. (AASO5227-AASO5242) for XX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 42; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New DNA fragments from the rpoB gene of mycobacteria, useful for diagnosis and identification of many mycobacterial species by restriction fragment length polymorphism -
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Query Match
Best Local
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      181
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                                                                                               61
                                                                                                                      61
                                                                                                                                  GCGGCGTCGAGGTGCCGGTGGATGTGGACGACAT 214
                                                                                                  GCCTGGGCGCACCAATCCGGCTCAGGTGACCACCACCACCCTCACCGAGGAAGAACGTCG 120
GCGGCCTCGAGGTCCCGGTCGAGGTCGACGACAT
                                        TCGCCACCATCGGGTACCTGGTGCGCCTGCACGAGGGCCAGACCACGATGACCGCCCCG
                                                      TCGCCACCATCGAGTACCTGGTGCGCCTGCACGAGGGCCAGACCACGATGACCGCCCCG
                                                                                       GTCTTGGCGGTGCCAACCCGGCTCTGGTGACTGCCACCACGCTCACCGAGGAAGACGTCG
                                                                                                                                                                                                   Similarity
                                                                                                                                                                                        Conservative
                                                                                                                                                                                                87.3%;
92.1%;
                                                                                                                                                                                 Score 186.8; DB 22; Length Pred. No. 4.6e-32; 0; Mismatches 17; Indels
 214
                                                                                                                                                                                                         214;
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                                           180
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Sequence 214 BP; 41 A; 72 C; 72 G; 29 T; 0 other;

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AC XX 
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07-SEP-2001

(first entry)

γQ Дb οy В Ş ₽ δ

Mycobacterium Non-tuberculous PCR-restriction Mycobacterium fortuitum rpoB gene fragment WO200131061-A1 fortuitum. mycobacteria; rpoB gene fragment; NTM; HIV; fragment length polymorphism analysis; ds.

27-OCT-2000; 2000WO-KR01223.

03-MAY-2001

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В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence for Mycobacterium fortuitum rpoB gene
C fragment is 1 of 24 rpoB gene fragments (AASO5201-AASO5224) from
CC various Mycobacterial species. These rpoB gene fragments can be used
CC in the diagnosis and identification of Mycobacterium species using a
CC novel pCR restriction fragment length polymorphism analysis (pRA)
CC method. The method comprises obtaining a restriction fragment length
CC polymorphism (RFLP) pattern of the 24 rpoB gene fragments; isolating,
CC amplifying and digesting the DNA fragment from the microorganism to
CC be identified and comparing the RFLP patterns from the known rpoB gene
CC fragments with the unidentified fragment. The rpoB gene fragments
CC are useful to identify a wide range of Mycobacterium species, e.g. for
CC diagnosis or to obtain epidemiological and pathogenesis information for
CC selection of appropriate therapies including M. tuberculosis, M. leprae
CC and non-tuberculous mycobacteria (NTM) encountered in subjects infected
CC with human immunodeficiency virus (HIV). Analysis of the rpoB gene
CC required), and can differentiate between many species in a single
CC experiment, including those difficult to distinguish by usual blochemical
CC detecting specific Mycobacterial species.
Mycobacterium avium
                      Non-tuberculous mycobacteria; rpoB gene fragment; NTM; HIV; PRA; RFLP; PCR-restriction fragment length polymorphism analysis; ds.
                                                                             Mycobacterium avium rpoB gene
                                                                                                                07-SEP-2001
                                                                                                                                                 AAS05215;
                                                                                                                                                                               AAS05215 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 208 BP; 43 A; 69 C; 69 G; 27 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 46; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New DNA fragments from the rpoB gene of mycobacteria, useful for diagnosis and identification of many mycobacterial species by
                                                                                                                                                                                                                                                                                                  181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         h 71.8%;
Similarity 86.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                specific
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                                                                                                             (first entry)
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                                                                                                                                                                               ВР
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 153.6; DB 22; Pred. No. 7.8e-25; 0; Mismatches 24;
                                                                           fragment
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   novel PCR-restriction fragment length polymorphism analysis (PRA)

Comethod. The method comprises obtaining a restriction fragment length

Complifying and digesting the DNA fragment from the microorganism to

Complifying and digesting the DNA fragment from the microorganism to

Complifying and digesting the PDA fragment from the microorganism to

Complifying and digesting the RFLP patterns from the known rpoB gene

Complifying and comparing the RFLP patterns from the known rpoB gene

Complifying and comparing the RFLP patterns from the known rpoB gene

Complifying and comparing the RFLP patterns from the known rpoB gene

Complifying and comparing the RFLP patterns from the known rpoB gene

Complifying and comparing the RFLP patterns from the known rpoB gene

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Complifying and comparing the RFLP patterns from the known rpoB gene

Complifying and comparing the RFLP patterns from the known rpoB gene

Complifying and comparing the RFLP patterns from the known rpoB gene

Complifying and digesting the patterns from the known rpoB gene

Complifying and digesting the patterns from the known rpoB gene

Complifying and comparing the patterns from the known rpoB gene

Complifying and comparing the RFLP patterns from the known rpoB gene

Complifying and digesting the patterns from the known rpoB gene

Complifying and comparing the RFLP patterns from the known rpoB gene

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Complifying and comparing the RFLP patterns from the known rpoB gene

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Complifying and complication patterns from the known rpoB gene

Complifying and digesting the RFLP patterns from the known rpoB gene

Complifying and digesting the RFLP patterns from the known rpoB gene

Complifying and digesting the RFLP patterns
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 179;
       07-SEP-2001
                                                                                              AAS05214 standard;
                                                      AAS05214;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 208 BP; 44 A; 69 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence for Mycobacterium avium rpoB gene fragment is 1 of 24 rpoB gene fragments (AASO5201-AASO5224) from various Mycobacterial species. These rpoB gene fragments can be used in the diagnosis and identification of Mycobacterium species using a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 44; 50pp; English.
                                                                                                                                                                                                      New DNA fragments from the rpoB gene of mycobacteria, useful for diagnosis and identification of many mycobacterial species by restriction fragment length polymorphism -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-OCT-2000; 2000WO-KR01223
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                                                                                                                                                                                                                                                                                                                                                                                                             61
                                                                                                                                                                                                                                                                                                                                                                                                                       61 GCCTGGGCGCACCAATCCGGCTCAGGTGACCACCACCACCCTCACCGAGGAAGACGTCG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         <u>-</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 TCAAGGAGAAGCGCTACGATCTGGCCCGGCGTGGGTTGGGTACAAGGTGAACAAGAAGCTGG
                                                                                                                                                                                                                                                                                             TCGCCACCATCGAGTACCTGGTGCGCCTGCACGAGGGTCAGCCCACGATGACCGTCCCCG
                                                                                                                                                                                                                                                                                                                         TCGCCACCATCGAGTACCTGGTGCGCCTGCACGAGGGCCAGACCACGATGACCGCCCCCG
                                                                                                                                                                                                                                                                                                                                                                                            GCCTGCACGCCGGTGAGCC-----GATCACCAGCTCGACGCTGACCGAGGAAGACGTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCAAGGAGAAGCGCTACGACCTGGCCCGGGTGGGCCGCTACAAGGTCAACAAGAAGCTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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(first entry)
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                                                                                                DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 145.6; DB 22;
Pred. No. 4.3e-23;
0; Mismatches 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69 G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ś
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RESULT 6
AAS05201
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                                                                                                                                                                                                                                                                                         Matches 171; Conservative
                                                                                                                                                                                                                                                                                                            Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                    Sequence 214 BP;
                                                        181
                                                                                     181
                                                                                                                  121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New DNA fragments from the rpoB gene of mycobacteria, useful for diagnosis and identification of many mycobacterial species by restriction fragment length polymorphism .
                                                                                                                                               121
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PCR-restriction
                                                                                                                                                                                                        61
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                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                       GCGGCGTCGAGGTGCCGGTGGAGACCGACGACAT 214
                                                                             GCGGCGTCGAGGTGCCGGTGGATGTGGACGACAT 214
                                                                                                      TCGCCACCATCGAGTACCTGGTGCGCCTGCACGAGGGCCAGACCACGATGACCGCCCCG
                                                                                                                                                                GGCTGCCGGCGGGCGAGTCGGCCGTACCCGCCTCGACCACGCTGACCGAAGCGGATGTCG
                                                                                                                                                                                   GCCTGGGCGCACCAATCCGGCTCAGGTGACCACCACCACCACCCTCACCGAGGAAGACGTCG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Park YK, Bai G, Kim S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99KR-0046795.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mycobacteria; rpoB gene fragment; NTM;
fragment length polymorphism analysis;
                                                                                                                                                                                                                                                                                                                                                 42 A; 68 C;
                                                                                                                                                                                                                                                                                                    67.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rpoB
                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                    Score 145.2; DB 2
Pred. No. 5.3e-23;
                                                                                                                                                                                                                                                                                                                                               75 G; 29 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene fragment
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                                                                                                                                                                                                                                                                                                                 DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kim
                                                                                                                                                                                                                                                                                        43;
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                                                                                                                                                                                                                                                                                                                 214;
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В Ş В δÃ 밁 Qy

181 GCGGCGTCGAGGTGCCGGTGGATGTGGACGACAT 214

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The present sequence for Mycobacterium gordonae type I rpoB gene CC fragment is 1 of 24 rpoB gene fragments (AASO5201-AASO5224) from CC various Mycobacterial species. These rpoB gene fragments can be used in the diagnosis and identification of Mycobacterium species using a convel pcR-restriction fragment length polymorphism analysis (PRA) cc method. The method comprises obtaining a restriction fragment length polymorphism (RELP) pattern of the 24 rpoB gene fragments; isolating, cc amplifying and digesting the DNA fragment from the microorganism to cc indentified and comparing the RELP patterns from the known rpoB gene care useful to identify a wide range of Mycobacterium species, e.g. for diagnosis or to obtain epidemiological and pathogenesis information for selection of appropriate therapies, including M. tuberculosis, M. leprae cc and non-tuberculous mycobacteria (NTM) encountered in subjects infected fragments is rapid, precise, simple and cost effective (only 1 pcr crequired), and can differentiate between many species in a single capteria. Also described are oligonuclectide probes (AASO5227-AASO5242) for XX
                                                                                                                                                                                                          Query Match
Best Local S
Matches 177
                                                                                                                                                                                                                                                                      Sequence 208 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New DNA fragments from the rpoB gene of mycobacteria, useful for diagnosis and identification of many mycobacterial species by restriction fragment length polymorphism .
               115
                                                121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 40; 50pp; English.
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                                                                             61
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                                                                                                            61
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                                                                                                                                                 1 TCAAGGAGAAGCGCTACGATCTGGCCCGCGTGGGTCGGTACAAGGTGAACAAGAAGCTGG
                                                                                                                             1 TCAAGGAGAAGCGCTACGACCTGGCCCGGGTAGGCCGCTACAAGGTCAACAAGAAGCTCG
TCGCCACCATCGAGTACCTGGTCCGCCTGCACGAGGGCCAGCACGATGACCGTCCCGG
                  TCGCCACCATCGAGTACCTGGTGCGCCTGCACGAGGGCCAGACCACGATGACCGCCCCG 180
                                                                  GCCTGCACGTCGGCGATCC------GATCACCAGCTCCACGCTGACCGAGGAAGAAGACGTCG
                                                                                GCCTGGGCGGCACCAATCCGGCTCAGGTGACCACCACCACCCTCACCGAGGAAGACGTCG 120
                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                   66.5%;
82.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kim S,
                                                                                                                                                                                                     0,
                                                                                                                                                                                                 Score 142.4; DB 22;
Pred. No. 2.1e-22;
0; Mismatches 31;
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                                                                                                                                                                                                                                                             26 T; 0 other;
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                                                                                                                                                                                                 Indels
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                                                                                                                                                                                            Gaps
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                                                                                                                                                                                             The present sequence for Mycobacterium kansasii rpoB gene CC fragment is 1 of 24 rpoB gene fragments (AAS05201-AAS05224) from CC various Mycobacterial Species. These rpoB gene fragments can be used CC in the diagnosis and identification of Mycobacterium species using a CC movel PCR restriction fragment length polymorphism analysis (PRA) CC method. The method comprises obtaining a restriction fragment length CC polymorphism (RFLP) pattern of the 24 rpoB gene fragments; isolating, CC amplifying and digesting the DNA fragment from the microorganism to CC diagnosis and comparing the RFLP patterns from the known rpoB gene CC fragments with the unidentified fragment. The rpoB gene fragments CC diagnosis or to obtain epidemiological and pathogenesis information for CC selection of appropriate therapies, including M. tuberculosis, M. leprae CC and non-tuberculous mycobacteria (NTM) encountered in subjects infected CC with human immunodeficiency virus (HIV). Analysis of the rpoB gene CC required), and can differentiate between many species in a single CC experiment, including those difficult to distinguish by usual biochemical CC deterting specific Mycobacterial species.
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AAS05208
ID AASO
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                                                                                                                                              Ouery Match
Best Local
                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 42; 50pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New DNA fragments from the rpoB gene of mycobacteria, useful for diagnosis and identification of many mycobacterial species by restriction fragment length polymorphism \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lee
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     61
                                 61
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                                                                             TCAAGGAGAAGCGCTACGATCTGGCCCGCGTGGGTCGGTACAAGGTGAACAAGAAGCTGG 60
GCCTGAACACCAATCATCC-----GATCACCACGACGACGCTGACCGAAGAAGACGTCG
                          GCCTGGGCGGCACCAATCCGGCTCAGGTGACCACCACCACCCTCACCGAGGAAGACGTCG 120
                                                          TCAAGGAGAAGCGCTACGACCTGGCCCGTGTCGGCCGATACAAGGTCAACAAGAAGCTGG
                                                                                                                               al Similarity
177; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Park YK, Bai G, Kim
                                                                                                                                                                                            208 BP;
                                                                                                                            66.5%;
ilarity 82.7%;
Conservative
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                                                                                                                                                                                        51 A; 65 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 English.
                                                                                                                               0
                                                                                                                       Score 142.4; DB 22; Pred. No. 2.1e-22; "Mismatches 31;
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                                                                                                                                                                                        65 G; 27 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kim Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Park
                                                                                                                                                        Length 208;
                                                                                                                          6
                                                                                                                        Gaps
114
                                                            60
                                                                                                                        1;
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1 TCAAGGAGAAGCGCTACGATCTGGCCCGCGTGGGTCGGTACAAGGTGAACAAGAAGCTGG 60

Matches Query Match Best Local Sequence

al Similarity 177; Conserv

Conservative

0;

Mismatches

Indels

6. Gaps 66.5%;

Score 142.4; Pred. No. 2.1

.1e-22

DB 22; 31;

Length

208 BP; 45 A; 68 C; 67 G;

28 T; 0 other;

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The present sequence for Mycobacterium ulcerans rpoB gene CC fragment is 1 of 24 rpoB gene fragments (AAS05201-AAS05224) from CC various Mycobacterial species. These rpoB gene fragments can be used CC in the diagnosis and identification of Mycobacterium species using a convel pCR-restriction fragment length polymorphism analysis (PRA) CC method. The method comprises obtaining a restriction fragment length polymorphism analysis (PRA) CC polymorphism (RFLP) pattern of the 24 rpoB gene fragments; isolating, complifying and digesting the DNA fragment from the microorganism to CC de identified and comparing the RFLP patterns from the known rpoB gene fragments with the unidentified fragment. The rpoB gene fragments care useful to identify a wide range of Mycobacterium species, e.g. for CC diagnosis or to obtain epidemiological and pathogenesis information for selection of appropriate therapies, including M. tuberculosis, M. leprae CC and non-tuberculous mycobacteria (NTM) encountered in subjects infected fragments is rapid, precise, simple and cost effective (only 1 PCR crequired), and can differentiate between many species in a single experiment, including those difficult to distinguish by usual blochemical cests. Also described are oligonucleotide probes (AAS05227-AAS05242) for detecting specific Mycobacterial species.
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                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 43; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                          New DNA fragments from the rpoB gene of mycobacteria, useful for diagnosis and identification of many mycobacterial species by restriction fragment length polymorphism -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-300520/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lee H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Non-tuberculous mycobacteria; rpoB gene fragment; NTM; HIV; PRA; PCR-restriction fragment length polymorphism analysis; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mycobacterium ulcerans.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAS05210 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCGCCACCATCGAGTACCTGCGCGCCTGCACGAGGGCCAGACCACGATGACCGCCCCCG 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCGCCACCATCGAGTATCTGGTCCGCCTGCACGAGGCCCAGGCCACGATGACCGTGCCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ERUME BIOTECH CO LTD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bai G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BP
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RESULT 9
AASO5218
ID AASO
XX AASO
XX AASO
XX AASO
XX WYCO
XX NON-
KW PCR-
XX WYCO
XX WYCO
XX WYCO
XX PPN W02(
XX Y CO
PN W02(
XX Y CO
PN W27-(
XX Z7-(
                                                        The present sequence for Mycobacterium flavescens rpoB gene (C fragment is 1 of 24 rpoB gene fragments (AASO5201-AASO5224) from (C various Mycobacterial species. These rpoB gene fragments can be used (C in the diagnosis and identification of Mycobacterium species using a (C novel PCR-restriction fragment length polymorphism analysis (pRA) (C method. The method comprises obtaining a restriction fragment length polymorphism (RRILP) pattern of the 24 rpoB gene fragments; isolating, (C amplifying and digesting the DNA fragment from the microorganism to be identified and comparing the RFLP patterns from the known rpoB gene fragments with the unidentified fragment. The rpoB gene fragments (C are useful to identify a wide range of Mycobacterium species, e.g. for (C selection of appropriate therapies, including M. tuberculosis, M. leprae (C and non-tuberculous mycobacteria (NTM) encountered in subjects infected (ragments is rapid, precise, simple and cost effective (only 1 PCR (C required), and can differentiate between many species in a single (experiment, including those difficult to distinguish by usual blochemical (tests, Also described are oilgonucleotide probes (AASO5227-AASO5242) for detecting specific Mycobacterial species.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New DNA fragments from the rpoB gene of mycobacteria, useful diagnosis and identification of many mycobacterial species
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        restriction
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-SEP-2001
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211 BP; 49

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70 <u>.</u>

27 T; 0

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The present sequence for Mycobacterium marinum rpoB gene
C fragment is 1 of 24 rpoB gene fragments (AAS05201-AAS05224) from
CC various Mycobacterial species. These rpoB gene fragments can be used
CC in the diagnosis and identification of Mycobacterium species using a
CC movel PCR-restriction fragment length polymorphism analysis (pRA)
CC method. The method comprises obtaining a restriction fragment length
CC polymorphism (REPLP) pattern of the 24 rpoB gene fragments; isolating,
CC amplifying and digesting the DNA fragment from the microorganism to
CC diagnosis and comparing the RFLP patterns from the known rpoB gene
CC are useful to identify a wide range of Mycobacterium species, e.g. for
CC diagnosis or to obtain epidemiological and pathogenesis information for
CC selection of appropriate therapies, including M. tuberculosis, M. leprae
CC with human immunodeficiency virus (HIV). Analysis of the rpoB gene
CC fragments is rapid, precise, simple and cost effective (only 1 pCR
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Best Local :
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                                                                                                                                                                                                                                                                                                                New DNA fragments from the rpoB gene of mycobacteria, useful for diagnosis and identification of many mycobacterial species by
                                                                                                                                                                                                                                                                                                      restriction fragment length polymorphism
                                                                                                                                                                                                                                                                                                                                                                                                      Lee H,
                                                                                                                                                                                                                                                                                                                                                                                                                               (ERUM-) ERUME BIOTECH CO LTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                99KR-0046795.
                                                                                                                                                                                                                                                                                                                                                                                                   Bai G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66.48;
                                                                                                                                                                                                                                                                            English
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Pred. No. 2.6e
0; Mismatches
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.6e-22;
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RESULT 11
AASO5217
ID AASO5
XX AASO5
AC AASO5
XX AASO5
XX AASO5
XX AASO5
XX AASO5
XX NON-
XX NON-
XX PCR-
XX PCR-
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The present sequence for Mycobacterium celatum rpoB gene fragment is 1 of 24 rpoB gene fragments (AASO5201-AASO5224) from various Mycobacterial species. These rpoB gene fragments can be used in the diagnosis and identification of Mycobacterium species using a novel PCR-restriction fragment length polymorphism analysis (PRA) method. The method comprises obtaining a restriction fragment length polymorphism (RFLP) pattern of the 24 rpoB gene fragments; isolating, amplifying and digesting the DNA fragment from the microorganism to be identified and comparing the RFLP patterns from the known rpoB gene fragments with the unidentified fragment. The rpoB gene fragments
                                                                                                                                                                                                                                                                                                            Claim 1; Page 45;
                                                                                                                                                                                                                                                                                                                                             New DNA fragments from the rpoB gene of mycobacteria, useful for diagnosis and identification of many mycobacterial species by restriction fragment length polymorphism .
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fragment length polymorphism analysis;
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The present sequence for Mycobacterium gordonae type II rpoB fragment is 1 of 24 rpoB gene fragments (AASUS201-AASUS224) f various Mycobacterial species. These rpoB gene fragments can in the diagnosis and identification of Mycobacterium species
                                                                                             restriction fragment length polymorphism
                                                                                                         New DNA fragments from the rpoB gene of mycobacteria, useful diagnosis and identification of many mycobacterial species
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CC method. The method comprises obtaining a restriction fragment length
CC polymorphism (RFLP) pattern of the 24 rpoB gene fragments; isolating,
CC amplifying and digesting the DNA fragment from the microorganism to
CC be identified and comparing the RFLP patterns from the known rpoB gene
CC fragments with the unidentified fragment. The rpoB gene fragments
CC are useful to identify a wide range of Mycobacterium species, e.g. for
CC diagnosis or to obtain epidemiological and pathogenesis information for
CC diagnosis or to obtain epidemiological and pathogenesis information for
CC election of appropriate therapies, including M. tuberculosis, M. leprae
CC and non-tuberculous mycobacteria (NTM) encountered in subjects infected
CC with human immunodeficiency virus (HIV). Analysis of the rpoB gene
CC fragments is rapid, precise, simple and cost effective (only 1 pCR
CC experiment, including those difficult to distinguish by usual biochemical
CC tests. Also described are oligonucleotide probes (AASO5227-AASO5242) for
CC defection anaecific Mycobacterial species
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              New DNA fragments from the rpoB gene of mycobacteria, useful for diagnosis and identification of many mycobacterial species by restriction fragment length polymorphism \,
                                                                                                                                                                                                                                                                                                           27-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Non-tuberculous mycobacteria; rpoB gene fragment; NTM; PCR-restriction fragment length polymorphism analysis;
                                                                                                                                                                                                                                                     (ERUM-) ERUME BIOTECH CO LTD
                                                                                                                                                                                                                                                                                                                                                             27-OCT-2000; 2000WO-KR01223
                                                                                                                                                                                                                                                                                                                                                                                                                           03-MAY-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200131061-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mycobacterium gordonae type III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mycobacterium gordonae type III rpoB gene fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAS05203;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAS05203 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 208 BP; 45 A; 62 C; 73 G; 28 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   175
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Local Similarity 81.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCGGCGTCGAGGTGCCGGTGGATGTGGACGACAT
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                                                                                                                                                                                                Park
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                                                                                                                                                                                             YK, Bai G,
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 Mismatches

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Pred. No. 2.4e-21
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RESULT 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence for Mycobacterium gordonae type III rpoB gene CC fragment is 1 of 24 rpoB gene fragments (AASO5201-AASO5224) from CC various Mycobacterial species. These rpoB gene fragments can be used CC in the diagnosts and identification of Mycobacterium species using a CC novel PCR restriction fragment length polymorphism analysis (PRA) CC method. The method comprises obtaining a restriction fragment length CC polymorphism (RFLP) pattern of the 24 rpoB gene fragments; isolating, CC amplifying and digesting the DNA fragment from the microorganism to be identified and comparing the RFLP patterns from the microorganism to gene useful to identify a wide range of Mycobacterium species, e.g. for CC arguments with the unidentified fragment. The rpoB gene fragments of appropriate therapies, including M. tuberculosis, M. leprae CC and non-tuberculous mycobacteria (NTM) encountered in subjects infected CC with human immunodeficiency virus (HIV), Analysis of the rpoB gene CC required), and can differentiate between many species in a single CC experiment, including those difficult to distinguish by usual biochemical CC tests. Also described are oligonucleotide probes (AASO5227-AASO5242) for XX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 173;
                                                                                                                                        03-MAY-2001.
                                                                                                                                                                                                    Mycobacterium xenopi.
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                                                                        27-OCT-1999;
                                                                                                     27-OCT-2000; 2000WO-KR01223
                                                                                                                                                                                                                              Non-tuberculous mycobacteria; rpoB gene fragment; NTM; PCR-restriction fragment length polymorphism analysis;
                                                                                                                                                                                                                                                                                Mycobacterium xenopi rpoB gene fragment
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80.8%;
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5.3e-21;
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(ERUM-) ERUME BIOTECH CO

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RESULT 15
AAS05205
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CC fragment is 1 of 24 rpoB gene fragments (AASO5201-AASO5224) from
CC various Mycobacterial species. These rpoB gene fragments can be used
CC in the diagnosis and identification of Mycobacterium species using a
CC movel PCR-restriction fragment length polymorphism analysis (PRA)
CC method. The method comprises obtaining a restriction fragment length
CC polymorphism (RRILP) pattern of the 24 rpoB gene fragments; isolating,
CC amplifying and digesting the DNA fragment from the microorganism to
CC defense that the unidentified fragment from the known rpoB gene
CC are useful to identify a wide range of Mycobacterium species, e.g. for
CC diagnosis or to obtain epidemiological and pathogenesis information for
CC gelection of appropriate therapies, including M. tuberculosis, M. leprae
CC and non-tuberculous mycobacteria (NTM) encountered in subjects infected
CC fragments is rapid, precise, simple and cost effective (only 1 PCR
CC required), and can differentiate between many species in a single
CC experiment, including those difficult to distinguish by usual biochemical
CC detecting specific Mycobacterial species.
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         27-OCT-2000; 2000WO-KR01223
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                                                                                                                                                                        Mycobacterium tuberculosis rpoB gene fragment.
                                                                                                    Mycobacterium tuberculosis
                                                                                                                                   PCR-restriction
                                                                                                                                                 Non-tuberculous
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                                                                                                                                                                                                                                           AAS05205;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           121
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173; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 208 BP; 51 A; 65 C; 67 G; 25 T; 0 other;
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                                                                                                                                                                                                        (first entry)
                                                                                                                           mycobacteria; rpoB gene fragment; NTM;
fragment length polymorphism analysis;
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80.8%;
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Pred. No. 5.3e-21
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                                                                                                                            HIV; PRA; RFLP; ds.
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Search completed: November Job time: 142.151 secs

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                                                                                                                                                                                                                                                                                                                             C polymorphism (RFLP) pattern of the 24 rpoB gene fragment; isolating, and digesting the DNA fragment from the microorganism to be identified and comparing the RFLP patterns from the known rpoB gene fragments with the unidentified fragment. The rpoB gene fragments with the unidentified fragment. The rpoB gene fragments or to obtain epidemiological and pathogenesis information for diagnosis or to obtain epidemiological and pathogenesis information for selection of appropriate therapies, including M. tuberculosis, M. leprae with human immunodeficiency virus (HIV). Analysis of the rpoB gene fragments is rapid, precise, simple and cost effective (only 1 PCR required), and can differentiate between many species in a single experiment, including those difficult to distinguish by usual blochemical tests. Also described are oligonucleotide probes (AAS05227-AAS05242) for xxx
                                                                                                                                                                                                                                                     Matches
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Best Local
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         175
                                     181
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                                                                                 121 TCGCCACCATCGAGTACCTGGTGCGCCTGCACGAGGGCCAGACCACGATGACCGCCCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               novel PCR-restriction fragment length polymorphism analysis (PRA) method. The method comprises obtaining a restriction fragment length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        restriction fragment length polymorphism
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ERUM-) ERUME BIOTECH CO LTD.
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                                                         TGGCCACCATCGAATATCTGGTCCGCTTGCACGAGGGTCAGACCACGATGACCGTTCCGG
                                                                                                                  GGCTGCATGTCGGCGAGCC-----CATCACGTCGTCGACGCTGACCGAAGAAGACGTCG
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Similarity 79.0%;
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Pred. No. 1.3e
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Minimum DB seq length: 0
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   GenEmbl:*
1: gb_ba:*
2: gb_htg:
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1 tcaaggagaagcgctacgat.....ccggtggatgtggacgacat 214
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Listing first 45 summaries
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ALIGNMENTS

REFERENCE AUTHORS TITLE		ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	Locus	MSU24494	RESULT 1
<pre>1 (bases 1 to 3752) Hetherington, S.V., Watson, A.S. and Patrick, C.C. Sequence and analysis of the rpoB gene of Mycobacterium smegmatis</pre>	Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.	Mycobacterium smegmatis	Mycobacterium smeqmatis.		U24494.1 GI:790347	U24494	(rnoB) gene	MSU24494 3752 bp DNA linear BOT 02-MAB-2000		

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TN 38101, USA
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/db_xref="taxon:1772"
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                                                                                                     Mycobacterium tuberculosis partial beta subunit, isolate 1417-97. AJ318819. 1 GI:22208414 RNA polymeraea bee
                                   Mycobacterium tuberculosis. Mycobacterium tuberculosis
                                                                                      RNA polymerase beta subunit;
           Bacteria; Actinobacteria;
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Nacional Microbiologia., Ctra. Majadahonda-Pozuelo,
Majadahonda. Madrid. 28220, SPAIN
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Molecular analysis of rifampin-resistant Mycobacterium tuberculosis
isolated in Spain (1996-2001). Description of new alleles into rpoB
gene and review
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RLRTVGELIQHOLTAVGMSRMERVVRERMTTQDVEAITPQTLINIRPVVAAIKEFFGTS
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/isolate="1415-97"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGGCCACCATCGAATATCTGGTCCGCTTGCACGAGGGTCAGACCACGATGACCGTTCCGG
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                                                                                                                                                MTU318813
616 bp DNA circular BCT 09-Al Mycobacterium tuberculosis partial rpoB gene for RNA polymer; beta subunit, isolate 1763-97.
AJ318813
AJ318813.1 GI:22208402
RNA polymerase beta subunit; rpoB gene.
Mycobacterium tuberculosis.
Mycobacterium tuberculosis
Bacteria; Actinobacteridae; Actinomycetales; Portughacteria; Actinobacteridae; Actinomycetales; Portughacteriae; Actinobacteriae; Actinobacteridae; Actinobacteriae; Actinobacteridae; Actinobacteriae; Portughacteridae; Po
                   Molecular analysis of rifampin-resistant Mycobacterium tuberculosis isolated in Spain (1996-2001). Description of new alieles into rpoB
                                                                                                                                  Corynebacterineae; Mycobacteriaceae;
                                                                   Herrera, L., Jimenez, M.S. and Saez, J.A.
                                                                                                                      tuberculosis complex.
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Molecular analysis of rifampin-resistant Mycobacterium tuberculosis
Isolated in Spain (1996-2001). Description of new alleles into rpoB
gene and review
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2 (bases 1
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/protein_id="CAC87036.1"
/protein_id="CAC87036.1"
/db_xref="Gi:22208415"
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RLRTVGELIQNQIRVGMSRMERVVREHTYTQDVEAITPOTLINIRPVVAAIKEFFGTS
QPSGFMGQNNPLSGLTHKRRLSALGPGGLSRERAGLEVRDVHP"
a 191 c 202 g 95 t
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/transl_table=11
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<1. .>610
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/isolate="1417-97"
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79.0%;
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Pred. No. 1.6e-12;
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ozuelo, Km 2.5,
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                                                                                                                                                                                                                                         Mycobacterium tuberculosis.
Mycobacterium tuberculosis
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacteriaceae;
  Direct Submission
Submitted (07-AUG-2001) Herrera
                                                                                                                             Herrera,L., Jimenez,M.S. and Saez,J.A.
Molecular analysis of rifampin-resistant Mycobacterium tubercul
isolated in Sain (1996-2001). Description of new alleles into
                                                  Herrera, L
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                                                                                                                                                                                                                                                                                                                                          RNA polymerase beta subunit;
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                                                                                                                                                                                                                                    tuberculosis
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AJ318815
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                                                                        (bases 1 to 618)
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/codon_start=1
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/product="RNA polymerase beta subunit"
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RLRTVGELIQNQIRVGMSRMERVVRERMTTQDVEAITPOTLINIRPVVAAIKEFFGTS
QLSQFIFMDQNNPLSGLTHKRLSALGPGGLSRERAGLEVRDVHP"
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<1. .>615
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/isolate="1763-97"
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Pred. No. 1.6e-12;
""" artches 39;
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dahonda-Pozuelo, Km 2.5,
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                                             Direct Submission
Submitted (07-AUG-2001) Herrera L., Servicio Bacteriologia,
Nacional Microbiologia., Ctra. Majadahonda-Pozuelo, Km 2.5,
Majadahonda. Madrid. 28220, SPAIN
                                                                                                                                               gene and review
                                                                                                                                                      Herrera,L., Jimenez,M.S. and Saez,J.A.
Molecular analysis of rifampin-resistant Mycobacterium tuberculosis
isolated in Spain (1996-2001). Description of new alleles into rpoB
                                                                                                                                                                                                                        Mycobacterium tuberculosis
Mycobacterium tuberculosis
Mycobacteria; Actinobacteria; Actinobacteria; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobact
                                                                                                                                                                                                                                                                           AJ318817
AJ318817.1 GI:22208410
RNA polymerase beta subunit; rpoB
                                                                                                         Herrera, L.
                                                                                                                                   Unpublished
                                                                                                                                                                                                                                                                                                                         MTU318817

Mycobacterium tuberculosis partial beta subunit, isolate 2348-98.
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                                                                                                                                                                                                                  tuberculosis complex.
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a 190 c 207 g 97 t
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<1. .>618
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Query Match
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                                                                                                                                                               Submitted (07-AUG-2001) Herrera L., Servicio Bacteriologia, Nacional Microbiologia., Ctra. Majadahonda-Pozuelo, Km 2.5, Majadahonda. Madrid. 28220, SPAIN
                                                                                                                                                                                                                                                                                                                           Herrera,L., Jimenez,M.S. and Saez,J.A. Molecular analysis of rifampin-resistant My isolated in Spain (1996-2001). Description
                                                                                                                                                                                                                                                                         Unpublished 2 (bases 1 to 633)
                                                                                                                                                                                                                                    Direct Submission
                                                                                                                                                                                                                                                         Herrera,L
                                                                                                                                                                                                                                                                                                                 gene and review
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Corynebacterineae; Mycobacteriaceae; Mycobac
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AJ318814.1 GI:22208404
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MYCOJABCTETIUM T.Jberculosis partial rpoB gene for RNA polymerase beta subunit, isolate 1058-97.
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Submitted (07-AUG-2001) Herrera L., Servicio Bacteri
Nacional Microbiologia., Ctra. Majadahonda-Pozuelo,
Majadahonda. Madrid. 28220, SPAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mycobacterium tuberculosis. Mycobacterium tuberculosis
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AJ318816.1 GI:22208408
RNA polymerase beta subunit; rpoB
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ABIKEFGTSQLSQFMOQNNPLSGLTYKRRLSALGPGGLSRERAGLEVRDV"
195 c 210 g 99 t
                                                                                                                    /codon_start=1
                                                                                                                                          /gene="rpoB"
                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                   /db_xref="taxon:1773"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /transl_table=11
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No. 1.6e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene
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dahonda-Pozuelo, Km 2.5,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mycobacterium; Mycobacterium
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gene for RNA polymerase
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RNA polymerase beta subunit; rpoB gene.
Mycobacterium tuberculosis.
Mycobacterium tuberculosis
Bacteria; Actinobacteria; Actinobacteridae; Actinom
Corynebacterineae; Mycobacteriaceae; Mycobacterium;
                                                                                                                                                                                                                                                                                                                                                               Submitted (07-AUG-2001) Herrera L., Servicio Bacter Nacional Microbiologia., Ctra. Majadahonda-Pozuelo, Majadahonda. Madrid. 28220, SPAIN
                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene and review
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Herrera,L., Jimenez,M.S. and Saez,J.A.
Molecular analysis of rifampin-resistant Mycobacterium tuberculosis
isolated in Spain (1996-2001). Description of new alleles into rpoB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mycobacterium tuberculosis partial rpoB gene for RNA polymerase beta subunit, isolate 1071-98.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Herrera,L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        (bases 1 to 639)
                                              126
                       /gene="rpob"
/gene="rpob"
/codon_start=1
/codon_start=1
/transl_table=11
/transl_table=11
/product="RIA polymerase beta subunit"
/protein_id="CaC87038.1"
/db_xref="GI:22208419"
/db_xref="GI:22208419"
/translation="RRTDEALLDIYRKLRPGEPPTKESAQTLLENLFFKEKRYDLARV
frykvnkklglhygepirssmilfeddvariffylvrihegQfmmfvpGgveypveTdb
IDHFGNRRLRTYGELIONGIRYGMSRMERVVRERMTTQDVEAITPQTLINIRPAVAAI
KEFFGTSQLSOFMVQNNPLSGLTQKRRLSALGPGGLSRERAGLEVRDVHPSHS"
26 a 202 c 212 g 99 t
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KEFFGTSQLSOFMDQNNPLSGLTHKRRMFALGPGGLSRERAGLEVRDVHPSH*
a 198 c 210 g 101 t
                                                                                                                                                                                                                                                /gene="rpoB"
                                                                                                                                                                                                                                                                                                /organism="Mycobacterium
/isolate="1071-98"
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ozuelo, Km 2.5,
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Best Local Similarity
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Matches 169; Conservative
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                                                                                                                                                                GCGGCGTCGAGGTGCCGGTGGATGTGGACGACAT 214
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                                                              Sequence
AX111339
Mycobacterium tuberculosis.
Mycobacterium tuberculosis
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                     AX111339.1
                                                                                        AX111339
                                                                                                                                                                                                                                                                                                                                                                                                                                            l (bases 1 to 970)
Persing,D.H., Hunt,J.J., Young,K.K.Y., Felmlee,T.
and Whelan,A.Christian.
Detection of a genetic locus encoding resistance
mycobacterial cultures and in clinical specimens
Patent: US 5643723-A 1 01-JUL-1997;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1 from patent US 150706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unclassified
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2072 from Patent WO0123604
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302 c 330 g
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                                                    GI:13927631
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79.0%;
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0; Mismatches 39;
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Mycobacterium tuberculosis

Mycobacterium tuberculosis

Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;

Actinomycetales; Corynebacterineae; Mycobacteriaceae;

Mycobacterium; Mycobacterium tuberculosis complex.

1 (bases 1 to 3853)

Characteriacy monarce acceptance accep
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Mycobacterium tuberculosis H37Rv
gene, partial cds.
U12205
                                                                                                                                                                                                                                                                                                                         Submitted (11-JUL-1994) Paul Imboden, Institute for Microbiology, University of Berne, Friedbuehlstrasse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Imboden, P., Troller, R., Marchesi, F., Telent Cole, S., Schopfer, K. and Burkart, T. The rpoB gene of Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                Imboden, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mycobacterium; Mycobacterium tuberculosis complex 1 (bases 1 to 3534) Bergeron, M.G., Boissinot, M., Huletsky, A., m Nard, C Picard, F.J. and Roy, P.H.
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Pred. No. 1.3
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                                                                                                                                                                                                                                                                                                                                     Berne,
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                                                                                                                                                                                                                                        1 (bases 1 to 5084)
Miller,L.P., Crawford,J.T. and Shinnick,T.M.
The rpoB gene of Mycobacterium tuberculosis
Antimicrob. Agents Chemother. 38 (4), 805-811 (1994)
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Mycobacterium tuberculosis (strain Rv) DNA.
Mycobacterium tuberculosis
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TEKGTE I I NGTERVVVSQLVRSPGVYEDET I DKSTEKTLHSVK V JESRGAMLEEDVOK
RDTVGVR I DKKRQDVTVLKALGWTSGD I VERRGESELMRSTLEKDNTYGTDEALLD
IYRKLRGEPPTKESAQTLLENLFYKEKRYDLARVGRYKNKLIGLHVGEP I TSSTLT
EEDVVAR I TEYLVRLHEGOTTMTVPGG VEVE PVETDD I DHFGNRRLETVGEL I QNQLRV
MSRMER VVRERWITQDVEA I TPQTL I NI TRVVAAI KEFFGTSQLSGPMQONUPLSGLT
HKRRLSALGPGGLSRERAGLEVRDVHPSHYGRWCP I ETPEGPNIG LIGSLSVYARVNP
FGFIETPYRKVVDGVVSDG I VVLTADEEDHTVVAAN KS JEDFSCHAURAURARVR
FGFIETPYRKVVDGVVSDG I VVLTADEEDHTVVAAN SPI DADGREVEERVLVRSEAP
LVGTGMELRAA I DAATS SSQESGV I EEVSADY I TVMHDNGTRRTY RHRKFARSHRGTC
ANQCPTYDAGGNVEAGQV I ADGCTDDGEMALGK NLLVA I MPWEGHNYEDA I I LSURL
VEEDVLTS I HI EEHE I DARDT KLGAEET IT DI ENI SDEVLADLDERG I VRISRED
DILVGKVTPKGCTELFPBERLLRA I FGEKAREVRDTSLKYPHGESGKVI GI RVESRED
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                                                        /organism="Mycobacterium tuberculosis"
/strain="Rv"
/db_xref="taxon:1773"
1065. .4598
                                                                                                                                                        Location/Qualifiers
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/protein_id="AAA20242.2"
/db_xref="G1:7144499"
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Pred. No. 1.3e-12;
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                                   ACCESSION
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                                                                                                                                                                                                                                                                  GCGGCGTCGAGGTGCCGGTGGAAACCGACGACAT 2173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  169;
                   complete genome.
AE006964 AE000516
                                                                              Mycobacterium tuberculosis CDC1551,
AE006964.1
                                                                                                                        AE006964
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/product="RNA polymerase beta'-subunit"
/protein_id="AaA21417.1"
/db_xref="GI:537608"
/translation="MLDVNFFDELRIGLATAEDIRQWSYGEVKKPETINYRTLKPEKD
GLFCEKIFGPTRDWECYCGKYKRVFKGIICERCGVEVTRAKVERENGHIELAAPVT
HHWYFKOVPSRLGYLLDLAPKDLEKIIYFAAYVITSVDEEMRHNEL"
a 1534 c 1691 g 890 t
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1065. .4598
/gene="rpoB"
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4641. .>5084
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/gene="rpoC"
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/protein_id="AAA21416.1"
/db_xref="GI:468334"
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GI:13880217
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Pred. No. 1.2e-12;
                                                                                                                  19352 bp
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2 (bases 1 to 19352)
Fleischmann,R.D., Alland,D., Eisen,J.A., Carpenter,L., White,O., Peterson,J., DeBoy,R., Dodson,R., Gwinn,M., Haft,D., Hickey,E., Kolonay,J.F., Nelson,W.C., Umayan,L.A., Ermolaeva,M., Salzberg,S.L., Delcher,A., Utterback,T., Weidman,J., Khouri,H., Salzberg,S.L., Delcher,A., Utterback,T., Weidman,J., Khouri,H., Salzberg,S.L., Mikula,A. and Bishai,W.
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Mycobacterium tuberculosis CDC1551
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (25-APR-2001) The Institute for Medical Center Dr. Rockville, MD 20850, US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fleischmann, R.D., Alland, D., Eisen, J.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mycobacterium; Mycobacterium tuberculosis complex.
1 (bases 1 to 19352)
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CANQC PIVDAGGRVEAGQVIADGPCTDDGEMALGKNLLVAINEMEGHNYEDAIILSNR
LVEEDVLTS-HIEEHELDAROTKLGAEEITROIDNISSDEVLADLDERGIVRTIGAEVRD
GDILVGKVTPKGETELTPEERLLRAIFGEKAREVRDTSLKVPHGESGKVIGIRVFSRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HKRRLSALGPGGLSRERAGLEVRDVHPSHYGRMCPIETPEGPNIGLIGSLSVYARVNP
FGFIETPYRKVVDGVVSDEIVYLTADEEDRHVVAQANSPIDADGRFVEPRVLVRRKAG
EVEYYPSSEVDYMDVSPRQMVSVATAMIPFLEHDDANRALMGANMQRQAVPLVRSEAP
                                                                                                                                                           similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEDELPAGVNELVRVYVAQKRKISDGDKLAGRHGNKGVIGKILPVEDMPFLADGTPVD
IILNTHGVPRRMNIGQILETHLGWCAHSGWKVDAAKGVPDWAARLPDELLEAQPNAIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EEDVVATIEYLVRLHEGQTTMTVPGGVEVPVETDDIDHFGNRRLRTVGELIQNQIRVG
MSRMERVVRERMTTODVEAITPQTLINIRPVVAAIKEFFGTSQLSQFMDQNNPLSGLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REPLEVPGLLDVQTDSFEWLIGSPRWRESAAERGDVNPVGGLEEVLYELSPIEDFSGS
MSLSFSDPRFDDVKAPVDECKDKDMTYAAPLFVTAEFINNNTGEIKSQTVFMGDFPMM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="similar to GB:L27989 GB:L05910 GB:U12205 SP:P47766 PID:149992; identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                               LREGEDEDLERAAANLGINLSRNESASVEDLA"
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IYRKLRPGEPPTKESAQTLLENLFFKEKRYDLARVGRYKVNKKLGLHVGEPITSSTLT
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/db_xref="GI:13880218"
/translation="MLEGCILADSRQSKTAASPSPSRPQSSSNNSVPGAPNRVSFAKL
                               /product="DNA-directed RNA polymerase,
/protein_id="AAK44922.1"
                                                                                                                                                                                      /note="similar to
                                                                                                                                                                                                                                                                                                                                                                                           LTIKSDDTVGRVKVYEAIVKGENIPEPGIPESFKVLLKELQSLCLNVEVLSSDGAAIE
                                                                                                                                                                                                                                                                                                                                                                                                                       MKLHHLVDDKIHARSTGPYSMITQQPLGGKAQFGGQRFGEMECWAMQAYGAAYTLQEI
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/strain="CDC1551"
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/db_xref="GI:13880219"
                                                                                             /transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note="clinical strain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:83331"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "MT0695"
                                                                                                                                                                                             SP:P37871;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               d RNA polymerase, beta subunit",1"
                                                                                                                                                                                             identified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Carpenter, L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genomic Research, 9712
                                                          beta-prime subunit"
                                                                                                                                                                                          by sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           White, O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         White, O.,
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gene

ITIVDSGATGNFTQTRTLAGMKGLVTNPKGEFIPRPVKSSFREGLTVLEYFINTHGA
RKGLADTALRTADSGYLJRRLVDVSQDVIVREHDCQTERGIVVELAERAPDGTLJRDP
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GVCATCYGRSMATGKLVDIGEAVGIVAAQSIGEPGTQLTMRTFHQGGVCEDITGGLPR
VQELFEARVPRGKAPIADVTGRVRLEDGERFYKITIVPDDGGEEVYYDKISKRQRLRV complement(7691. .8065) /gene="MT0697" VSIHDKHIEVIVRQMLRRVTIIDSGSTEFLPGSLIDRAEFEAENRRVVAEGGEPAAGR PVLMGITKASLATDSWLSAASFQETTRVLTDAAINCRSDKLNGLKENVIIGKLIPAGT GINRYRNIAVQPTEEARAAAYTIPSYEDQYYSPDFGAATGAAVPLDDYGYSDYR" GVLSVRAKIKVRLTQLRPPVEIEAELFGHSGWQPGDAWMAETTLGRVMFNELLPLGYPFVNKQMHKKVQAAIINDLAERYPMIVVAQTVDKLKDAGFYWATRSGVTVSMADVLVPPRKKEILDHYEERADKVEKQFQRGALNHDERNEALVEIWKEATDEVGQALREHYPDDNP GPGNRPLKSLSDLLKGKQGRFRQNLLGKRVDYSGRSVIVVGPQLKLHQCGLPKLMALE LFKPFVMKRLVDLNHAQNIKSAKRMVERGPQWWDLVLESVIAEHEVLLNHAPTLHRLG IQAEBPMLVEGKAIQLHPLVCEAFNADFDGDQMAVHLPLSAEAQAEARILMLSSNNLI IQAEBPMLVEGKAIQLHPLVCEAFNADFDGDQMAVHLPLSAEAQAEARILMLSSNNLI LEDIWSTFTKLAPKQLIVDENLYRELVDRYGEYFTGAMGAESIQKLIENFDIDAEAES LRDVIRNGKGQKKLRALKRLKVVAAFQQSGNSPMGMVLDAVPVIPPELRPMVQLDGGR FKHEDGSERVLSDGDHVEVGQQLMEGSADPHEVLRVQGPREVQIHLVREVQEVYRAQG HIWYFKGVPSRLGYLLDLAPKDLEKIIYFAAYVITSVDEEMRHNELSTLEAEMAVERK /translation="MLDVNFFDELRIGLATAEDIRQWSYGEVKKPETINYRTLKPEKDGLFCEKIFGPTRDWECYCGKYKRVRFKGIICERCGVEVTRAKVRRERMGHIELAAPVT ${ t FATSDLNDLYRRVINRNNRLKRLIDLGAPEIIVNNEKRMLQESVDALFDNGRRGRPVT}$

complement(7691. .8065) /gene="MT0697" 'note="identified by Glimmer2; putative"

gene

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/db_xref="GI:13880220" /transl_table=11 /codon_start=1

Glimmer2; putative; co authentic frameshift" 'note="This region ote-"This region contains an authentic frame shift and not the result of a sequencing artifact; identified by conserved hypothetical protein, ş

10167

/gene="MT0699" 10167. .10925 /gene="MT0699"

PF01261* 'note-"identified by match ç PFAM protein family HMM

/transl_table=11 /codon_start=1

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LDTCHTWAAGEALTDAVDRIKAITGRIDLVHHNDSRDEAGSGRDRHANLGSGQIDPDL

/gene="MT0700" 10957. .11799 10957.

LVAAVKAAGAPVICETADQGRKDDIAFLRERTGS"

/::ore="similar to GB:U00012 PID:466863; identified sequence similarity; putative" /transl_table=11 /gene="MT0700" codon_start=:

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/product="hydrolase/esterase, putative"
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SYRLYKPYGLPSSAPLVYMLHGGFGSAKQAERSYGWDELADSEKFLVAYPDGYHRAWN
ANGGGCCGRPAREGYDDIGFVRAVVADIANNVSIDPARVYYTGMSNGAIMSYTLACNT

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Matches 169
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                                                                                                                                                                                             61
                 GCGGCGTCGAGGTGCCGGTGGATGTGGACGACAT 214
                                                                                                                                            GGCTGCATGTCGGCGAGCC-----CATCACGTCGTCGACGCTGACCGAAGAAGACGTCG 1177
                                                                                                                                                                                GCCTGGGCGGCACCAATCCGGCTCAGGTGACCACCACCACCCTCACCGAGGAAGACGTCG 120
                                                                                        TCGCCACCATCGAGTACCTGGTGCGCCCTGCACGAGGGCCAGACCACGATGACCGCCCCG 180
GCGGCGTCGAGGTGCCGGGTGGAAACCGACGACAT 1271
                                                                 Similarity
                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="MT0702"
13498. 11/-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /TTANSIATION "MSDTHVYTNQVPPLENYNPASSPVLIEALIQEGGOWGLDEVNEY
OAISASCQAQRWGELADRNRFILHTHDAYGYRVDEVEYDPAYHELMRTAITHGMHAAP
WADDRPGAHVVRAAKTSVWTVEPGHICPISMTYAVVPALRYNSELAAVYEPLLTSREY
DPELKPATTKAGITTAGKSMTEKQGGSDVRAGTTYAVPALRYNSELAAVYEPLLTSREY
DFELKPATTKAGITTAGKSMTEKQGGSDVRAGTTYATPNADGSYSLTCHKWFTSAPMCD
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GEEGRGVPTIIEMVNLTRLDCALGSATSMRTGLTRAVHHAQHRKAFGQAYLDOPLMRN
VLADLAVWBAEAATIVANRMAGATDNAVRGNETEALLRAIGLAKKWYCKRSTAHAAE
ALECLGGNGYVEDSGMPRLYREAPLMGIWEGSGNVSALDTLRAMATRPACVEFUFDEL
ARSAGQDPRLDGHVERLRPQLGDLDTIGYRARKIAEDICLALQGSLLVRHGHPAVAEA
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ELSALVERADLDPGVHYILVSGRGEGFCAGFDLSAYAEGSSSTGGGGAYQGTVLDGKT
QAVNHLPNQPWDPMIDYQMMSREYRGEASLMHADKPTVYKIHGYCVAGGTDIALHADQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="MT0702"
/note="similar to GP:
similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PEPADLDERTERLVARIAALPVNQLIMVKLALNSALLQQGVATSRMYSTVFDGAARHT
PEGHAFVADAVEHGFRDAVRRRDEPFGDYGRQASRV"
                                                                                                                                                                                                                                                                                                                                                                           /product="hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                               /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                             /note="identified by Glimmer2; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="MT0703"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VIAAADAKIGYPPTRVWGVPAAGLWAHRLGDQRAKRLLFTGDCITGAQAAEWGLAVEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="enoyl-CoA hydratase/isomerase family protein"
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/db_xref="GI:13880224"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="acyl-CoA deh
/protein_id="AAK44926.
/db_xref="GI:13880223"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FLATRLGGOWGGAYGTMPAGLDLAPILERALVKG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon_start=:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PID:457174 PID:537028;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /transi_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="similar to SP:P33224 GB:L20915 PID:457172
PID:457174 PID:537028; identified by sequence similarity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="MT0701"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AFWREVNRCGALDTTTEGPVTTSGATCADNRRVVLLTVDDAGHRWPSFATQTLWRFFA
                                                                                                                                                                                                                                                                                                                        60.6%;
79.0%;
                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                  Score 129.6; DB Pred. No. 1e-12;
                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GP:3885480;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          dehydrogenase, putative"
)26.1"
                                                                                                                                                                                                                                                                                                                                    DB 1;
                                                                                                                                                                                                                                                                                                    39,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       identified
                                                                                                                                                                                                                                                                                                                                    Length 19352;
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                                                                                                                                                                                                                                                                                                6;
                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                              1.
                                                                                                                                                                                                                                                                                                                              FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMMENT
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DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JOURNAL
MEDLINE
PUBMED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM
                                                                                                                                                                              gene
                                                                                                                                                                                                                                                                                                            source
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been renumbered from the original cosmid submissions but the old gene designations are in brackets after the new gene numbers. Gene prediction was based on a Hidden Markov Model of TB genes implemented in TBparse (Krogh) supplemented with visual inspection of positional base preference in codons, especially where there is nicrease in the observed/expected third position G + C. CAUTION: In some cases we may not have predicted the correct initiation codon. Where possible we choose an initiation codon binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most upstream initiation codon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (11-JUN-1998) Submitted on behalf of the Mycobacterium tuberculosis sequencing and mapping teams, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CBIO 1SA Unite de Genetique Moleculaire Bacterienne, Institut Pasteur, 28 rue du Docteur Roux, 75724 Paris Cedex 15, France E-mail: parkhill@sanger.ac.uk On Jun 27, 1998 this sequence version replaced gi:2143285.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Details of M. tuberculosis sequencing at the Sanger Centre are available on the World Wide Web.
(URL, http://www.sanger.ac.uk/Projects/M_tuberculosis/) CDS have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cole, S.T., Brosch, R., Parkhill, J., Garnier, T., Churcher, C., Harris, D., Gordon, S.V., Elglmeier, K., Gas, S., Barry III, C.E., Tekala, F., Badcock, K., Basham, D., Brown, D., Chillingworth, T., Connor, R., Davies, R., Devlin, K., Fellwell, T., Gentles, S., Hamlin, N., Holroyd, S., Hornsby, T., Jagels, K., Krogh, A., McLean, J., Moule, S., Murphy, L., Oliver, S., Osborne, J., Quail, M. A., Rajandream, M. A., Rogers, J., Rutter, S., Seeger, K., Skelton, S., Squares, S., Squares, R., Sulston, J.E., Taylor, K., Whitehead, S. and Barrell, B.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    initiation codon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Parkhill, J.
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Nature 393 (6685), 537.544 (1998)
98295987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Deciphering the biology of Mycobacterium tuberculosis from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mycobacterium tuberculosis H37Rv.
Mycobacterium tuberculosis H37Rv
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mycobacterium; Mycobacterium tuberculosis complex.

1 (bases 1 to 19770)
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                                                                                                                                                                          /note-"Rv0654, (MTCI376.22), len: 501. unknown, FASTA score: Q53353 LIGNOSTILBENE ALPHA, BETA-DIOXYGENASE (485 aa) opt:280 z-score: 330.1 E(): 2.3e-11, (28.5% identity in 523 aaoverlap). Also similar to M. tuberculosis protein MTCY2IC12.07c (29.5% identity in 522 aa overlap).
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                                                                                                                                                          codon_start-1
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/clone="1376"
                                                                                                                                                                                                                                                                                                                                                                                                 /gene="Rv0654"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="Rv0654"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /strain="H37Rv"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note="agga, possible rbs upstream of Rv0654"
8. .1573
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gene

CDS

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misc_feature
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2074. . 2118
/gene-"Rv0655"
/note-"PS00211 ABC transporters family signatu
complement(3052. .3435)
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complement(3052. .3435)
/gene-"Rv0656c"
/note-"Rv0656c, (MTC1376.20, unknown), len: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="Rv0655"
1585..2664
/gene="Rv0655"
                                                                                                                                                             /note-"RV0657c, (MTC1376.19),unknown, len: 51 aa; similar /note-"Rv0657c, (MTC1376.19),unknown, len: 51 aa; similar to several other M. tuberculosis hypothetical proteins eg. Yw08, MYCTU 010848 hypothetical 8.9 kd protein CY39.08c (80 aa), fasta scores; opt: 107 z-score: 182.3 E(): 0.0038, 45.8% identity in 48 aa overlap. Also similar to MTCY48_5 andAL020958|SC4H8_7 Streptomyces coelicolor cosmid 4H8 (66 aa), 41.0% identity in 39 aa overlap."
                                                                                                                                                                                                                                                                                                                                                                                                                     complement(3530...3685)
/gene="Rv0657c"
complement(3530...3685)
/gene="Rv0657c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="hypothetical protein Rv0656c"
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DDADYELAERHLEDIRVRRVYSADD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="hypothetical protein Rv0655"
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PGEISGGMRKARGLARALVLDPQIILCDEPDSGLDPVRTAVLSQLIMDINAQIDATIL
IVTHNINIARTVPDNMGMLFRKHLVMFGPREVLLTSDEPVVRGFLNGRRIGPIGMSEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="mttaqaaesqupylegflapysteytatdlpytgripehldgry 
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RPHPRTGIIEGGPNTNVLTHAGRTLALVEAGVVNYELTDELDTYG PCDFDGTLHGGYT 
AHPQRDPHTGELHAVSY SFARGHRQYSVIGTDGHARRYDIEVAGSPWHMSFSLTDN 
YVVIYDLPYTFDPMQVVPASVPRWLQRPARLVIQSVLGRVRIPDPIAALGNRMGGHSD 
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1762. .1785
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                              u protein Rv0657c"
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CDS gene

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181 GCGGCGTCGAGGTGCCGGTGGATGTGGACGACAT 214
                                                                                                                                                                                    61 GCCTGGGCGGCACCAATCCGGCTCAGGTGACCACCACCACCCTCACCGAGGAAGACGTCG
                                                                                                                                                                                                                                                    1 TCAAGGAGAAGCGCTACGATCTGGCCCGCGGTGGGTCGGTACAAGGTGAACAAGAAGCTGG
                                                              TCGCCACCATCGAGTACCTGGTGCGCCTGCACGAGGGGCCAGACCACGATGACCGCCCCCG
                                                                                                                                            GGCTGCATGTCGGCGAGCC-----CATCACGTCGTCGACGCTGACCGAAGAAGACGTCG
                                                                                                                                                                                                                              TCAAGGAGAAGCGCTACGACCTGGCCCGCGTCGGTCGCTATAAGGTCAACAAGAAGCTCG
                                                                                                                                                                                                                                                                                                                           169;
                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(4480. 4483)
/note-"possible RBS upstream of Rv0658c"
complement(4753. 5061)
/gene-"Rv0659c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IPASLYYTAIVGPEANSAVVRIFGGVRASWPWALVVFLVVVFVAPLCEEIIYRGLLWG
AVDRRWGRWAALVVTTVVFALAHLEFARAPLLVVVAIPIALARFYSGGLLASIVTHOV
TNLLPGIVLLLGLTGAISLP
                                                                                                                                                                                                                                                                                                                                                                                                                         /note-"Rv0660c, (MTC1376.16), len:
|AF016485_130 Halobacterium sp; NRC
32.4%ldentity in 74 aa overlap"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="SPTREMBL:006780"
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LVSELELTAVENRVPSDCVVNFDNIHTLPRTAFRRRITRLSPARLHEACQTLRASTGC
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/gene="Rv0659c"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(5048. .5293)
/gene="Rv0660c"
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complement(3761. .4477)
                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="SPTREMBL:006782"
                                                                                                                                                                                                                                                                                                                                         60.68;
79.08;
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                                                                                                                                                                                                                                                                                                                   Score 129.6; DB Pred. No. 1e-12; O; Mismatches
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NRC-1 plasm (100 aa),
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Db 10932 GCGGCGTCGAGGTGCCGGTGGAAACCGACGACAT 10965

Scarch completed: November 13, 2002, 01:27:35 Job time: 679.07 secs

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                    Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Perfect score:
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   EST:*
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Gapop 10.0 , Gapext 1.0
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208
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em_htc: *
gb_est1: *
gb_est2: *
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em_gss_inv:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

6	5	C 4	c 3	2	c 1	No.	Result
43.4	44.2	44.2	4.5	50.2	174.4	Score	
20.9	21.3	21.3	21.6	24.1	83.8	Match Length DB ID	Query
370	562	٠ د د	877	568	1282	Length	
10		5 :	17	13	9	DB.	
BE227740	BQ752716	RE415602	A0687771	B1995346	AI770311	Length DB ID	
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19.4				20.9 20.9 20.5 20.5 20.3 20.3 20.3 20.1
564 566 567	0.000000000000000000000000000000000000	360 421 501 509 516	96 455 449 573 700	391 496 550 925 495 638 1072 453 468 400 876
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ALIGNMENTS

FEATURES Source	COMMENT		JOURNAL &	TITLE	AUTHORS 1	REFERENCE		ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	LOCUS	RESULT 1 AI770311/c
Mycobacterium Laboratory Institute of Molecular and Cell Biology 30 Medical Drive, Singapore 117609, Republic of Singapore Tel: 65 874 3011 Fax: 65 779 1117 Email: mcbbom@incb.nus.edu.sg Insert Length: 1282	Contact: Murugasu-Oei, B.	20092472	anaerobic stationary-phase Mycobacterium smegmatis	Upregulation of stress response genes and ABC transporters in	<pre>furugasu-Oei,B., Tay,A. and Dick,T.</pre>	Corynebacterineae; Mycobacteriaceae; Mycobacterium. 1 (bases 1 to 1282)	Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;	Mycobacterium smegmatis	Mycobacterium smegmatis.	SST.	A1770311.1 GI:6742680	smegmatis cDNA, mRNA sequence. AI770311	ionary phase library	AI770311 1282 bp mRNA linear FST 24-TAN-2000	

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DEFINITION
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCGAGGTTCCCGTCGAGGTCGACGACAT 29
                                                                                                             Contact: Charles Hauser
DCMB Box 91000
Duke University
Durham, NC 27708-1000
                                                                                                                                                                                                                                              l (bases 1 to 568)
Grossman,A., Chang,C.-W., Davies,J., Harris,E., Hauser,C.,
.P., McDermott,J.P., Shrager,J., Silflow,C. and Stern,D.
Analyses of the Chlamydomonas reinhardtii Genome: A Model,
Unicellular System for Analyzing Gene Function and Regulati
                                                                                                                                                                                                                                                                                                                                                                              Chlamydomonas reinhardtii Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             blyb346 pmRNA linear EST 25-OCT-2001 1031026E07.y2 C. reinhardtii CC-1690, Stress II (normalized), Lambda Zap II Chlamydomonas reinhardtii cDNA, mRNA sequence. BI99546
                                                                                                                                                                                                            Vascular Plants. Project:
Unpublished (2001)
                                                Email: chauser@duke.edu
                                                                                                                                                                                                                                                                                                                                                                     Chlamydomonadaceae; Chlamydomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                         Chlamydomonas reinhardtii.
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                                                                    919 613 8159
919 613 8177
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DNase I was heat-inactivated at 75cC for 5 min. and removed by using RNeasy columns followed by phenol extraction and ethanol precipitation. The RNA preparations were confirmed to be free of genomic DNA contamination by carrying out PCR and RT-PCR using the Access kit (Promega) and primers specific for the histone-like protein gene hip (Lee et al., 1998). cDNA as synthesized using random hexamer primers (Promega) and Stratagene's cDNA synthesis kit. cDNA fragments were ligated into lambda ZAP II vector and packaged in vitro using Stratagene reagents. "
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Location/Qualifiers
1. .568
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395 c 405 g 252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Mycobacterium smegmatis"
/strain="mc2155"
/db_xref="taxon:1772"
/clone_lib="Mycobacterium anaerobic stationary phase
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Pred. No. 1.1e
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ches 21;
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KEYWORDS SOURCE ACCESSION VERSION

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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CGAGGTCCCGGTCGAGGTGGACGACAT 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CATCGAGTACCTGGTGCGCCTGCACGAGGGCCAGACCACGATGACCGTCCCCGGCGGCGT 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             109;
                                                                                                                                                              Contact: Wing RA
Clemson University Genomics Institute
Clemson University
                  High quality sequence stop: 85
                                       Email: rwing@clemson.edu
Seq primer: TAATACGACTCACTATAGGG
Class: BAC ends
                                                                                                           Tel: 864 656 7288 Fax: 864 656 4293
                                                                                                                                                                                                                                        A BAC End Sequencing Framework to Sequence the Unpublished (1998)
                                                                                                                                                                                                                                                                                 Wing, R.A. and Dean, R.A.
                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoldeae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                           Oryza sativa.
Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nbxb0075L01f CUGI Rice BAC Library Oryza sativa genomic clone
                                                                                                                                                     100 Jordan Hall,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             AQ687771.1 GI:5328939
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         //note="Vector: pBluescript II SK-; Site_1: EcoRI; Site_2: XhoI; Stress condition II library, constructed by John Davies and Jeffrey McDermott, combines cDNAs from CC-1690 cells grown to mid-log phase in TAP (NH4+ containing) and shifted to TAP - NO3- (24hrs); H2 production conditions (0, 12hr, 24hr) see Melis et al., (2000) Plant Phys. 122: 127-135; TAP + H2O2 (1, 12, 24 hr); TAP + Sorbitol (1, 2, 6, 24 hr); TAP + Cd (1, 2, 6, 24 hr). PolyA mRNA was purified from each sample, pooled and cDNA synthesized. The cDNA was directionally cloned into lambda ZaP II (Stratagene) in the EcoRI (5') and XhoRI (3') sites. pBluescript II SK- plasmids were excised from the lambda ZAP clones by superinfection with ExAssist (Stratagene) phage. The library was normalized using method 4 described in Bonaldo et al., (1996) Genome Research 6: 791-806."
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Chlamydomonas reinhardtii"
/strain="CC-1690 wild type mt+ 21gr"
/db_xref="taxon:3055"
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), Lambda Zap II"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29 CGTGGGCCGCTACAAGGTCAACAAGAAGCTGGGCCTGAACGCCGGCCCAGCCGATCACGTC 88
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                                                              Anderson,O.A., Appéls,R., Bailey,P., Blake,T., Close,T., Cloutier, S., Dubcovsky,J., Feuillet,C., Gale,M., Graner,A., Gustafson,P., Herrmann,R.G., Holton,T., Jacquemin,J.M., Jia,J., Joudrier,P., Langridge,P., Lazo,G.R., Lin,J.J., McGulre,P., Ogihara,Y., Pecchioni,N., Qualset,C., Schuch,W., Selvaraj,G., Shariflou,M., Sorrells,M., Warburton,M. and Wenzel,G. International Triticeae EST Cooperative (ITEC): Production of Expressed Sequence Tags for Species of the Triticeae
                         Expressed Sequence Tags Unpublished (2000) Contact: Warburton M
                                                                                                                                                                                                                                                                                                             Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
Triticeae; Triticum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BE415602 354 bp mRNA linear EST 24-JUL-
MWL036.B05000414 ITEC MWL Wheat Root Library Triticum aestivum
Clone MWL036.B05, mRNA sequence.
Applied Biotechnology Center, CIMMYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EST
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//note="Vector: pBeloBACII; Site_1: HindIII; Site_2:
HindIII; Rice is one of two most popular grains in the
world, Half of the world population especially those
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="nbxb0075L01f"
/clone_lib="CUGI Rice BAC Library"
/tissue_type="Leaf"
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/strain="Japonica"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /cultivar "Nipponbare"
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53.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGGGCTGGAAGACGAGCTACATCGTCATCCTCGCCACGCTCGCCGGGGGTCGCGCTCGTCC 186
                                                                                                                               Email: oandersn@pw.usda.gov
Sequences have been trimmed to rem
quality sequence with phred score
                                                                                                                                                                                                                 Unpublished (2002)
Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center 800 Buchanan Street, Albany, CA 94710, USA
Tel: 510595773
                                                                                                                                                                                                                                                                                                                           Anderson,O.D., Akhunov,E., Chao,S., Crossman,C., Deal,K., Dvorak, Lazo,G.R., Pham,J., Rausch,C.J., Wilson,C. and Woo,J.
The structure and function of the expressed portion of the wheat genomes: Salt-stressed root cDNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BQ752716 562 bp mRNA linear EST 23-JUL-2002 WHE4118_C11_E228S Wheat salt-stressed root cDNA library Triticum aestivum cDNA clone WHE4118_C11_E22, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; Pooidea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Triticum aestivum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: mwarburton@cgnet.com
International Triticeae EST Cooperative (ITEC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fax: 52-5-7267558/59
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Tel: 52-5-7269091 ext 1381
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/cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="WHE4118_C11_E22"
                                                         /organism="Triticum aestivum'
                                                                                                Location/Qualifiers
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/db_xref="taxon:4565"
/clone="MFL05.B05"
/clone="MFL05.B05"
/clone="MFL05.TIEC MML Wheat Root Library"
/tissue_type="root"
/dev_stage="8 day old"
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91 c
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insert size."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Triticum aestivum"
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Pred. No. 3
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/clone_lib="Wheat salt-stressed root cDNA library"

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RESULT 6
BE227740
LOCUS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Grossman,A., Davies,J., Federspiel,N., Harris,E., Lefebvre,P., McDermott,J.P., Sifflow,C., Stern,D. and Surzycki,R. Analyses of the Chlamydomonas reinhardtii Genome: A Model, Unicellular System for Analyzing Gene Function and Regulation in Vascular Plants; project phase 2 Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chlamydomonas reinhardtii.
Chlamydomonas reinhardtii
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BE227740 370 bp mRNA linear EST 894034G12.yl C. reinhardtii CC-1690, normalized, Lambda Chlamydomonas reinhardtii cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                 Duke University
Durham, NC 27708-1000, USA
Tel: 919 613 8164
Fax: 919 613 8177
                                                                                                                                                                                                                                                                                                                                                                                              Contact: Elizabeth H. Harris DCMB Box 91000
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//dev_stage="Full tillering"
//deb_host="E. coli SOLR"
//note="Vector: Lambda Uni-ZAP XR, excised phagemid
/note="Vector: Lambda Uni-ZAP XR, excised phagemid
pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI; Hydroponic
plants grown to full tillering stage were treated with 150
mM NaCl for either 12 hours or 7 days. Root tissues of the
plants subjected to both types of treatment were collected
separately at University of California, Davis (E. Akhunov
and K. Deal in J. Dvorak's Lab). Total RNA was prepared
separately from the two samples (12h and 7day treatments),
and equal amount of RNA was then pooled PolyA RNA was
purified from the pooled RNA, a cDNA library was made, and
the cDNA clones were in vivo excised to give pBluescript
SK(-) phagemids in J. Dvorak's lab (E. Akhunov, J. Dvorak)
at the University of California, Davis. Colony plating,
plasmid DNA preparations and DNA sequencing were performed
in the OD Anderson lab (all other authors)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92
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                                                                                                                                                                                                                     chlamy@duke.edu.
Location/Qualifiers
                                                                          /organism="Chlamydomonas reinhardtii"
/strain="CC-1690 wild type mt+ 21gr"
/db_xref="faxon:3055"
/clone_lib="C. reinhardtii CC-1690, normalized, Lambda Zap
XhoI; This library, constructed
                          /note="Vector: pBluescript II SK-; Site_1: EcoRI; Site_
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by John Davies and Jeffrey
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        173 CGAGCCCGCGCGCGCAGCGCATCACCGACAAGATCTTTGGCGAGACCTCCAAGGTGGCCAC 232
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B0767689
B0767689.1 GI:21976163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hedley,P., Liu,H., Caldwell,D., McCallum,N., Mudie,S., Cardle,L., Ramsay,L., Machray,G., Marshall,D.F.M. and Waugh,R. Development of Barley Transcriptome Resources
                                                                                                                                                                                                                                                                                                                         Invergowrie, Dundee, DD2 5DA,
Tel: 00 44 1382 562731
Fax: 00 44 1382 562426
                                                                                                                                                                                                                                                                                                                                                                                            Genome Dynamics/Computational Biology Scottish Crop Research Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae; Triticeae; Hordeum.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Waugh R, Marshall DF
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (2001)
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                                                                                                                                                                                                                                                                                                      est@scri.sari.ac.uk.
                                                                                                                     /clone_lib="root, 3
EBro08"
                                                                                                                                                                                        /cultivar="Optic"
/db_xref="taxon:4513"
/note="Vector: pSPORT1; Site_1: Sal I; Site_2: Not I;
Non-normalised library, directionally cloned into pSPORT1
                                                  /dev_stage="3 wee|
/lab_host="DH10B"
                                                                                             /tissue_type="root"
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Pred. No. 4.8;
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Tel: 919 613 8159
Fax: 919 613 8177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Charles Hauser
DCMB Box 91000
Duke University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vascular Plants; p
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BE724777 496 bp mRNA linear EST 894078F06.yl C. reinhardtii CC-1690, normalized, Lambda Chlamydomonas reinhardtii cDNA, mRNA sequence.
BE724777
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                                                                                                                                                                                                                                                                                                                                                                                                                         chauser@duke.edu
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                mid-log phase in TAP (acetate containing) medium in the light, TAP medium in the dark, HS (minimal) medium in ambient levels of CO2 and HS medium bubbled with 5% CO2 POLYA mRNA was purified from each sample, pooled and cDNA synthesized. The cDNA was directionally cloned into lambda ZAP II (Stratagene) in the EcoRI (5') and XhoI (3') sites. PBluescript II SK plasmids were excised from the lambda ZAP clones by superinfection with ExAssist (Stratagene)
                                                                                                                                                                                              XhoI; This library, constructed by John Davies and Je McDermott, combines cDNAs from CC-1690 cells grown to
                                                                                                                                                                                                                                                                                                        /organism="Chlamydomonas reinhardtii"
/strain="CC-1690 wild type mt+ 21gr"
/db_xref="taxon:3055"
                                                                                                                                                                                                                                                                   /clone_lib="C.
II"
                                                                                                                                                                                                                                   /note="Vector: pBluescript II SK-; Site_1: EcoRI; Site_2:
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Pred. No. 4.8;
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                                                                                                                                                                                                                                                                                                                                                                                             Genome Dynamics/Computational Biology Scottish Crop Research Institute Invergowrie, Dundee, DD2 5DA, Scotlandel: 00 44 1382 562731

Fax: 00 44 1382 562426
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BQ767542.1
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Waugh R, Marshall DF
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                                                                                                                                                                                                                                                                                                                                                                          est@scri.sari.ac.uk
    /note="Vector: pSPORT1; Site_1: Sal I; Site_2: Not I; Non-normalised library, directionally cloned into pSPORT1. Derived from roots of 3 week old drought stressed barley plants. Developed as part of the barley transcriptome resources of BBSRC/SERRAD funded cereal IGF (Investigating Gene Function) project."

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EBro08"
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/dev_stage="3 week"
/lab_host="DH10B"
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/clone_lib="root, 3 week, drought-stressed,
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/cultivar="Optic"
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159 c 164 g 80 t 1 others
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Pred. No. 4.9;
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Query Match Best Local Similarity 54.(Matches 87; Conservative

20.5%;

Score 42.6; D: Pred. No. 7.4; 0; Mismatches

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                                                                                                                                                                 2 CAAGGAGAAGCGCTACGACCTGGCCCGCGTGGGCCGCTACAAGGTCAACAAGAAGCTGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Adron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial Ecognic strain y2; cn bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be Location/Qualifiers
                                                       CCTGAACGCCGGCCAGCCGATCACGTCGTCGACTCTGACCGAGGAAGACGTCGTCGCCAC 121
                                                                                                                             TCGAGGCCATCACCTGGGCCATCGTCCTGCGCCGGCGCAAG
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29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (02-JUN-1999) Genoscope · Centre BP 191 91006 EVRY Cedex · FRANCE (E-mail :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanoĝaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                      /clone="BACR19D16"
/clone_lib="RPCI-98"
/note="end : TET3"
a 61 c 61 g
                                                                                                                                                                                                                                                                                                                                                                                  /organism≃"Drosophila melanogaster"
/db_xref="taxon:7227"
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Pred. No. 7.7;
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segref@genoscope.cns.fr
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272 GAGGAAGA 279
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                                                                 CGCCTGCACGAGGCCCAGACGATGACCGTCCCCGGCGGCGGCGTCGAGGTCCCGGTCGAG 197
                                                 CCGATCACGTCGTCGACCTCTGACCGAGGAAGAACGTCGTCGCCCACCATCGACTACCTGGTG
                                                                                                                                                                        GACCTGGCCCGCGTGGGCCGCTACAAGGTCAACAAGAAGCTGGGCCTGAACGCCGGCCAG
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC

clade; Panicoldeae; Andropogoneae; Sorghum.

1 (bases 1 to 495)

Cordonnier-Pratt, M.-M., Gingle, A., Marsala, C., Sudman, M. and Pratt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: mmpratt@uga.edu
Sequences have been trimmed to exclude PolyA, vector and regions
below Phred quality 16. The threshold for highest quality sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
                                                                                                                                                                                                                                           Similarity 51.6
97; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POLYA-No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seq primer: JEN REV
High quality sequen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     An EST database from Sorghum: water-stressed Unpublished (2000)
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BE592949
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WS1_92_D09.b1_A002 Water-stressed 1 (WS1) Sorghum bicolor cDNA,
                                                                                                                                                                                                                                                                                                                           70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     quality sequence stop:
                                                                                                                                                                                                                                                                                                       /organism="Sorghum bicolor"
/db_xref="taxon:4558"
/clone_lib="Nater-stressed 1 (WS1)"
/clone_lib="Nater-stressed 1 (WS1)"
/note="Organ: Mix of 5-week old plants on days 7 & 8 after water was withheld: Vector: Lambda Zap: Site_1: xhoI:
Site_2: EcoRI; The library was made from poly-A RNA in the cloning vector lambda Zap II. Clones to be sequenced were prepared by mass excision."

189 c 153 g 82 t 1 others
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1. .495
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Pred. No. 8.1;
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Matches 104; Conserv
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: rwing@clemson.edu
Total hq bases = 326
Seq primer: AATTAACCCTCACTAAAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clemson University
100 Jordan Hall, Clemson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wing, R., Close, T.J., Kleinhofs, A., Wise, R., Kannangara, G., von Wetstein, D., Akhunov, E., Chin, A., Choi, D.W., Fenton, R.D., Kianian, P., Otto, C., Simons, K., Zhang, D., Begum, D., Frisch, D., Yu, Y., Henry, D., Palmer, M., Rambo, T., Simmons, J., Oates, R. and Main, D. Development of a genetically and physically anchored EST resource for barley genomics: Morex testa/pericarp cDNA library Unpublished (2001)
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638 bp mRNA linear EST 23-OCT-2001
HVSMEK0007M21f Hordeum vulgare testa/pericarp EST library
HVcDNA0013 (normal) Hordeum vulgare cDNA clone HVSMEk0007M21f, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 864 656 7288
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Wing RA
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              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note-"vector: lambdaZAP; Site_1: EcoR1; Site_2: Xhol; plants were raised from seeds in a Controlled Environments growth chamber maintained in continuous light at 18oC, and testa and pericarp were dissected from developing kernels at Washington State University, Pullman, WA (Kannangara, von Wetstein). Total RNA was prepared, poly(A) RNA was purified, one cDNA library was made, and 1 million pfu were in vivo excised to give pBluescript SK(-) cDNA phagemids in the TJ Close lab at the University of California, Riverside (Akhunov, Chin, Choi, Close, Fenton, Kianian, Otto, Simons, Zhang). Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI)
                                                                                                                                          Genetically and physically anchored EST resources for
barley genomics. Barley Genetics Newsletter 31:29-30.
(http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"
241 c 196 g 94 t
                                                                                                                                                                                                                                                                                                                                (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or above. For more details on library preparation and sequence analysis see
                                                                                                                                                                                                                                                                           http://www.genome.clemson.edu/projects/barley. To order this clone see http://www.genome.clemson.edu/orders Also
                                                                                                                                                                                                                                                      see Close TJ, Wing R, Kleinhofs A, Wise R (2001)
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/lab_host="TJC121"
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/db_xref="taxon:4513"
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                                                              CTGCTGGCGACGGCTCTGGCGCTGCCCGCCGACGGCAAGGTCATCGCATTCGACGTGAGC
                                                                                       ATCACGTCGTCGACTCTGACCGAGGAAGACGTCGTCGCCACCATCGAGTACCTGGTGGCG 140
                                                                                                                               CTGATCAAGCTGAGCGGCGCGCGGCGGACGCTGGAGGTGGGCGTGTTCACGGGCTACTCG
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                                                                                                                                                                                                            95;
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                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Zea mays"
/db_xref="MaizeDB:637686"
/db_xref="taxon:4577"
/db_xref="taxon:4577"
/clone="PCO131734"
/clone="lib="Maize Mapping Project/DuPont Cornsensus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This clone is available through: ResGen, Invitrogen Corp. South Memorial Parkway Huntsville, AL 35801 For further in call: (800)-533-4363 or contact via email: ccu@resgen.com High quality sequence stop: 180.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
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Contact: Shoemaker R/Public Soybean EST Project
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//db_xref="taxon:3847"
/clone="cenoME YSTEMS CLONE ID: Gm-c1032-3450"
/clone_lib="Gm-c1032"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="Cotyledons of 8-day-old 'Williams'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               161 GATGACCGTCCCCGGCGGCGTCGAGGTCCGAGGTCGAGGTGGACGAC 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        282 CGACAACGACGGCGTCGTCACGCGCCCAGGACCTCGAGGCCCTCCTCACGTGCCTTGCCGC 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     101 CGAGGAAGACGTCGTCGCCACCATCGAGTACCTGGTGCGCCTGCACGAGGGCCAGACCAC 160
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                                                                                                                                                                                                                                                                                                                                                                                                              Email: mmpratt@uga.edu
Sequences have been trimmed to exclude PolyA, vector, and regions
below Phred quality 16. The threshold for highest quality sequence
is 20. Three-prime sequences, which are obtained with PolyTMix or
T7 sequencing primer, are presented as the reverse complement.
Seq primer: JEN REV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant
Plant Sciences Building, Rm. 2502, Athens, GA 3
Tel: 706 542 1860
Fax: 706 583 0210
                                                                                                                                                                                                                                                                                                                                                                                  High quality sequence stop: 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Lillopsida; Poales; Poaceae; PACC clade; Panicoldeae; Andropogoneae; Sorghum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sudman,M. and Pratt,L.H.

An EST database from Sorghum: plants infected with a compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cordonnier-Pratt, M.-M., Gingle, A., Fang, G.C., Dean, R., Wing, R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sorghum bicolor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         bicolor cDNA, mRNA sequence.
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Colletotrichum graminicola"

(notes Vector: pBluescript II SK(-) from Lambda Zap II;

Site_1: XhoI; Site_2: EcoRI; Four-week-old sorghum

seedlings were sprayed with spore suspension prepared from

3-week-old FRM42I, a sorghum isolate of the anthracnose

pathogen Colletotrichum graminicola. Inoculated plants

were kept in a 25 C dark growth chamber with 100% relative
                                                                                                                                                                                             /db_xref="taxon:4558"
/clone_lib="Pathogen-infected compatible 1 (PIC1)"
/tissue_type="Leaves"
                                                                                                                                                               /dev_stage="4-week-old seedlings infected with
                                                                                                                                                                                                                                                                       /organism="Sorghum bicolor"
/cultivar="BTx623"
                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fractionation column. The column eluent was then precipitated, redissolved, and ligated into Stratagene's pBluescript II XR predigested vector (pBluescript II SK(+) vector that has been digested with EcoRI and XhoI, and phosphorylated by Stratagene). 100% of the white and 87.5% of the blue colonies appear to contain recombinant plasmids with cDNA inserts, based on size (n=28 and 8 respectively). This library was constructed by Dr. Paul Keim and Dr. Virginia Coryell."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GI:18065216
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Pred. No. 9.
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GA 30602-7271,
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Search completed: November 13, 2002, 04:00:27 Job time: 1122.63 secs
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ORIGIN
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                                                                                        342 ACGGCA 347
                                                                                                                                   202 ACGACA 207
                                                                                                                                                               282 AGCGTGGGTTCGAGTCCATCATCCACGCCATCGGCAGCTCCTACCTCTCCCACCGACGCCA 341
                                                                                                                                                                                            142 TGCACGAGGGCCAGACCACGATGACCGTCCCGCGCGGCGCGCTCGAGGTCCCGGTCGAGGTGG 201
                                                                                                                                                                                                                                                     22 TGGCCCGCGTGGGCCGTACAAGGTCAACAAGAAGCTGGGCCTGAACGCCGGCCAGCCGA 81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              humidity for 24 hr, followed by 12/12 hr of light/dark cycle at 25 C with 90% relative humidity for another 24 hr. All leaves were harvested and quick frozen with liquid nitrogen and stored in a -80 C freezer. The library was made from poly-A RNA in the cloning vector lambda ZAP II. Clones to be sequenced were prepared by mass excision. WARNING: While most or all ESTs are expected to derive from the host plant, no effort was made to eliminate ESTs deriving from the pathogen."
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Result
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Perfect score:
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Sequence 7771, Ap
Sequence 7717, Ap
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16.5	16.6	16.6	16.6	16.7	16.7	16.7	16.8	16.8	16.9	16.9	17.0	17.0	17.0	17.0	17.0	17.0	17.0	17.1	17.1	17.1	17.3	17.4	17.5	17.5	17.5
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Sequence 2873, Ap		107,	1000	7025,	7000	Sequence 32324 A		Sequence J, Appli	Sequence 4000, Ap	sequence 1024, Ap	Todaciice I, April	Sequence 1, Appli	Sequence 1 Appli	Sequence 1, appli		٠,		rddence or whole	Seguence 1232, Ap			7,	ocquence 1/, Appl	30	3 7 0 0

ALIGNMENTS

US-09-984-711-5

GENERAL INFORMATION:

Sequence 5, Application US/09984711 Patent No. US20020119549A1

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FEATURE:

NAME/KEY: CDS

LOCATION: (702)..(4196)

OTHER INFORMATION:

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                                                                                                                                                                                                                                                                           SEQ ID NO 5
LENGTH: 5096
TYPE: DNA
ORGANISM: Corynebacterium glutamicum
                                                                                                                                     Query Match 42.3%;
Best Local Similarity 68.5%;
Matches 137; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: MOECKEL, Bettina
APPLICANT: STEPHAN, Hans
APPLICANT: STEPHAN, Hans
APPLICANT: KEUTZER, Caroline
APPLICANT: HERNANN, Thomas
APPLICANT: HERNANN, Thomas
APPLICANT: BINDER, Michael
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE TPSL GENE
FILE REFERENCE: 204209USO
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CURRENT FILING DATE: 2001-10-31
PRIOR APPLICATION NUMBER: DE10108230.9
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin version 3.1
Score 88; DB 10; Length 5096;
Pred. No. 8.4e-14;
0; Mismatches 60; Indels
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CURRENT APPLICATION NUMBER: US/10/075,460
: CURRENT FILING DATE: 2002-02-15
: PRIOR APPLICATION NUMBER: DE 10107230.9
: PRIOR FILING DATE: 2001-02-16
: PRIOR APPLICATION NUMBER: DE 10162386.0
: PRIOR FILING DATE: 2001-12-19
: NUMBER OF SEQ ID NOS: 14
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 5
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Patent No. US20020119537A1
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APPLICANT: PFEFFERLE, Walter
APPLICANT: BINDER, Michael
TITLE OF INVENTION: NUCLEOTIDE SEEQUENCES WHICH CODE FOR THE rpob GENE
                                 APPLICANT: MOECKEL, Bettina APPLICANT: BATHE, Brigitte APPLICANT: HERMANN, Thomas APPLICANT: PREFFERLE, Walte APPLICANT: BINDER, Michael
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Best Local :
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APPLICANT: HANS, STEFAN
APPLICANT: HANS, STEFAN
APPLICANT: HERMANN, THOMAS
APPLICANT: HERMANN, THOMAS
APPLICANT: PFEFFERLE, WALTER
APPLICANT: BINDER, MICHAEL
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE TPSL GENE
FILE REFERENCE: 218472USOX
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LOCATION: (702)..(4196)
OTHER INFORMATION:
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ORGANISM: Corynebacterium glutamicum
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                                                                                                                                                                                                                                                                                                                                  1695
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Pred. No. 8.4e-14;
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; LOCATION: (702)..(4196)
US-09-887-052-3
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US-09-887-052-3
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CURRENT FILING DATE: 2001-06-25
PRIOR APPLICATION NUMBER: DE10107229.5
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin version 3.0
SEQ ID NO 1
SEQ ID NO 1
LENGTH: 5099
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; LOCATION: (702)..(4196)
US-09-887-052-1
                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 8

SOFTWARE: PatentIn version 3.0

SEQ ID NO 3

LENGTH: 5099

TYPE: DNA

ORGANISM: Corynebacterium glutamicum
FEATURE:
                                                                                               Query Match
Best Local Similarity
                                                                                     Matches
                                                                                                                                                                                                                                                                                                     APPLICANT: MACKEL, Bettina
APPLICANT: MATHE, Brigitte
APPLICANT: HERMANN, Thomas
APPLICANT: PEEFERLE, Walter
APPLICANT: BINDER, Michael
TITLE OF INVENTION: NUCLEOTIDE SEEQUENCES WHICH CODE FOR THE rPOB GENE
FILE REFERENCE: 204212USOX
CURRENT APPLICATION NUMBER: US/09/887,052
CURRENT APPLICATION NUMBER: US/09/887,052
PRIOR APPLICATION NUMBER: DE101107229.5
PRIOR FILING DATE: 2001-06-25
PRIOR FILING DATE: 2001-02-16
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Best Local :
1578 AAGCGCTACGACCTGGCCTCGCGTTGGTCGTTACAAGATCAACCGCAAGCTCGGCCTTGGT 1637
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                      9 AAGCGCTACGACCTGGCCCGCGTGGGCCGCTACAAGGTCAACAAGAACCTGGGCCTGAAC 68
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5. US20020119537A1
                                                                                Conservative
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                                                                     Score 88; DB 10; I
Pred. No. 8.4e-14;
0; Mismatches 60;
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Pred. No. 8.4e-14;
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GCCGGCCAGCCGATCACGTCGTCGACTCTGACCGAGGAAGACGTCGTCGCCACCATCGAG 128

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US-09-452-239-5
; Sequence 5, Application US/09452239
; Patent No. US20020081693A1
; GENERAL INFORMATION:
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TITLE OF INVENTION: NUCLEOTIDE SEEQUENCES WHICH CODE FOR THE rPOB GENE
FILE REFERENCE: 2042120S0X
CURRENT APPLICATION NUMBER: US/09/887,052
CURRENT FILING DATE: 2001-06-25
PRIOR APPLICATION NUMBER: DEIO107229.5
PRIOR APPLICATION NUMBER: DEIO107229.5
NUMBER OF SEO ID NOS: 8
SOFTWARE: Patentin version 3.0
SEO ID NO 5
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APPLICANT: Rafalski, Antoni J.
APPLICANT: Rafer, Gary M.
APPLICANT: Cabboon, Rebecca E.
TITLE OF INVENTION: Plant Caffeoyl-CoA O-Methyltransferase
FILE REFERENCE: BB1284 US NA
CURRENT APPLICATION NUMBER: US/09/452,239
CURRENT FILING DATE: 1999-12-01
EARLIER APPLICATION NUMBER: 60/110,594
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LOCATION: (702)..(4196)
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TYPE: DNA
ORGANISM: Corynebacterium
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137; Conserv
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APPLICATION Gene Expression Profiles in FILE REFERENCE: 44921-5028-W0 CURRENT APPLICATION GENE EXPRESSION PROFILES IN FILE REFERENCE: 44921-5028-W0 CURRENT APPLICATION NUMBER: US/09/880,107 CURRENT FILING DATE: 2001-06-14 PRIOR APPLICATION NUMBER: US 60/211,379 PRIOR FILING DATE: 2000-06-14 PRIOR FILING DATE: 2000-06-14 PRIOR FILING DATE: 2000-06-14 PRIOR FILING DATE: 2000-06-14 PRIOR FILING DATE: 2000-10-02 SOFTWARE: PATENTIAL DATE: 2000-10-02 NUMBER OF SEQ ID NO3678 SEQ ID NO 3678 LENGTH: 2693 TYPE: DNA ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FARLIER FILING DATE: 1998-December-02
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Microsoft Office 97
SEQ ID NO 5
LENGTH: 1057
TYPE: DNA
ORGANISM: Zea mays
US-09-452-239-5
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US-09-880-107-3678/c
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Best Local
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Patent No. US20020142981A1
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Horne, Darci
APPLICANT: Vockley, Jos
APPLICANT: Scherf, Uwe
APPLICANT: Gene Logic,
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                                                                                                                                                                                                                                                         OTHER INFORMATION: Genbank Accession No. US20020142981A1 X04654
156 GCCAACAAGTTCGTCGCCATCAAGGGCAAGGGCGCGCGCCAG
                 156 ACCACGATGACCGTCCCCGGCGGCGGCGTCGAGGTCCCGGTCGAG
                                                                                                                   36 CGCTACAAGGTCAACAAGAAGCTGGGCCTGAACGCCGGGCCAGCCGATCACGTCGTCGACT 95
                                                                                                                                                                                           Local Similarity
nes 87; Conserv
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                                                        GTGTGCCTGGTGGCGGTGACCATGCCGCTGGTGATGCTGCAGCGCTGGCTCGTGCGCTCG
                                                                            CTGACCGAGGAAGACGTCGTCGCCACCATCGAGTACCTGGTGCGCCTGCACGAGGGCCAG 155
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Pred. No. 0.023;
0; Mismatches
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Sequence 3598, Application US/09878574
Patent NO. US20020110548A1
GENERAL INFORMATION:
APPLICANT: Byrum, Joseph R.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Thompson, Michael D.
TITLE OF INVENTION: Nucleic Acid Molecules and TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(15401)B
CURRENT APPLICATION NUMBER: US/09/878,574
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PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/205,848

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR FILING DATE: 2000-11-27

PRIOR PRIOR PILING DATE: 2000-12-29

PRIOR PRIOR PILING DATE: 2000-12-27

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR FILING DATE: 2000-12-29

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR FILING DATE: 2001-02-16

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Best Local
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APPLICANT:
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APPLICANT:
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TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA, 011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 141 CTGCACGAGGCCAGACCACGATGACCGTCCCGGCGGCGTCGAGGTCCCGGTCGA 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                          262 CTGGTGAAGGTCAAGGCCACGGGGGGGCGCCAGGGGCGAGGTCAAGGGGCACCACCGA 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    202 ATCGAAGTGGTCAAGCTGGTGGATCTGTCGGAAAGCGCCCATATCGAGCGCGAGCTGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21 CTGGCCCGCGTGGGCCGCTACAAGGTCAACAAGAAGCTGGGCCTGAACGCCGGCCAGCCG 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATCACGTCGACTCTGACCGAGGAAGACGTCGTCGCCACCATCGAGTACCTGGTGCGC 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTGACCACCGTGGGGCACGATGAGGTGATCGAGCAGATCACCAAGAACCTCAACAAGCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wall, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Carr, Grant J.
Yamamoto, Robert T.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zyskind, Judith W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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Pred. No. 0.026;
0; Mismatches 84;
                                                                                              and Other Molecules Associated
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; LENGTH: 1050
; TYPE: DNA
; ORGANISM: Coral
US-10-060-857-7
RESULT 11
US-09-934-778-1
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PRIOR APPLICATION NUMBER: 09/333,535
PRIOR FILING DATE: 1999-06-14
NUMBER OF SEQ ID NOS: 15775
SEQ ID NO 3598
LENGTH: 392
TEPE: DNA
OPERATINE (Blycine max
OPERATINE (MORANTION: Clone ID: LIB3028-008-Q1-B1-C6
US-09-878-574-3598
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US-10-060-857-7
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PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 7, Application US/10060857 Patent No. US20020132318A1
GENERAL INFORMATION:
APPLICANT: AntiCancer, Inc.
APPLICANT: Zhao, Ming
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Best Local
                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Jiang, Ping
APPLICANT: Xu, Mingxu
APPLICANT: Yang, Meng
TITLE OF INVENTON: IMPROVED FLUORESCENT PROTEINS
FILE REFERENCE: 31276-20032.00
CURRENT APPLICATION NUMBER: US/10/060,857
CURRENT FILING DATE: 2002-01-29
CURRENT FILING DATE: 1002-01-29
CURRENT FILING DATE: 1002-01-29
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                                                                                                   181
                                                             554 AGGGCTTCAAGTGGGAG
                                                                                                                                   494
                                                                                                                                               121 CCATCGAGTACCTGGTGCGCCTGCACGAGGGCCAGACCACGATGACCGTCCCCGGCGGCG
                                                                                                                                                                                  434 CCAAGGGCCGCCCCCTCCCCTTCGCCTGGGACATCCTGTCCCCCCAGTTCCAGTACGGCT
                                                                                                                                                                                                                                            61 GCCTGAACGCCGGCCAGCCGATCACGTCGTCGACTCTGACCGAGGAAGACGTCGTCGCCA 120
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Local Similarity 49.7%;
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                                                                                           TCGAGGTCCCGGTCGAG 197
                                                                                                                   CCAAGGTGTACGTGAAGCACCCCGCCGACATCCCCGACTACAAGAAGCTGTCCTTCCCCG
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                                                                                                                                                                                                                                                                                                                         98; Conservative
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Pred. No. 0.15;
0; Mismatches 99;
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Pred. No. 0.051;
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Sequence 1, Application US/09934778
Patent No. US20020106772A1

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APPLICANT: Wang, X.

APPLICANT: Cooper, Bret

TITLE OF INVENTION: Promotters for regulation of plant expression

FILE REFERENCE: 1360.001US1

CURRENT APPLICATION NUMBER: US/09/887,576

CURRENT FILING DATE: 2001-06-25

PRIOR APPLICATION NUMBER: US 60/213,848

PRIOR FILING DATE: 2000-06-23

PRIOR APPLICATION NUMBER: US 60/214,087

PRIOR APPLICATION NUMBER: US 60/214,087

PRIOR FILING DATE: 2000-06-23

PRIOR FILING DATE: 2000-12-29

PRIOR FILING DATE: 2000-12-29

PRIOR FILING DATE: 2000-12-29
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CUBRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: 09/420,211
PRIOR FILING DATE: 1999-10-18
PRIOR FILING DATE: 1998-10-15
PRIOR FILING DATE: 1998-10-15
PRIOR APPLICATION NUMBER: 08/951,924
PRIOR APPLICATION NUMBER: 08/951,924
PRIOR FILING DATE: 1997-10-16
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 1
LENGTH: 1131
SOFTWARE: Fas
SEQ ID NO 777
LENGTH: 1467
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: LOCATION: (1)..(1131)
US-09-934-778-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -09-887-576-777
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Best Local :
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APPLICANT: Croteau, Rodney B
APPLICANT: Burke, Charles C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: GERANYL DIPHOSPHATE SYNTHASE LARGE SUBUNIT, AND METHODS FILE REFERENCE: WSUR117920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Mentha piperita
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     595 CT 596
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       147 GAGGGCCAGACCACGATGACCGTCCCCGGCGGCGTCGAGGTCCCGGGTCGAGGTGGACGAC 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           415 CTCGTCGGCGGCGACGAGTCCACGGCGGTGCGCGCGTCGAGATGATCCAC 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          87 TCGTCGACTCTGACCGAGGAAGACGTCGTCGCCACCATCGAGTACCTGGTGCGCCTGCAC 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27 CGCGTGGGCCGCTACAAGGTCAACAAGAAGCTGGGCCTGAACGCCGGCCAGCCGATCACG 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACGATGTCGCTGATGCACGACGACCTCCCATGCATGGACAACGACGACCTCCGCCGCGGC 534
1467
                                  FastSEQ for Windows Version 4.0
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1 Similarity 50.5%;
92; Conservative
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                                                                                                                                                                                                                                                                                                                   Han, B.
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0.21;
hes 90; Indels
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: LOCATION: (479)
US-09-854-731-1
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SEQ ID NO 1
LENGTH: 484
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
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Best Local Similarity
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                                                                                                                                                                       Matches
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Patent No. US20020120949A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/854,731 CURRENT FILING DATE: 2001-05-14 PRIOR APPLICATION NUMBER: 60/092,438 PRIOR FILING DATE: July 10, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Allen, Steve
APPLICANT: Lee, Jian Ming
TITLE OF INVENTION: Plant Protein Kinases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: BB-1171
                                                                                                                                                                                                                                                                                                             NAME/KEY: unsure LOCATION: (467)
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LOCATION: (402)
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148 AGGGCCAGACCACGATGACCGTCCCCGGCGGCGTCGAGGTCCCGGTCGAGGTG 200
                              260 CACCGACGACGA-CGTGGAGGACGTCCGCCGGGAGATCCAGATAATGCACCACCTGGCGG
                                                                                          200 GCGTGGAGCGGGCCACGGGCAAGGAGTTCGCGTGCAAGTCCATCCTGAAGCGCAACTCGT 259
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                                                         88 CGTCGACTCTGACCGAGGAAGACGTCGTCGCCACCATCGAGTACCTGGTGCGCCTGCACG 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1174 ATCGTGCCGGCGTACACCATGCCGGCCAACGCCGAGCACGTCGCCGTCCTCCGCGTCGTC 1233
                                                                                                                       28 GCGTGGGCCGCTACAAGGTCAACAAGAAGCTGGGCCTGAACGCCGGCCAGCCGATCACGT 87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    69 GCCGGCCAGCCGATCACGTCGTCGACTCTGACCGAGGAAGACGTCGTCGCCACCATCGAG 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9 AAGCGCTACGACCTGGCCCGCGTGGGCCGCTACAAGGTCAACAAGAAGCTGGGCCTGAAC 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCGGTCGAGGTGGACGAC 206
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(469)
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                                                                                                                                                                                18.2%;
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                                                                                                                                                          Score 37.8; DB 10;
Pred. No. 0.23;
0; Mismatches 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 38; DB 10; Length 1467; Pred. No. 0.22; 0; Mismatches 100; Indels
                                                                                                                                                        77;
                                                                                                                                                                                          Length 484;
                                                                                                                                                           Indels
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RESULT 15
US-10-052-586-545
Sequence 545, Application US/10052586
Patent No. US20020127584A1
GENERAL INFORMATION:
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; LOCATION: (1).
US-09-815-242-7696
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CURRENT FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR FILING DATE: 2000-10-23

PRIOR FILING DATE: 2000-10-23
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APPLICANT: Ohlsen, Kar
APPLICANT: Ohlsen, Kar
APPLICANT: Eyskind, Ju
APPLICANT: Wall, Danie
APPLICANT: Trawick, Jo
APPLICANT: Carr, Grant
APPLICANT: Yamamocto, F
APPLICANT: Xu, H. Howa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 7696 LENGTH: 1164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/253,625
PRIOR TILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR PILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                           738
                                                                                                                                                                                                                                                                                                 143
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                                                                                                                                                                  CGCCA 742
                                                                                                                                                                                                                                        ACACAAGGTCGGCAAGTCACTGTACGAGGCCGACCTGGTCGAGACCGCCAAGGCCATCGC 737
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93; Conservat
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Zyskind, Judith W.
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Pred. No. 0.24;
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                                                                                   PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/078886
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078939
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079664
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PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063120
PRIOR FILING DATE: 1997-10-24
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PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059266
PRIOR FILING DATE: 1997-09-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/052,586 CURRENT FILING DATE: 2002-01-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3430R1C1
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OR FILING DATE: 1997-11-24
OR APPLICATION NUMBER: 60/066772
OR FILING DATE: 1997-11-24
OR APPLICATION NUMBER: 60/06935
OR FILING DATE: 1997-12-11
OR APPLICATION NUMBER: 60/069425
OR FILING DATE: 1997-12-12
OR APPLICATION NUMBER: 60/069870
OR FILING DATE: 1997-12-17
OR APPLICATION NUMBER: 60/068017
OR FILING DATE: 1997-12-18
OR FILING DATE: 1997-12-18
OR APPLICATION NUMBER: 60/077450
OR FILING DATE: 1998-03-11
OR APPLICATION NUMBER: 60/077632
OR FILING DATE: 1998-03-11
OR APPLICATION NUMBER: 60/077632
OR FILING DATE: 1998-03-11
OR APPLICATION NUMBER: 60/077632
OR FILING DATE: 1998-03-11
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DR FILING DATE: 1997-10-31
DR APPLICATION NUMBER: 60/065311
DR FILING DATE: 1997-11-31
DR APPLICATION NUMBER: 60/066120
DR FILING DATE: 1997-11-21
                                                         APPLICATION NUMBER: 60/
FILING DATE: 1998-03-27
                                         APPLICATION
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FILING DATE: 1997-10-28
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FILING DATE: 1997-10-21
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FILING DATE: 1997-10-24
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Godowski, Paul
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                                       NUMBER:
NUMBER: 60/080107
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OR APPLICATION NUMBER: 6070
PR FILLING DATE: 1998-06-03
PR APPLICATION NUMBER: 6070
PR FILLING DATE: 1998-06-04
PR APPLICATION NUMBER: 6070
PR FILING DATE: 1998-06-04
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OR APPLICATION NUMBER: 60/082797
OR FILING DATE: 1998-04-22
OR APPLICATION NUMBER: 60/083322
OR FILING DATE: 1998-04-28
OR APPLICATION NUMBER: 60/083495
OR FILING DATE: 1998-04-29
OR APPLICATION NUMBER: 60/083496
OR FILING DATE: 1998-04-29
OR APPLICATION NUMBER: 60/083499
OR FILING DATE: 1998-04-29
OR APPLICATION NUMBER: 60/083559
OR APPLICATION NUMBER: 60/08356
OR APPLICATION NUMBER: 60/084366
OR FILING DATE: 1998-05-05
OR APPLICATION NUMBER: 60/08414
OR FILING DATE: 1998-05-05
OR APPLICATION NUMBER: 60/084639
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RE APPLICATION NUMBER: 60/08
REFILING DATE: 1998-05-15
PR APPLICATION NUMBER: 60/08
REFILING DATE: 1998-05-18
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FILING DATE: 1998-05-22
APPLICATION NUMBER: 60/
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PR APPLICATION NUMBER: 60/081195

PR FILING DATE: 1998-04-09

PR APPLICATION NUMBER: 60/081838

PR FILING DATE: 1998-04-15

PR APPLICATION NUMBER: 60/082568

PR FILING DATE: 1998-04-21
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R APPLICATION NUMBER: 60/08
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APPLICATION NUMBER: 60/085579
FILING DATE: 1998-05-15
APPLICATION NUMBER: 60/085580
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APPLICATION NUMBER:
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FILING DATE: 1998-05-07
APPLICATION NUMBER: 60/084643
FILING DATE: 1998-05-07
APPLICATION NUMBER: 60/085573
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FILING DATE: 1998-04-21
APPLICATION NUMBER: 60/082704
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FILING DATE: 1998-04-08
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PRIOR APPLICATION NUMBER: 60/088825
PRIOR FILLING DATE: 1998-05-10
PRIOR APPLICATION NUMBER: 50/088826
PRIOR FILLING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088861
PRIOR FILLING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088863
PRIOR FILLING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088876
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PRIOR APPLICATION NUMBER: 60/089876
PRIOR FILLING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/089990
PRIOR FILLING DATE: 1998-06-12
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OR FILING DATE: 1998-06-05
OR APPLICATION NUMBER: 60/088326
OR APPLICATION NUMBER: 60/088326
OR FILING DATE: 1998-06-09
OR APPLICATION NUMBER: 60/088722
OR FILING DATE: 1998-06-10
OR APPLICATION NUMBER: 60/088738
OR FILING DATE: 1998-06-10
OR APPLICATION NUMBER: 60/088740
OR APPLICATION NUMBER: 60/088811
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OR APPLICATION NUMBER: 60/088811
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APPLICATION NUMBER: 60/089538
FILING DATE: 1998-06-17
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FILING DATE:
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FILING DATE: 1998-06-16
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FILING DATE:
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FILING DATE: 1998-06-05
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FILING DATE: 1998-06-04
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                           NUMBER: 60/089653: 1998-06-17
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1998-06-17
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В 밁 õ 밁 Qy Query Match Best Local s Matches 80 121 CCATCGAGTACCTGGTGCGCCTGCACGAGGG 912 852 61 -TCAAGGAGAAGCGCTACGACCTGGGCCGGCGGGGGCGCTACAAGGTCAAGAAGCTGG GCATGCATGCAGCCATGAAGTACATCAACACGACTCTGGTTTCGCGCATCGGCTCCGTCA GCCTGAACGCCGGCCAGCCGATCACGTCGTCGACTCTGACCGAGGAAGACGTCGTCGCCA 120 TCCTGGAGACCCGCTACGCCGTGCCCGGGAAGAGCCTGGAGGAGCAGAACGAGGTCATAG ;08 Similarity Conservative 18.0%; Score 37.4; DB Pred. No. 0.31; 0; Mismatches 0; 151 DB 12; 71; Length 1535; Indels 0, Gaps 911 97] 60

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Search completed: November 12, Job time: 33.1607 secs

2002,

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Result
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Maximum DB
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Perfect score:
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Listing first 45 s
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/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
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1 US-07-923-692C-5
2 US-08-184-237-5
2 US-08-484-341-5
2 US-08-22-468A-1
5 195216-7
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2 US-09-248-335-65
3 US-09-272-35-3
3 US-09-072-435-3
3 US-09-072-317A-3
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US-09-082-614A-57
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Sequence 57, Appl
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Patent No. 5352575
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RESULT 1
US-08-250-030-1
                                                                                                                    GENERAL INFORMATION:
APPLICANT: Persing, D
TITLE OF INVENTION: D
TITLE OF INVENTION: C
TITLE OF INVENTION: C
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                  Sequence 1, Application US/08250030 Patent No. 5643723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schwegman,
STREET: 3500 IDS Centu
CITY: Minneapolis
STATE: MN
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US-09-568-102-1
US-09-568-480-1
US-09-568-486-1
US-09-568-472-1
US-09-568-472-1
US-09-568-472-1
US-09-105-537-17
US-09-105-537-3
US-09-105-537
                                                                                                                                                        Locus Encoding in Mycobacterial Cultures and
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Sequence 2, Appli
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Sequence 3, Appli
Sequence 1, Appli
Sequence 17, Appli
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COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: IBM PC COMPATIBLE
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/250,030
FILING DATE: 26-MAY-1994
ATTORNEY/ACENT INFORMATION:
NAME: MUSTION: 435
ATTORNEY/ACENT INFORMATION:
REGISTRATION NUMBER: 150.105US1
TELECHOME: 612-339-0331
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-339-3061
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 970 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: Linear
MOLECULE TYPE: DNA
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                                                                                                                                                     US-08-250-030-1
                                                                                   Best Loc
Matches
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                    1 TCAAGGAGAAGCGCTACGACCTGGCCCGCGTGGGCCGCTACAAGGTCAACAAGAAGCTGG 60
TCAAGGAGAAGCGCTACGACCTGGCCCGCGTCGGTCGCTATAAGGTCAACAAGAAGCTCG 85
                                                                                 al Similarity
182; Conserv
                                                                              Conservative
                                                                                          80.0%;
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                                                                      Score 166.4; DB 1;
Pred. No. 5.3e-31;
0; Mismatches 26;
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REFERENCE_DOCKET NUMBER: 150.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-339-031
TELEFAX: 612-339-3061
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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PCT-US95-06790-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: PCT/U
FILING DATE: 26-MAY-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0
                                  181
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                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Mayo Foundation for Medical Education and Research APPLICANT: and Hoffmann-La Roche Inc.
TITLE OF INVENTION: Detection of a Genetic Locus Encoding TITLE OF INVENTION: Resistance to Rifampin
NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Schwegmar
                                                                                                                           86
                                                                                                                                 61 GCCTGAACGCCGGCCAGCCGATCACGTCGTCGACTCTGACCGAGGAAGACGTCGTCGCCA 120
                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: sing
TOPOLOGY: linear
                                                                                                                                                                                            1 TCAAGGAGAAGCGCTACGACCTGGCCCGCGTGGGCCGCTACAAGGTCAACAAGAAGCTGG
                                                                                                                                                                                                                                                                                                                                                                                     LENGTH:
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TCGAGGTGCCGGTGGAAACCGACGACAT 233
                         TCGAGGTCCCGGTCGAGGTGGACGACAT 208
                                                     CCATCGAATATCTGGTCCGCTTGCACGAGGGTCAGACCACGATGACCGTTCCGGGCGGCG
                                                                     CCATCGAGTACCTGGTGCGCCTGCACGAGGGCCAGACCACGATGACCGTCCCCGGGGGGC 180
                                                                                                                GGCTGCATGTCGGCGAGCCCATCACGTCGTCGTCGACGCTGACCGAAGAAGACGTCGTGGCCA
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3500 IDS Center
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87.5%; Pred. No. 5.3e-31;
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INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 3447 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
FOOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-313-185-57
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Best Local Similarity 80...
167; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION UMBER: US/08/313
FILING DATE: 12-OCT-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 0235
REFERENCE/DOCKET NUMBER: 0235
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 57, Appli
Patent No. 5851763
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/313,185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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           989
                                                                                  121 CCATCGAGTACCTGGTGCGCCTGCACGAGGGGCCAGACCACGATGACCGTGCCCGGCGGCG 180
                                                                                                                                                                                                       809 TCAAGGAGAAACGCTACGACCTGGCCAGGGTTGGTCGTTACAAGGTCAACAAGAAGCTCG 868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Honore, Nadine
APPLICANT: Telenti, Amalio
APPLICANT: Bodmer, Thomas
TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
TITLE OF INVENTION: in Mycobacterium Tuberculosis
NUMBER OF SEQUENCES: 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                    61 GCCTGAACGCCGGCCAGCCGATCACGTCGTCGACTCTGACCGAGGAAGACGTCGTCGCCA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
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                                                                                                                                                                                                                        1 TCAAGGAGAAGCGCTACGACCTGGCCCGCGTGGGCCGCTACAAGGTCAACAAGAAGCTGG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & ADDRESSEE: Dunner STREET: 1300 I Street, N.W.
CITY: Washington STATE: D.C.
COUNTRY: USA
TAGAAGTGCCAGTGGAAACTGACGATAT 1016
                                                                CCATAGAGTACCTGGTTCGTCTGCATGAGGGTCAGTCGACAATGACTGTCCCAGGTGGGG
                                                                                                                                   GGTTGCACGCCGGTGAGTTGATCACGTCGTCCACGCTGACCGAAGAGGATGTCGTCGCCA
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Young, Douglas
Zhang, Ying
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                                                                                                                                                                                                                                                                                                                                                                             DNA (genomic)
                                                                                                                                                                                                                                                                                                68.5%; Score 142.4; DB 2
80.3%; Pred. No. 2.5e-25;
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                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02356.0068-00000
                                                                                                                                                                                                                                                                                                                   DB 2;
                                                                                                                                                                                                                                                                                 41; Indels
                                                                                                                                                                                                                                                                                                                   Length 3447;
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                                                                   988
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US-09-082-614A-57

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RESULT 5
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Patent No. 5352575;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 3447 base pairs
TYPE: nucleic acid
STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                         Best Local Similarity Matches 167; Conservat
                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 57, Application US/09082614A Patent No. 6124098
                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: 11
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 02
TELECOMMUNICATION INFORMATION:
                                                                                             181 TCGAGGTCCCGGTCGAGGTGGACGACAT 208
                                                                                                                                 869
                                                                                                                                                                                                                                                              CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08
APPLICATION OF 12-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: MANGE 12-OCT-1994
NAME: MANGE 12-OCT-1907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/082,614A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Honore, Nadine
APPLICANT: Telenti, Amalio
APPLICANT: Telenti, Amalio
APPLICANT: Bodmer, Thomas
TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
TITLE OF INVENTION: in Mycobacterium Tuberculosis
NUMBER OF SEQUENCES: 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                    61 GCCTGAACGCCGGCCAGCCGATCACGTCGTCGACTCTGACCGAGGAAGAAGACGTCGTCGCCA 120
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APPLICANT: Cole, Stewart
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Finnegan, Henderson, Farabow, Garrett ADDRESSEE: Dunner STREET: 1300 I Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
                                                                          TAGAAGTGCCAGTGGAAACTGACGATAT 1016
                                                                                                                                                                                                 GGTTGCACGCCGGTGAGTTGATCACGTCGTCCACGCTGACCGAAGAGGATGTCGTCGCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION:
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                                                                                                                                                                                                                                                                                                                                          Conservative
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Zhang, Ying
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Pred. No. 2.5e-25;
0; Mismatches 41
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                                                                                                                                                                                                                                                                                                                                                                 DB_3; Length 3447;
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APPLICANT: Fafaiski, Antoni J.

APPLICANT: Fafaiski, Antoni J.

APPLICANT: Fafaiski, Antoni J.

APPLICANT: Fafaiski, Antoni J.

APPLICANT: Cahoon, Rebecca E.

TITLE OF INVENTION: Plant Caffeoyl-CoA O-Methyltransferase
FILE REFERENCE: BB1284 US NA

CURRENT APPLICATION NUMBER: US/09/452,239

CURRENT APPLICATION NUMBER: 00/110,594

EARLIER APPLICATION NUMBER: 60/110,594

NUMBER OF SEQ ID NOTE: 1998-December-02

SOFTWARE: Microsoft Office 97

SEQ ID NO 5

LENGTH: 1057

TYPE: DNA

ORGANISM: Zea mays

TICLURIANT: 200 MICROSOFT OFFICE 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
Matches 68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1174 ACCCCGTGGGGCCGCGGCGGCGGCGACGACGCGATCTACGTGGACGGCGT 1223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1114 ACCGCGGCCGAGTACGTCACGGTCATCAAGGAGCTGACGGCCCGGGCCCGGGCCCCGGGC
                                                          352
                                                                                                                                                                                                                                                                    292 CTGATCAAGCTGAGCGGCGCGCGCGCGCACCCTGGAGGTGGGCGTGTTCACGGGCTACTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 100,817
FILING DATE: 29-JUN-1987
APPLICATION NUMBER: 886,260
FILING DATE: 16-JUL-1986
APPLICATION NUMBER: 784,787
FILING DATE: 04-OCT-1985
APPLICATION NUMBER: 801,799
FILING DATE: 26-NOV-1985
APPLICATION NUMBER: 844,113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/(
FILING DATE: 20-APR-1990
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: PETROVSKIS, ERIK A.; POST, LEONARD E.; TIMMINS, JAMES G. TITLE OF INVENTION: PSEUDORABIES VIRUS PROTEIN NUMBER OF SEQUENCES: 12
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         159 ACGATGACCGTCCCCGGCGCGTCGAGGTCCGAGGTCGAGGTGGACGACAT 208
                                                                                                                                                                                                      81 ATCACGTCGTCGACTCTGACCGAGGAAGACGTCGTCGCCACCATCGAGTACCTGGTGCGC 140
                                                                                                                                                                                                                                                                                                           21 CTGGCCCGCGTGGGCCGCTACAAGGTCAAGAAGAAGCTGGGCCTGAACGGCGGGCCAGCCG 80
                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity es 95; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99 ACCGAGGAAGACGTCGTCGCCACCATCGAGTACCTGGTGCGCCCTGCACGAGGGCCAGACC 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 1734
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                             CTGCTGGCGACGGCTCTGGCGCTGCCGGCGACGGCAAGGTCATCGCATTCGACGTGAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    h 20.6%;
Similarity 61.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                          20.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                0;
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Pred. No. 0.07;
0; Mismatches 88; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
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RESULT 8
US-07-923-692C-5
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: OTHER INFORMATION: H37Rv
US-09-103-840A-1
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US-09-103-840A-1/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 92; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       595825 CCTGGGCACCGTCGCCGAGTCGGTCGACGGGATATTCACCGGCAGACTGGTCGGC 595771
                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT FAPPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
                                                                                                                                                                                                                                                                                                                                   APPLICANT: Donson, APPLICANT: Dawson, APPLICANT: Grantham, APPLICANT: Turpen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: FLEISCHMAN, ROBERT D.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin
                  SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/923,692C
FILING DATE: 31-JUL-1992
                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                         TITLE OF INVENTION: RECOMBINANT PLANT VIRAL NUCLEIC ACIDS NUMBER OF SEQUENCES: 11
                                                                                                                                           STATE: 04111
                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   152
CLASSIFICATION:
                                                                                                                                                                                                    STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92 GACTCTGACCGAGGAAGACGTCGTCGCCACCATCGAGTACCTGGTGCGCCTGCACGAGGG 151
                                                                                                                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCAGACCACGATGACCGTCCCCGGCGGCGTCGAGGTCCCGGTCGAGGTGGACGAC
                                                                                                                                                                                    San Francisco
                                                                                                                                                                                                   E: Limbach & Limbach
2001 Ferry Building
                                                                                                                                                                                                                                                                                    Turpen, Ann Myers
Garger, Stephen J.
Grill, Laurence K.
                                                                                                                                                                                                                                                                                                                                      Dawson, William 0.
Grantham, George L.
Turpen, Thomas H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
31-JUL-1992
N: 435
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Pred. No. 0.13;
0; Mismatches 83;
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RESULT 9
US-08-184-237-5
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Best Local Similarity 52.5%,
Matches 85; Conservative
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; LOCATION:
US-07-923-692C-5
              Sequence 5, Application US/08184237 Patent No. 5589367
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 415-433-8716
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 160
FILING DATE: 26-FEB-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 347
FILING DATE: 05-MAY-1989
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                        HYPOTHETICAL: NO ANTI-SENSE: NO ORIGINAL SOURCE: ORGANISM: Oryza IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (9)
                                                                                               1011 GGTCATGCAGGGCTACGCATACATCCTCACCCCACCCCGGCAA 1052
                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
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APPLICATION NUMBER: US 16
FTI.TING DATE: 26-FEB-1988
                                                                                                                            155 GACCACGATGACCGTCCCCGGCGGCGTCGAGGTCCCGGTCGA 196
                                                                                                                                                       951 CTTCGTCGACAACCACGACACCGGCTCGACGCAGCACCTGTGGCCGTTCCCCTCCGACAA 1010
                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION: NAME: Halluin, Albert P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE: 08-JUN-PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 160,771
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FILING DATE: 22-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 6.
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                                                                                                                                                                                                                                             95
                                                                                                                                                                                                                                                                                                                                                                                                        CLONE: alpha-amylase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: FILING DATE: 15-JUI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Halluin, Albert REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH:
                                                                                                                                                                          TCTGACCGAGGAAGACGTCGTCGCCACCATCGAGTACCTGGTGCGCCTGCACGAGGGCCA 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1450 base pairs
                                                                                                                                                                                                                                                                                                                                                             CDS (B) LOCATION: 12. .1316
                                                                                                                                                                                                                                                                                                                                                                                                                                    Oryza sativa
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O
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                                                                                                                                                                                                                                                                                               18.7%;
52.5%;
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                                                                                                                                                                                                                                                                                Score 38.8; DB 1;
Pred. No. 0.45;
0; Mismatches 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BIOG-20121
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APPLICANT:

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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-43-4150
TELEPAX: 415-433-4716
TELEPAX: 415-433-8716
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                  CLONE:
FEATURE:
                                                                                                                   MOLECULE TYPE: DI
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 363,138
FILING DATE: 08-JUN-1989
                                                                   ORGANISM: Oryza sativa 
IMMEDIATE SOURCE:
                                                                                                    ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION: NAME: Halluin, Albert P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 26-FEB-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 34
FILING DATE: 05-MAY-1989
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APPLICATION NUMBER: US 97
FILING DATE: 31-JUL-1992
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APPLICANT:
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APPLICATION NUMBER:
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FILING DATE: 22-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 64
FILING DATE: 16-JAN-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
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NAME/KEY:
LOCATION:
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                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: BIOG-20121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 3: FILING DATE: 17-FEB-1989
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                                                                                                                                                                      TOPOLOGY: linear
                                                                                                                                                                                                         TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER:
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                                                                                                                                                                                                                           LENGTH:
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CLASSIFICATION:
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                                                   alpha-amylase
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                                                                                                                                                                                                                        1450 base pairs
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Turpen, Ann Myers
Garger, Stephen J.
Grill, Laurence K.
CDS (B) LOCATION: 12. .1316
12. .1316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Grantham, George L.
Turpen, Thomas H.
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                                                                                                                                                    DNA (genomic)
                                                                                                                                                                                       single
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                                                                                                                                                                                                                                                                                                                                                                                                                  US 219,279
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US-08-482-920-5
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Sequence 5, Appiter
No. 5866785
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Best Local
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                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/4
FILING DATE: 07-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 184,
FILING DATE: 19-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 600,
FILING DATE: 22-OCT-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
             APPLICATION NUMBER:
FILING DATE: 08-JUN-
PRIOR APPLICATION DATA:
                                                          APPLICATION NUMBER:
FILING DATE: 05-MAY-
PRIOR APPLICATION DATA:
                                                                                                         FILING DATE: 26-FEB-PRIOR APPLICATION DATA:
                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 3:
FILING DATE: 17-FEB-1989
                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 641,617
FILING DATE: 16-JAN-1991
                                                                                                                                  PRIOR APPLICATION DATA:
PRIOR APPLICATION US 160,771
                                                                                                                                                                                                       PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
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                                                                                                                                                                          APPLICATION NUMBER: FILING DATE: 26-FE
                                                                                                                        APPLICATION NUMBER: US 10 FILING DATE: 26-FEB-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    155 GACCACGATGACCGTCCCGGGCGGCGTCGAGGTCCCGGTCGA 196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: New
ZIP: 10036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95 TCTGACCGAGGAAGACGTCGTCGCCACCATCGAGTACCTGGTGCGCCTGCACGAGGGCCA 154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      35 CCGCTACAAGGTCAACAAGAAGCTGGGCCTGAACGCCGGCCAGCCGATCACGTCGTCGAC 94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INVENTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Application US/08482920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2: Pennie & Edmonds
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Garger, Stephen J.
Grill, Laurence K.
VENTION: RECOMBINANT PLANT VIRAL NUCLEIC ACIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Turpen, Thomas H.
Turpen, Ann Myers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Donson, Jon
Dawson, William O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Grantham, George L.
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                                                                           UMBER: US 347,637
05-MAY-1989
                               08-JUN-1989
                                                                                                                                                                       26-FEB-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18.7%;
52.5%;
                                             US 363,138
                                                                                                                                                                                      US 160,766
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US 219,279
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FILING DATE:

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US-08-484-341-5
; Sequence 5, Application US/08484341
; Sequence 5, Application US/08484341
; GENERAL INFORMATION:
; APPLICANT Dawson, William 0.
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MOLECULE TYPE: DO
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 415-854-3594
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1011 GGTCATGCAGGGCTACGCATACATCCTCACCCCACCCCGGCAA 1052
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                UNGANISM: Oryza sativa IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 1450 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            155 GACCACGATGACCGTCCCCGGCGGCGTCGAGGTCCCGGTCGA 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Halluin, Albert P.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 8129-112
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-3660
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLONE:
                                                                                COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                               Grantham, George L.
Turpen, Thomas H.
Turpen, Ann Myers
Garger, Stephen J.
Grill, Laurence K.
TITLE OF INVENTION: RECOMBINANT PLANT VIRAL NUCLEIC
NUMBER OF SEQUENCES: 11
                          PRIOR
                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Limbach & Limbach
STREET: 2001 Ferry Building
CITY: San Francisco
STATE: CAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTTCGTCGACACCACGACACCGGCTCGACGCAGCACCTGTGGCCGTTCCCCTCCGACAA 1010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCTGACCGAGGAAGACGTCGTCGCCACCATCGAGTACCTGGTGCGCCCTGCACGAGGGCCA 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   85;
APPLICATION NUMBER: US/08/484,341 FILING DATE: 07-Jun-1995 CLASSIFICATION: CUNKNOWN> R APPLICATION DATA: APPLICATION NUMBER: 08/184,237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alpha-amylase
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12. .1316
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                                                                                                 Version #1.25
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RESULT 12
US-09-232-468A-1
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                                                                                                                  Sequence 1, Application US/09232468A
Patent No. 6207165
GEMERAL INFORMATION:
APPLICANT: AUDONNET et al.
             APPLICANT: AUDONNET et al.

TITLE OF INVENTION: POLYNUCLEOTIDE VACCINE FORMULA AGAINST PORCINE
TITLE OF INVENTION: REPRODUCTIVE AND RESPIRATORY PATHOLOGIES
FILE REFERENCE: 454313-2230
CURRENT APPLICATION NUMBER: US/09/232,468A
CURRENT FILLING DATE: 1999-01-05
RUMBER OF SEO ID NOS: 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
 SOFTWARE:
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Local Similarity 52.5%;
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APPLICATION NUMBER: US 219,279

FILING DATE: 15-JUL-1988

ATTORNEY_AGENT INFORMATION:

NAME: Halluin, Albert P.

REGISTRATION NUMBER: 28,957

REFERENCE_DOCKET NUMBER: 810G-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE DESCRIPTION: SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Oryza sativa IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: DNA (9: HYPOTHETICAL: NO ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-433-4150
PatentIn
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LOCATION: 12. .1316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLONE: alpha-amylase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
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APPLICATION NUMBER: US 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 641,617 FILING DATE: 16-JAN-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 60 FILING DATE: 22-OCT-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 26-FEB-1988
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5196516-7
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; LOCATION: (1)..(2742)
US-09-232-468A-1
                                                                                                                                                                                           Sequence 4, Application US/09029603
Patent No. 6210935
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO:7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMON,
                                                              APPLICANT: Schupp, Thomas
APPLICANT: Engel, Natalie
APPLICANT: Bietenhader, Jurg
APPLICANT: Toupet, Christine
APPLICANT: Pospiech, Andreas
TITLE OF INVENTION: Staurosporin Biosynthesis Gene Clusters
FILE REFERENCE: 4-20555/A/PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Loc
Matches
CURRENT APPLICATION NUMBER: US/09/029,603
CURRENT FILING DATE: 1998-03-20
EARLIER APPLICATION NUMBER: PCT/EP96/03643
EARLIER FILING DATE: 1996-08-19
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                      3475 GTCGGCCCTCGAGCAGCAGGAGCACA 3500
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TITLE OF INVENTION: PSEUDORABIES VIRUS VACCINE NUMBER OF SEQUENCES: 8
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/07/383,833
FILING DATE: 21-JUL-1989
                                                                                                                                                                                                                                                                                                                                                                                    3415 CGACGTGGACGACGCCAAGCTGGACCAGGCCCGGGACATGATCCGGTACATGTCCATCGT 347/
                                                                                                                                                                                                                                                                                                                                                                                                                                                        3355 CATGAAGGCCCTGTACCCCGTCACGACGACGCCTCAAGGAGGACGGCGTCGACGAGGG 3414
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                                                                                                                                                                                                                                                                                                                                                      182 CGAGGTCCCGGTCGAGGTGGACGACA 207
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54.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18.7%; Score 38.8; DB 6; 54.1%; Pred. No. 0.49;
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RESULT 15
US-07-640-476-6
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NAME/KEY: misc_RNA
LOCATION: (5071)..(6085)
OTHER INFORMATION: ORF
US-09-029-603-4
                                                                                                                                                                                                                                                                                                                                                                                              Sequence 6, Application US/07640476 Patent No. 5376536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 91; Conserv
                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                               APPLICANT: QUAX, WILHELMUS
APPLICANT: LUITEN, RUDOLF G.
APPLICANT: SCHUUHRUIZEN, PAU
APPLICANT: MRABET, NADIR
TITLE OF INVENTION: NOVEL GL
TITLE OF INVENTION: THEIR US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 4
                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                               CURRENT APPLICATION DATA
                                                                                                                                                                                                          NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 545 Middlefield Road, Suite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1137 ACCGCCGGCCACGAGACCACCAACTGCCTCGCCAGGGCGGTCCTCACCCTGCGCG 1194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_RNA
LOCATION: (4013)..(4999)
OTHER INFORMATION: ORF
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LOCATION: (1747)..(2553)
OTHER INFORMATION: ORF
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OTHER INFORMATION: ORF
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LOCATION: (2593)...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Streptomyces longisporoflavus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1077 CGGGACACCGGATCACUGCTCAGCGTGGACGGCATCGTCGGCACCTGCGTCCATCTGCTC 1136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1017 GAGGTGGACCGGCGGCGGCGACGACCGACGATCTGCTCACCCTCCTCGTCCGCGCC 1076
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              138 CGCCTGCACGAGGGCCACACCACGATGACCGTCCCGGCGGCGGCGTCGAGGTCCCGGTCG 195
APPLICATION NUMBER: US/07/640,476 FILING DATE: 19910110
                                                                                                                                                                                     STREET: 545 Midd.
CITY: Menlo Park
STATE: CA
                                                                                                                                                      COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    78 CCGATCACGTCGTCGACCTCTGACCGAGGAAGACGTCGTCGCCACCACCATCGAGTACCTGGTG 137
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                                                                                                                                                        CA
USA
                                                                                                                                                                                                                                                                                                             LUITEN, RUDOLF G.M.
SCHUURHUIZEN, PAUL W.
MRABET, NADIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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ON: ORF
                                                                                                                                                                                                                                                                               NOVEL GLUCOSE ISOMERASE ENZYMES AND THEIR USE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 38.8;
Pred. No. 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                 Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB
                                                                #1.25
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Search completed: November 12, Job time: 2703.89 secs
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INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 1164 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Streptomyces murinus
FFATHER: DSM 40091
                                                                                                                                                                                                                                                                                                                                                                       Query Match 18.6%; Score 38.6; DB 1; Best Local Similarity 49.7%; Pred. No. 0.49; Matches 98; Conservative 0; Mismatches 99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
NAME/KEY: CDS
LOCATION: 1..1164
LOCATION: 1..1164
IDENTIFICATION METHOD: (
OTHER INFORMATION: /PCI
OTHER INFORMATION: /PVI
OTHER INFORMATION: /Sta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kate H. Murashige
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 24615-2009.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 327-7250
TELEFAX: (415) 327-2951
TELEFAX: 706141
                                                                        897 GTGGGCCTCGGCCGCGG 913
                                                                                                                                       837 TTACGAGGGCCCGCGCACTTCGACTTCAAGCCGCGGGGACCGAGGACTTCGACGGCGT 896
                                                                                                                                                                         122 CATCGAGTACCTGGTGCGCCTGCACGAGGGCCAGACCACGATGACCGTCCCCGGCGGGGT 181
                                                                                                                                                                                                               777 GTTCGGCCCCGGCGACCTGCGGGCGGCGTTCTGGCTGGTCGACCTCCTGGAGACCGCCGG 836
                                                                                            182 CGAGGTCCCGGTCGAGG 198
                                                                                                                                                                                                                                                                                        717 CAAGCTCTTCCACATCGACCTCAACGGCCAGTCCGGCATCAAGTACGACCAGGACCTGCG 776
                                                                                                                                                                                                                                         62 CCTGAACGCCGGCCAGCCATCACGTCGTCGACTCTGACCGAGGAAGACGTCGTCGCCAC 121
                                                                                                                                                                                                                                                                                                              2 CAAGGAGAAGCCCTACGACCTGGCCCGCGTGGGCCGCTACAAGGTCAACAAGAAGCTGGG 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                             OD: experimental
/EC_number= 5.3.1.5
/PCGnumber= 7xylose isomerase (glucose isomerase)"
/evidence= EXPERIMENTAL
/standard_name= "D-xylose ketol isomerase"
              2002, 21:00:00
                                                                                                                                                                                                                                                                                                                                                                                                           Length 1164;
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Result
No.
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Maximum DB
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Perfect score:
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                                                         765460
                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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179.2
174.4
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Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-697-123B-19
208
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Copyright (c) 1993 - 2002 Compugen Ltd
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            208
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        AAS05219
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Mycobacterium tube	PRV glycoprotein g	Pseudorables virus	DNA encoding gI of	ouro	companiate gene	Capatiacus	;	Drosophila melanos	Drosophila melanor	Streptomyces ambof	Swine pendorabion	Psendorables :: :::	C grucamicum codin	c grucamicum codin	Mycobacterium gast	mal			_	Mycobacterium gord					Mycobacterium intr		Mycobacterium gord		M. tuberculosis rp	copacterium						į	

ALIGNMENTS

07-SEP-2001 (first entry)

AAS05219 standard; DNA; 208 BP.

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New DNA fragments from the rpoB gene of mycobacteria, useful for diagnosis and identification of many mycobacterial species by restriction fragment length polymorphism .
                                          WPI; 2001-300520/31.
                                                               Lee
                                                                           (ERUM-) ERUME BIOTECH CO LTD.
                                                                                               27-OCT-1999;
                                                                                                              27-OCT-2000; 2000WO-KR01223.
                                                                                                                                   03-MAY-2001.
                                                                                                                                                                             Non-tuberculous mycobacteria; rpoB gene fragment; NTM; HIV; PRA; PCR-restriction fragment length polymorphism analysis; ds.
                                                                                                                                                  WO200131061-A1
                                                                                                                                                                                                          Mycobacterium fortuitum rpoB gene fragment.
                                                                                                                                                                   Mycobacterium fortuitum
                                                              Ή,
                                                          Park YK,
                                                                                             99KR-0046795.
                                                          Bai G,
                                                          Kim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence for Mycobacterium fortuitum rpoB gene fragment is 1 of 24 rpoB gene fragments (AASO5201-AASO5224) from CC various Mycobacterial species. These rpoB gene fragments can be used in the diagnosis and identification of Mycobacterium species using a cc method. The method comprises obtaining a restriction fragment length polymorphism analysis (pRA) cc method. The method comprises obtaining a restriction fragment length cc amplifying and digesting the DNA fragment from the microorganism to comprise with the unidentified fragment from the microorganism to be identified and comparing the RFIP patterns from the known rpoB gene cc are useful to identify a wide range of Mycobacterium species, e.g. for cd diagnosis or to obtain epidemiological and pathogenesis information for can non-tuberculous mycobacteria (NTM) encountered in subjects infected with human immunodeficiency virus (HIV). Analysis of the rpoB gene cc with human immunodeficiency virus (HIV). Analysis of the rpoB gene cc experiment; including those difficult to distinguish by usual blochemical cc tests. Also described are oligonucleotide probes (AASO5227-AASO5242) for xx
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match 100.0%; Score 208; DB 22; Length 208; Best Local Similarity 100.0%; Pred. No. 1e-37; Matches 208; Conservative 0; Mismatches 0; Indels 0
                              (ERUM-) ERUME BIOTECH CO LTD
                                                             27-OCT-1999;
                                                                                       27-OCT-2000; 2000WO-KR01223
                                                                                                                      03-MAY-2001
                                                                                                                                                                          Mycobacterium avium.
                                                                                                                                                                                                                                             Mycobacterium avium rpoB gene fragment.
                                                                                                                                                                                                                                                                        07-SEP-2001 (first entry)
                                                                                                                                                  WO200131061-A1
                                                                                                                                                                                              Non-tuberculous mycobacteria; rpoB gene fragment; NTM; HIV; PRA; PCR-restriction fragment length polymorphism analysis; ds.
                                                                                                                                                                                                                                                                                                                                    AAS05215 standard; DNA; 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 208 BP; 43 A; 69 C; 69 G; 27 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCGAGGTCCCGGTCGAGGTGGACGACAT 208
                                                                                                                                                                                                                                                                                                                                                                                                                         TCGAGGTCCCGGTCGAGGTGGACGACAT 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCATCGAGTACCTGGTGCGCCTGCACGAGGGCCAGACCACGATGACCGTCCCCGGCGGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCATCGAGTACCTGCGCCCTGCACGACGCCAGACCACGATGACCGTCCCCGGCGCGC
      Park
      Ϋ́,
                                                            99KR-0046795
   Bai G,
   Kim S,
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Park
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NX NPI; 2001-300520/31.

XX New DNA fragments from the rpoB gene of mycobacteria, useful for production of many mycobacterial species by restriction fragment length polymorphism.

CC Production fragment length polymorphism.

CC Production fragment length polymorphism.

CC Production fragment length polymorphism.

CC Crayment is 1 of 24 rpoB gene fragments (AASO5201-AASO5224) from CC fragment is 1 of 24 rpoB gene fragments (AASO5201-AASO5224) from CC fragment is 1 of 24 rpoB gene fragments (AASO5201-AASO5224) from CC fragment for production of mycobacteriam species using a cc method. The method comprises obtaining a restriction fragment length polymorphism analysis (PRA) CC polymorphism (RFLP) pattern of the 24 rpoB gene fragments; isolating, CC amplifying and digesting the DNA fragment from the microorganism to CC are useful to identify a wide range of Mycobacterium species, e.g. for celection of appropriate therapies, including M. tuberculosis, M. leprae CC and non-tuberculous mycobacteria (NFM) encountered in subjects infected fragments is rapid, precise, simple and cost effective (only 1 pCR cost). Also described are oligonacleotide probes (AASO5227-AASO5242) for xx xx Sequence 208 BP; 44 A; 69 C; 69 G; 26 T; 0 other;
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                                                                                                                                                           Query Match 86.2%;
Best Local Similarity 91.3%;
Matches 190; Conservative
      181
            181 TCGAGGTCCCGGTCGAGGTGGACGACAT 208
                                            121
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                                                                                   61
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                                                                                                               TCGAGGTGCCGGTGGAGACCGACGACAT
                                    CATCGAGTACCTGGTGCGCCTGCACGAGGGTCAGCCCACGATGACCGTCCCGGGCGCA
                                                    CCATCGAGTACCTGGTGCGCCTGCACGAGGGCCAGACCACGATGACCGTCCCCGGCGGCG 180
                                                                                   GCCTGAACGCCGGCCAGCCGATCACGTCGTCGACTCTGACCGAGGAAGACGTCGTCGCCA 120
                                                                       GCCTGCACGCCGGTGAGCCGATCACCAGCTCGACGCTGACCGAGGAAGACGTCGTCGCCA
                                                                                                                                                             0;
                                                                                                                                                                   Score 179.2; DB
Pred. No. 2.7e-31
                                                                                                                                                           Mismatches
                                                                                                                                                                           DB 22;
                                                                                                                                                           18;
                                                                                                                                                         Indels
                                                                                                                                                                            Length
                                                                                                                                                                           208;
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                                                                                                                                                       Gaps
                                    180
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AASO5211
ID AASO5211 standard: DNA; 208 BP.
XX
AC AASO5211;
XX
O7-SEP-2001 (first entry)
XX
Wycobacterium marinum rpoB gene fragment.
XX
KW Non-tuberculous mycobacteria; rpoB gene fragment; NTM;
XX
KW PCR-restriction fragment length polymorphism analysis;
XX
YX
PD WC00131061-A1.
XX
PPD 03-MAY-2001.
XX
27-OCT-2000; 2000WO-KR01223.
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HIV; PRA; RFLP; ds.

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RESULT 4
AASO5210
ID AASO
XX AASO
AC AASO
DT 07-S
XX
DE MYCO
XX
RW PCR-
XX
OS MYCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cc method. The method comprises obtaining a restriction fragment length CC polymorphism (RFLP) pattern of the 24 rpoB gene fragments; isolating, CC amplifying and digesting the DNA fragment from the microorganism to CC inflaments with the unidentified fragment. The rpoB gene fragments CC iragments with the unidentified fragment. The rpoB gene fragments CC are useful to identify a wide range of Mycobacterium species, e.g. for CC diagnosis or to obtain epidemiological and pathogenesis information for CC and non-tuberculous mycobacteria (NYM) encountered in subjects infected CC fragments is rapid, precise, simple and cost effective (only 1 PCR CC experiment, including those difficult to distinguish by usual biochemical CC tests. Also described are oligonucleotide probes (AASO5227-AASO5242) for XX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 187; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
Mycobacterium ulcerans
                            Non-tuberculous PCR-restriction
                                                                 Mycobacterium ulcerans rpoB gene fragment.
                                                                                                   07-SEP-2001 (first entry)
                                                                                                                                      AAS05210;
                                                                                                                                                            AAS05210 standard; DNA; 208 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 208 BP; 45 A; 69 C; 68 G; 26 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence for Mycobacterium marinum rpoB gene fragment is 1 of 24 rpoB gene fragments (AAS05201-AAS05224) from various Mycobacterial species. These rpoB gene fragments can be used in the diagnosis and identification of Mycobacterium species using a finite diagnosis and identification of mycobacterium species using a
                                                                                                                                                                                                                                             181
                                                                                                                                                                                                                                                                         181
                                                                                                                                                                                                                                                                                                       121
                                                                                                                                                                                                                                                                                                                                    121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     novel PCR-restriction fragment length polymorphism analysis (PRA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 43; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New DNA fragments from the rpoB gene of mycobacteria, useful for diagnosis and identification of many mycobacterial species by restriction fragment length polymorphism -
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                                                                                                                                                                                                                                                                                                                                                                                                                             1 TCAAGGAGAAGCGCTACGACCTGGCCCGCGTGGGCCGCTACAAGGTCAACAAGAAGCTGG 60
                                                                                                                                                                                                                                                                                                                                                                                                                            _
                                                                                                                                                                                                                                                                                       CCATCGAGTACCTGGTGCGCCTGCACGAGGGGCCAGACCATGACCGTCCCGGGCGGCG 180
                                                                                                                                                                                                                                    TCGAGGTGCCGGTCGAGACCGACGACAT 208
                                                                                                                                                                                                                                                         TCGAGGTCCCGGTCGAGGTGGACGACAT 208
                                                                                                                                                                                                                                                                                                                                                GCCTGAACGCCGGCCAGCCGATCACGTCGTCGACTCTGACCGAGGAAGACGTCGTCGCCA 120
                                                                                                                                                                                                                                                                                                                                                                                                            TCAAGGAGAAGCGCTACGACCTGGCCCGGGTGGGCCGGTACAAGGTCAACAAGAAGCTCG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                    mycobacteria; rpoB gene fragment; NTM;
fragment length polymorphism analysis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99KR-0046795
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           83.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 174.4; DB 22;
Pred. No. 3.1e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cho
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Park HJ
                      ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     208;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                   RFLP
                                                                                                                                                                                                                                                                                                                                                  120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
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Query Match Best Local S Matches 186

186;

Conservative

0;

Similarity

83.1%;

Score 172.8; | Pred. No. 7.1e 0; Mismatches

.le-30 DB 22;

Indels Length

0

60

208; 0, Gaps

RESULT 5
AAS05201
ID AASI
XX
AC AASI
XX

AAS05201 standard; DNA; 208 BP

07-SEP-2001

(first entry)

밁 Š В Ş 밁 Ş 밁 Ş

181 TCGAGGTCCCGGTCGAGGTGGACGACAT 181 TCGAGGTGCCGGTCGAGACCGACGACAT 208

CCATCGAATACCTGGTCCGCTTGCACGAGGGCCAGACCGCGATGACCGCTCCGGGCGGTG CCATCGAGTACCTGGTGCGCCTGCACGAGGGGCCAGACGATGACCGTCCCCGGCGGCG

180

121 121

61 61

GCCTGAACGCCGGCCAGCCGATCACGTCGTCGACTCTGACCGAGGAAGACGTCGTCGCCA 120

GCCTGAACGCCGGCCAGCCCATCACCAGCTCGACGCTGACCGAGGAAGACCTTCGTCGCCA

TCAAGGAGAAGCGCTACGACCTGGGCCGGGTGGGCCGCTACAAGGTCAACAAGAAGCTGG TCAAGGAGAAGCGCTACGACCTGGCTCGCGTGGTCGGTACAAGGTCAACAAGAAGCTCG

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method. The method comprises obtaining a restriction fragment length CC polymorphism (RPLP) pattern of the 24 rpoB gene fragments; isolating, CC amplifying and digesting the DNA fragment from the microorganism to be identified and comparing the RPLP patterns from the microorganism to CC fragments with the unidentified fragment. The rpoB gene fragments CC are useful to identify a wide range of Mycobacterium species, e.g. for CC selection of appropriate therapies, including M. tuberculous mycobacteria (NTM) encountered in subjects information for CC and non-tuberculous mycobacteria (NTM) encountered in subjects infected fragments is rapid, precise, simple and cost effective (only 1 pCR CC required), and can differentiate between many species in a single CC tests. Also described are oligonuclectide probes (AAS05227-AAS05242) for XX
     Sequence 208 BP; 45 A; 68 C; 67 G;
                                                                                                                                                                                                                                                                                     The present sequence for Mycobacterium ulcerans rpoB gene fragment is 1 of 24 rpoB gene fragments (AAS05201-AAS05224) from various Mycobacterial species. These rpoB gene fragments can be used in the diagnosis and identification of Mycobacterium species using a novel PCR-restriction fragment length polymorphism analysis (PRA)
                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 43; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                       restriction fragment length polymorphism
                                                                                                                                                                                                                                                                                                                                                                                                                                                  New DNA fragments from the rpoB gene of mycobacteria, useful for diagnosis and identification of many mycobacterial species by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lee H,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bai G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kim S,
28 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cho s,
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RESULT 6
AAS05202
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                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Sim
Matches 184;
                                                                                                                                                                                                                                                                                                                                                                                            Sequence 208 BP; 46
                                                        181 CCGAGGTGCCGGTTGAGACCGACGACAT 208
                                                                                             181
                                                                                                                              121
                                                                                                                                                              121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 40; 50pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New DNA fragments from the rpoB gene of mycobacteria, useful for diagnosis and identification of many mycobacterial species by restriction fragment length polymorphism .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mycobacterium gordonae type I.
                                                                                                                                                                                              61
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PCR-restriction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mycobacterium
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                                                                                                                                                                                                                                                             -
                                                                               TCGAGGTCCCGGTCGAGGTGGACGACAT 208
                                                                                                                                                                                                 GCCTGAACGCCGGCCAGCCGATCACGTCGTCGACTCTGACCGAGGAAGACGTCGTCGCCA 120
                                                                                                                                     CCATCGAGTACCTGGTGCGCCTGCACGAGGGCCAGACCACGATGACCGTCCCCGGGGGGG 180
                                                                                                                                                                                 GCCTGCACGTCGGCGATCCGATCACCAGCTCCACGCTGACCGAGGAAGACGTCGTCGCCA
                                                                                                                                                                                                                                                 CCATCGAGTACCTGGTCCGCCTGCACGAGGGCCCAGCACACGATGACCGTCCCGGGCGGCA 180
                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gordonae type I rpoB gene fragment.
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                                                                                                                                                                                                                                                                                                                                                                                       A; 71 C; 65 G;
                                                                                                                                                                                                                                                                                                                                       81.5%;
88.5%;
                                                                                                                                                                                                                                                                                                                    Score 169.6;
Pred. No. 3.7e
0; Mismatches
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                                                                                                                                                                                                                                                                                                                    3.7e-29;
nes 24;
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                                                                                                                                                                                                                                                                                                                    0;
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Ŷ В Q В ş В

181 TCGAGGTCCCGGTCGAGGTGGACGACAT 208

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                                                                                                                                                                                                                  The present sequence for Mycobacterium gordonae type II rpoB gene CC fragment is 1 of 24 rpoB gene fragments (AASO5201-AASO5224) from CC various Mycobacterial species. These rpoB gene fragments can be used in the diagnosis and identification of Mycobacterium species using a CC method. The method comprises obtaining a restriction fragment length polymorphism analysis (PRA) CC polymorphism (RPLP) pattern of the 24 rpoB gene fragments; isolating, CC polymorphism and digesting the DNA fragment from the microorganism to CC amplifying and digesting the DNA fragment from the known rpoB gene identified and comparing the RPLP patterns from the known rpoB gene CC are useful to identify a wide range of Mycobacterium species, e.g. for CC diagnosis or to obtain epidemiological and pathogenesis information for CC selection of appropriate therapies, including M. tuberculosis, M. leprae with human immunodeficiency virus (HIV). Analysis of the rpoB gene CC required), and can differentiate between many species in a single CC tests. Also described are oligonucleotide probes (AASO5227-AASO5242) for XX
                                                                                                                                                     Best Local Sin
Matches 184;
121
                                                                                                                                                                                                      Sequence 208 BP; 45 A; 62 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New DNA fragments from the rpoB gene of mycobacteria, useful for diagnosis and identification of many mycobacterial species by restriction fragment length polymorphism -
                       121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 40; 50pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mycobacterium gordonae type II.
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PCR-restriction
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                                                                          61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAS05202 standard; DNA; 208
                                                                                       CCATCGAGTACCTGGTGCGCCTGCACGACGGCCAGACCACGATGACCGTCCCCGGCGGCG
                                    GCCTGAACGCCGGCCAGCCGATCACGTCGTCGACTCTGACCGAGGAAGACGTCGTCGCCA 120
                                                                                                                                                                Similarity
                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gordonae type II rpoB gene fragment
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mycobacteria; rpoB gene fragment; NTM;
fragment length polymorphism analysis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bai G,
                                                                                                                                                              81.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kim S,
                                                                                                                                                   0;
                                                                                                                                               Score 169.6; DB 22;
Pred. No. 3.7e-29;
0; Mismatches 24;
                                                                                                                                                                                                73 G; 28 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kim Y,
                                                                                                                                              24;
                                                                                                                                               Indels
                                                                                                                                                                    Length
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                                                                                                                                            0,
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              180
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                                                                                                                                                                              The present sequence for Mycobacterium kansasii rpoB gene CC fragment is 1 of 24 rpoB gene fragments (AASO5201-AASO5224) from CC various Mycobacterial species. These rpoB gene fragments can be used in the diagnosis and identification of Mycobacterium species using a convel pcR-restriction fragment length polymorphism analysis (pRA) cc method. The method comprises obtaining a restriction fragment length cc polymorphism (RRLP) pattern of the 24 rpoB gene fragments; isolating, cc amplifying and digesting the DNA fragment from the known rpoB gene cc are useful to identify a wide range of Mycobacterium species, e.g. for cc diagnosis or to obtain epidemiological and pathogenesis information for and non-tuberculous mycobacteria (NTM) encountered in subjects infected fragments is rapid, precise, simple and cost effective (only 1 pcR crequired), and can differentiate between many species in a single cc estes. Also described are oligonucleotide probes (AASO5227-AASO5242) for xx
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                                                                                                                   Matches
                                                                                                                              Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 42; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New DNA fragments from the rpoB gene of mycobacteria, useful for diagnosis and identification of many mycobacterial species by restriction fragment length polymorphism .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ERUM-) ERUME BIOTECH CO LTD.
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            61
              61 GCCTGAACGCCGGCCAGCCGATCACGTCGACTCTGACCCGAGGAAGACGTCGTCGCCA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-300520/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-OCT-1999; 99KR-0046795.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Non-tuberculous mycobacteria; rpoB gene fragment; NTM; HIV; PRA; RFLP; PCR-restriction fragment length polymorphism analysis; ds.
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                                                                                        GCCTGAACACCAATCATCCGATCACCACGACGACGCTGACCGAAGAAGACGTCGTCGCCA 120
                                                                                                                           Similarity
                                                                                                                                                                    208
                                                                                                              Conservative
                                                                                                                                                                  BP; 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  kansasii rpoB gene fragment.
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                                                                                                                                                           A; 65 C; 65 G; 27 T; 0 other;
                                                                                                                        80.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kim S,
                                                                                                              0;
                                                                                                                   Score 168; DB 22;
Pred. No. 8.3e-29;
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                                                                                                            Mismatches
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                                                                                                                                 Length 208;
                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Park HJ;
                                                                                                         0
                                                                                                     Gaps
                                                                                                      0
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1 TCAAGGAGAAGCGGTACGACCTGGCCCGCGTGGGCCGCTACAAGGTCAACAAGAAGCTGG 60

Matches Query Match Best Local

Similarity

48 A; 71 C; 80.8%;

64 G;

25 T; 0 other;

Conservative

0

Mismatches

25;

Indels

0, Gaps

0;

Score 168; Pred. No. 1

; DB 22; Length 208, 8.3e-29;

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The present sequence for Mycobacterium celatum rpoB gene CC fragment is 1 of 24 rpoB gene fragments (AAS05221-AAS05224) from CC various Mycobacterial Species. These rpoB gene fragments can be used in the diagnosis and identification of Mycobacterium species using a method. The method comprises obtaining a restriction fragment length polymorphism analysis (PRA) cc method. The method comprises obtaining a restriction fragment length CC amplifying and digesting the DNA fragment from the microorganism to be identified and comparing the RFLP patterns from the known rpoB gene are useful to identify a wide range of Mycobacterium species, e.g. for CC diagnosis or to obtain epidemiological and pathogenesis information for Selection of appropriate therapies, including M. tuberculosis, M. leprae with human immunodeficiency virus (HTV). Analysis of the rpoB gene CC required), and can differentiate between many species in a single CC required, and can differentiate between many species in a single CC tests. Also described are oligonuclectide probes (AAS05227-AAS05242) for XX
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AAS05217
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 Sequence
                                                                                                                                                                                                                                                                                                                    Claim 1; Page 45; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                   New DNA fragments from the rpoB gene of mycobacteria, useful for diagnosis and identification of many mycobacterial species by
                                                                                                                                                                                                                                                                                                                                             restriction fragment length polymorphism
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-MAY-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mycobacterium celatum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Non-tuberculous mycobacteria; rpPCR-restriction fragment length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mycobacterium celatum rpoB gene fragment.
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208 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Park YK, Bai G,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rpoB gene fragment; NTM;
th polymorphism analysis;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Cho s,
                                                                                                                                                                                                                                                                                                                                                                                                                                 Kim Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                Park HJ;
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RESULT 9
AASO5205
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                                        CC fragment is 1 of 24 rpoB gene fragments (AASOS201-AASOS224) from CC various Mycobacterial species. These rpoB gene fragments can be used CC in the diagnosis and identification of Mycobacterian species using a CC movel PCR-restriction fragment length polymorphism analysis (PRA) CC method. The method comprises obtaining a restriction fragment length CC polymorphism (RFLP) pattern of the 24 rpoB gene fragments; isolating, CC polymorphism (RFLP) pattern of the 24 rpoB gene fragments; isolating, CC amplifying and digesting the DNA fragment from the microorganism to CC diagnosis with the unidentified fragment. The rpoB gene fragments for CC are useful to identify a wide range of Mycobacterium species, e.g. for CC diagnosis or to obtain epidemiological and pathogenesis information for CC selection of appropriate therapies, including M. tuberculosis, M. leprae and non-tuberculous mycobacteria (MYM) encountered in subjects infected fragments is rapid, precise, simple and cost effective (only 1 PCR required), and can differentiate between many species in a single tests. Also described are oligonucleotide probes (AASOS227-AASOS242) for detecting specific Mycobacterial species.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 41; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New DNA fragments from the rpoB gene of mycobacteria, useful for diagnosis and identification of many mycobacterial species by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            restriction fragment length polymorphism
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Sequence

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The present sequence for Mycobacterium terrae rpoB gene C fragment is 1 of 24 rpoB gene fragments (AAS05201-AAS05224) from CC various Mycobacterial Species. These rpoB gene fragments can be used in the diagnosis and identification of Mycobacterium species using a CC movel PCR-restriction fragment length polymorphism analysis (PRA) CC method. The method comprises obtaining a restriction fragment length CC polymorphism (RRILP) pattern of the 24 rpoB gene fragments; isolating, CC polymorphism (RRILP) pattern of the 24 rpoB gene fragments; isolating, CC polymorphism (RRILP) pattern of the 27 rpoB gene fragments; isolating, CC fragments with the unidentified fragment from the known rpoB gene CC are useful to identify a wide range of Mycobacterium species, e.g. for CC diagnosis or to obtain epidemiological and pathogenesis information for CC selection of appropriate therapies, including M. tuberculosis, M. leprae CC and non-tuberculous mycobacteria (NTM) encountered in subjects infected CC with human immunodeficiency virus (HIV). Analysis of the rpoB gene CC fragments is rapid, precise, simple and cost effective (only 1 pCR)
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Best Local Similarity
                                                                                                                                                                                                                                                                                                Claim 1; Page 42; 50pp; English.
                                                                                                                                                                                                                                                                                                                      New DNA fragments from the rpoB gene of mycobacteria, useful for diagnosis and identification of many mycobacterial species by restriction fragment length polymorphism
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Park YK, Bai G,
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Cho
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RESULT 11
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Best Local
The present sequence for Mycobacterium bovis rpoB gene fragment is 1 of 24 poB gene fragments (AAS05201-AAS05224) from various Mycobacterial species. These rpoB gene fragments can be used in the diagnosis and identification of Mycobacterium species using a novel PCR-restriction fragment length polymorphism analysis (PRA) a method. The method comprises obtaining a restriction fragment length polymorphism (RFLP) pattern of the 24 ppbB gene fragment; isolating, amplifying and digesting the DNA fragment from the microorganism to be identified and comparing the RFLP patterns from the known rpoB gene fragments.
                                                                                                                                                                                                                                                                      Claim 1; Page 45; 50pp; English.
                                                                                                                                                                                                                                                                                                           New DNA fragments from the rpoB gene of mycobacteria, useful for diagnosis and identification of many mycobacterial species by restriction fragment length polymorphism .
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Best Local :
         misc_feature
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                                                                                                                                                                                                                                                                                                Mycobacterium
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                                                                                                                                                                                                                                                                                                                                                                                    15-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                AAT09676 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                are useful to identify a wide range of Mycobacterium species, e.g. for diagnosis or to obtain epidemiological and pathogenesis information for selection of appropriate therapies, including M. tuberculosis, M. leprae and non-tuberculous mycobacteria (NTM) encountered in subjects infected with human immunodeficiency virus (HIV). Analysis of the rpoB gene required), and can differentiate between many species in a single experiment, including those difficult to distinguish by usual biochemical tests. Also described are oligonucleotide probes (AASO5227-AASO5242) for distortion of the properties of the probes (AASO5227-AASO5242) for distinguish by usual biochemical detecting specific Mycobacterial species.
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82; Conservative
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                                                                                                                                                                                                                                                                                                                disease diagnosis; oligonucleotide;
ain reaction; DNA amplification; rpob
                                                                                                                                                                                                                                                                                                                                                  tuberculosis rpoB gene DNA sequence
                                                                                                                                                                                                                                                                                              tuberculosis
   /*tag= g
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433..434
                                         /*tag= f
/note= "primer
372..373
                                                                                                                                                                                                                     /note= "primer |
226. 345
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/note= "primer ;
348..373
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226..240
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354..373
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            tuberculosis signature
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Pred. No. 1.9
                                                                                     rpo105
                                                                                                                         rpo95"
                                                                                                                                                                                               DDIDHL"
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26;
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This oligonucleotide DNA primer is specific for Mycobacterium tuberculosis, and may be used to amplify a sample DNA by targeting a portion of the gene encoding rpoB. The 1st several bases comprise nonhybridizing tail consisting of filler bases followed by a restriction site incorporated to facilitate cloning using the amplicon at a later date, if desired. The remaining bases hybridize to bacterial rpoB DNA. The method provides for the detection of M. susceptibility, particularly to rifamycin. The method can provide often greater than 95% sensitivity and 100% specificity. The biological sample is a fluid or tissue sample from a human.
                                                                                                                              Disclosure; Fig.3; 54pp; English.
                                                                                                                                                    Detection of Mycobacterium tuberculosis - with a primer set that targets portions o
                                                                                                                                                                                WPI; 1996-030581/03
                                                                                                                                                                                                     Felmlee TA,
Young KKY;
                                                                                                                                                                                                                                                            26-MAY-1994;
                                                                                                                                                                                                                                                                              26-MAY-1995;
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952..966
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536..562
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486
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438
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             signature
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                                                                                                                                            by amplifying sample DNA the gene encoding rpoB.
                                                                                                                                                                                                        Whelen
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Sequence

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156 T; 0 other;

This invention relates to a method for identifying a nucleotide or polypeptide sequence that may be a drug target, or essential for growth represent DNA encoding proteins. Polynucleotide sequences AAH51947 - AAH52092 tuberculosis proteins which are potential drug targets. The DNA and protein sequences are used to illustrate the method of the invention. The method involves providing an unknown nucleotide or polypeptide sequences, algorithm capable of analysing a functional relationship between characterising the function of nucleic acids and polypeptides sequences. The method is useful for useful as a target for a drug or essential for the growth or viability of an organism

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RESULT 1:
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Best Local
                                                                                                                                   Identifying nucleotide or polypeptide sequence for use as drug target, involves providing algorithm that analyzes a functional relationship between nucleotide or polypeptide sequences, and comparing the
                                                                                                                   Disclosure; Page 68-69;
                                                                                                                                                                                                                                  01-FEB-2000;
                                                                                                                                                                                                                                                                                                                                 Drug
                                                                                                                                                                                                                    (REGC ) UNIV
                                                                                                                                                                                                                                                                                  17-MAY-2001
                                                                                                                                                                                                                                                                                                 WO200135317-A1
                                                                                                                                                                                                                                                                                                                                         Mycobacterium tuberculosis potential drug target gene
                                                                                                                                                                                                                                          12-NOV-1999;
12-NOV-1999;
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                                                                                                                                                                                                                                                                                                                 Mycobacterium
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DB; AAG81125.
                                                                                                                                                                                                                                                                                                                                target;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCGAGGTCCCGGTCGAGGTGGACGACAT 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCATCGAGTACCTGGTGCGCCTGCACGAGGGCCAGACCATGATGACCGTCCCCGGCGGCG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                     TCGAGGTGCCGGTGGAAACCGACGACAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGCTGCATGTCGGCGAGCCCATCACGTCGTCGACGCTGACCGAAGAAGACGTCGTGGCCA 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCATCGAATATCTGGTCCGCTTGCACGAGGGTCAGACCACGATGACCGTTCCGGGCGGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCCTGAACGCCGGCCAGCCGATCACGTCGTCGACTCTGACCGAGGAAGACGTCGTCGCCA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                   'n
                                                                                                                                                                                                                                99US-0165086.
99US-0165124.
2000US-0179531.
                                                                                                                                                                                                                 CALIFORNIA
                                                                                                                                                                                                                                                                                                                          growth; organism viability; characterisation;
                                                                                                                                                                                                                                                                 2000WO-US31152
                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                 Rotstein
                                                                                                                                                                                                                                                                                                                tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                              DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            80.0%;
                                                                                                                207pp;
                                                                                                                                                                                                 SH,
                                                                                                                                                                                                                                                                                                                                                                                               3519
                                                                                                                                                                                                Marcotte
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                                                                                                                                                                                                                                                                                                                                                                                               ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 166.4;
Pred. No. 1.
                                                                                                                 English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                ΞX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .9e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 970
                                                                                                                                                                                                                                                                                                                                            SEQ
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Query Match
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                                                                                                                                                                                                                                                                                                                      61
                                                                                                                                                                                                                                                                                                                                                                  121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 15
            $$$$$$$$$$$$$$$$$$$$$$$
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes a method for generating a repertory of nucleic acids of tuf, fus, atpD and/or reca genes from which probes and/or primers are derived. The method comprises amplifying the nucleic acids of determined algal, archaeal, bacterial, fungal and parasitical species with a combination of defined primer pairs. The method can be used for producing probes and/or primers for detecting one or more related microorganisms e.g. algae, archaea, bacteria, fungi and parasites, for universal detection and for specific and ubiquitous detection and identification of an algal, archaeal, bacterial, fungal
                                                                                                                           Nucleic acid sequences are used to generate universal probes and primers which can be used to identify and detect the presence of algal, archaeal, bacterial, fungal and parasitical species in a test sample -
                                                                                                                                                         121 CCATCGAGTACCTGGTGCGCCTGCAGGGCCCAGACCACGATGACCGTCCCCGGCGGCG 180
                                                                               61 GCCTGAACGCCGGCCAGCCGATCACGTCGACTCTGACCGAGGAAGACGTCGTCGCCA 120
                                                                  1 TCAAGGAGAAGGGCTACGACCTGGCCGGTGGGCCGCTACAAGGTCAACAAGAAGGTGG 60
                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                           Species specific; genus specific; family specific; probe; detection; identification; algal; archaeal; bacterial; fungal; parasitical; microorganism; diagnosis; translation elongation factor fu; toxin; translation elongation factor G. RecA recombinase; resistance; catalytic subunit of proton-translocating ATPase; antimicrobial;
                              Length 3519;
                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouellette M;
                                                                                                                                                                                                                                                                                                                                                      Mycobacterium tuberculosis nucleotide sequence SEQ ID NO:2072.
                                                 Indels
Sequence 3519 BP; 675 A; 1081 C; 1183 G; 580 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Menard C,
                           DB 22;
                                                 26;
              80.0%; Score 166.4; DB 2.
                                      Pred. No. 1.9e-
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 1478-1479; 1580pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Huletsky A,
                                                                                                                                                                                                                    1064 TCGAGGTGCCGGTGGAAACCGACGACT 1091
                                                                                                                                                                                                       181 TCGAGGTCCCGGTCGAGGTGGACGACAT 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (INFE-) INFECTIO DIAGNOSTIC (IDI) INC.
                                                                                                                                                                                                                                                                                    AAH02079 standard; DNA; 3534 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-SEP-2000; 2000WO-CA01150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-SEP-1999; 99CA-2283458
19-MAY-2000; 2000CA-2307010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Boissinot M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                   (first entry)
                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                     /accine; primer; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-245006/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bergeron MG, Bolss.
                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200123604-A2.
                                   Best Local Sim
Matches 182;
                                                                                                                                                                                                                                                                                                                                  24-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-APR-2001
                      Query Match
                                                                                                                                                                                                                                                                                                            AAH02079;
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and parasitical species, genus, family and group. A nucleic acid (1)

cobtained using the method of the invention can be used for the universal
detection of any bacterium, fungus or parasite in a sample and for the
detection of at least one antimicrobial agent resistance gene or at
least one toxin gene. haxA nucleic acids are used for the specific and
tubiquitous detection and for identification of Streptococcus pneumoniae.

(1) can be used to design a therapeutic agent which is effective against
which can be detected include Abiotrophia adiacens, Bordetaila sp.,
which can be detected include Abiotrophia adiacens, Bordetaila sp.,
Mycobacteriaceae family, Pseudomonads group, Escherichia coli,
Nycobacteriaceae family, Pseudomonads group, Streptococcus as p.,
Nycobacteriaceae family, Pseudomonads group, Streptococcus as p.,
Drovides faster results than substrate specificity tests as results can
be determined in an hour and improved accuracy is also acideved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAH00010 to AAH002304 represent nucleotide sequences and primers/probes which are given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1022 CCATCGAATATCTGGTCCCCTTGCACGAGGTCAGACCACGATGACCGTTCCGGGCGCG 1081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCCTGAACGCCGGCCAGCCGATCACGTCGTCGACTCTGACCGAGGAAGACGTCGTCGCCA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCATCGAGTACCTGGTGCGCCTGCACGAGGCCAGACCACGATGACCGTCCCCGGCGCG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 TCAAGGAGAAGCGCTACGACCTGGCCCGCGTGGGCCGCTACAAGGTCAACAAGAAGCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 22; Length 3534;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mycobacterium tuberculosis; rpoB; RNA polymerase beta subunit;
rifampin resistance; mutation detection; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80.0%; Score 166.4; DB 22; Length
87.5%; Pred. No. 1.9e-28;
iive 0; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3534 BP; 679 A; 1081 C; 1188 G; 586 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1082 TCGAGGTGCCGGTGGAAACCGACGAT 1109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 TCGAGGTCCCGGTCGAGGTGGACAT 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mycobacterium tuberculosis rpoB gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ВЪ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAA74651 standard; DNA; 3853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99WO-US30377
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 182; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (DADE-) DADE BEHRING INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kurn N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200043546-A2.
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The present sequence is the rpoB gene from Mycobacterium tuberculosis. Rifamphin resistance is largely associated with point mutations localised in a small core region of 81 base pairs in the rpoB gene, which encodes the RNA polymerase beta subunit. To detect a mutation, a complex is formed comprising a first sequence representing the predetermined region of the gene of the organism and a second sequence representing the corresponding region of the gene of the wild type organism in double stranded form. Each member of at least one pair of non-complementary strands within the complex has a label. The association of the labels in the complex is related to the presence of the mutation. The presence of the mutation is related to the drug resistance of the strain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCATCGAGTACCTGGTGCGCCTGCACGAGGGCCAGACCACGATGACCGTCCCCGGCGGCG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 80.0%; Score 166.4; DB 21; Length Best Local Similarity 87.5%; Pred. No. 1.9e-28; Matches 182; Conservative 0; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3853 BP; 723 A; 1173 C; 1293 G; 664 T; 0 other;
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           Example 1; Fig 4; 86pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121
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Search completed: November 12, 2002, 16:50:23 Job time: 143.222 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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**Reading the completion of th	OM nucleic - nucleic search, using sw mode	model
US-09-697-123B-19 score: 208 table: Incaeggagaggctacgacccggtcgaggtggacgacat table: IDENTITY NUC Gapop 10.0 , Gapex 1.0 2054640 seqs, 14551402878 residues mber of hits satisfying chosen parameters: 4109280 BB seq length: 0 BB seq length:	on: November 12, 2002, 16	6; Search time 636.023 (Without alignments) 9517.553 Million cell
table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0 1	US-09-697-123B-19 t score: 208 ce: 1 tcaaggagaagcgctacgac.	ccggtcgaggtggacgacat
## 1651402878 residues mber of hits satisfying chosen parameters: DB seq length: 0 DB seq length: 200000000 Cessing: Minimum Match 100% Listing first 45 summaries GenEmbl:* 1 gb_ba:* 2 gb_htg:* 3 gb_lin:* 4: gb_ph:* 5: gb_ph:* 6: gb_ppi:* 11: gb_pai:* 7: gb_ph:* 8: gb_pi:* 11: gb_pi:* 12: gb_ri:* 13: gb_vi:* 14: gb_pi:* 15: gb_vi:* 16: em_ba:* 17: em_lun:* 18: em_lun:* 19: em_ov:* 20: em_ov:* 21: em_ov:* 22: em_lun:* 23: em_lun:* 24: em_lun:* 25: em_lun:* 26: em_lun:* 27: em_lun:* 28: em_lun:* 29: em_lun:* 21: em_lun:* 23: em_lun:* 24: em_lun:* 25: em_lun:* 26: em_lun:* 27: em_lun:* 28: em_lun:* 29: em_lun:* 31: em_lun:* 31: em_lun:* 32: em_lun:* 33: em_lun:* 34: em_lun:* 35: em_lun:* 36: em_lun:* 37: em_lun:* 38: em_lun:* 39: em_lun:* 41: em_lun:*	table: IDENTITY_NUC Gapop 10.0 ,	
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ø is the number of results predicted by chance to have . 9 Pred.

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AJ18813 Mycobacte
AJ18813 Mycobacte
AJ18815 Mycobacte
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AJ11839 Sequence AXIII339 Sequence U12205 Mycobacteri L27989 Mycobacteri AE006964 Mycobacteri AR06747 Sequence 214314 M. Leprae ge AL583923 Mycobacte AF242549 Amycolato AXI20631 Sequence AXI20631 Sequence U24494 Mycobacter1 score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. SUMMARIES MSU24494 MTU318818 MTU318819 MTU318815 MTU318817 MTU318817 MTU318814 MTU318816 AX111339 MTU12205 MSGRPOB AE006964 DB 3752 610 610 616 618 618 637 637 637 970 3853 19354 19352 19770 19473 3447 348950 Length Query 171.2 1166.4 Result No.

MTCI376 AR067447 MLB1790G MLEPRTN7

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AL772413 Oryza sat AL772413 Oryza sat U42212 Streptomyce AF171937 Suid herp 104901 Sequence 6 AE005722 Caulobact AE005722 Caulobact AE00299 Mesorhizo 230344 S. ambofacie X62287 S. coelicolo AL353862 Streptomy AY034826 Curvillari AY102669 Drosophil ALIGOAR STREETONIA ALG4070 RAISTONIA ABO70951 STREETONY Y19223 Thermus aqu X9423 S.f.mosus r AL391588 Streetony AL591787 Sinorhizo U04877 Streetomyce SCCB12 SME591787 SVU04837 CNSORC9R CNSO7YP9 SCU42212 AF171937 104901 AE005722 ALC46086 AP002999 SARECAG AX120631 AP005275 AX127144 SRRECAGEN AB070951 TAQ19223 AL646073 3941 32805 3495 349960 349960 204050 204050 32913 32913 329105 1416 329105 329105 135378 135378 1352 1736 13652 12112 92509 346294 3488 37898 1440 2206 9302 886.8 511.2 511.2 447.2 47.2 446.6 45.8 43.

ALIGNMENTS

MSU24494 3752 bp DNA linear BCT 02-MAR-2000 Mycobacterium smegmatis DNA polymerase (rpoB) gene, complete cds. U24494 Mycobacterium smegmatis.
Mycobacterium smegmatis
Mycobacterius; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycotacles; Corynebacterineae; Mycobacteriaceae;
Mycobacterium.
1 (bases 1 to 3752)
Hetherington,S.V., Watson,A.S. and Patrick,C.C.
Sequence and analysis of the rpob gene of Mycobacterium smegmatis GI:790347 U24494.1 RESULT 1
MSU24494
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SOURCE
ORGANISM REFERENCE AUTHORS TITLE

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2 (bases
Herrera, L.
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GRVKVYEAIVKGENIPEPGIPESFKVLLKELQSLCLNVEVLSSDGRAIEMROGDDEDL
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Antimicrob. Agents Chemother. 39 (9), 2164-2166 (1995)
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Hetherington,S.V.
Direct Submission
Submitted (11-APR-1995) Seth V. Hetherington,
St. Jude Children's Research Hospital, 332 N.
TN 38101, USA
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/organism="Mycobacterium smegmatis"
/db_xref="taxon:1772"
194. .3703
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Pred. No. 4.6e
0; Mismatches
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194. .3703
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                                                                                                                                                                                          Herrera,L., Jimenez,M.S. and Saez,J.A.
Molecular analysis of rifampin-resistant Mycobacterium tuberculosis
isolated in Spain (1996-2001). Description of new alleles into rpob
gene and review
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gene for RNA polymerase
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AJ318818
AJ318818.1 GI:22208412
RNA polymerase beta subunit; rpoB gene.
Mycobacterium tuberculosis.
Mycobacterium tuberculosis.
Addinobacterium tuberculosis
Corynebacteriae: Actinobacteria; Actinobacteriae: Mycobacterium
tuberculosis complex.
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Submitted (07-AUG-2001) Herrera L., Servicio Bacteriologia,
Nacional Microbiologia., Ctra. Majadahonda-Pozuelo, Km 2.5,
Majadahonda. Madrid. 28220, SPAIN
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Mycobacterium tuberculosis.
Mycobacterium tuberculosis
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
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rpoB
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Pred. No. 3.8e-18;
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AJ318819 GI:22208414
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/isolate="1415-97"
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87.5%;
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QLSQTIFMDQNNELSGLTHKRRLSALGPGGLSRERAGLEVRDVHP"

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Molecular analysis of rifampin-resistant Mycobacterium tuberculosis
isolated in Spain (1996-2001). Description of new alleles into rpob
gene and review
                                                                        Direct Submission
Submitted (07-AUG-2001) Herrera L., Servicio Bacteriologia, Centro
Nacional Microbiologia., Ctra. Majadahonda-Pozuelo, Km 2.5,
Majadahonda. Madrid. 28220, SPAIN
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Submitted (07-AUG-2001) Herrera L., Servicio Bacteriologia, Centro
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Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium
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gene for RNA polymerase
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Pred. No. 3.8e-18;
0; Mismatches 26;
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rpoB
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beta subunit, isolate 2540-97.

    .616
    /organism="Mycobacterium"

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/db_xref="taxon:1773"
                                                                                                                                              Location/Qualifiers
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Mycobacterium tuberculosis
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                                                                                                                                                                                                                                                                               /gene="rpoB"
                                                                                                                                                                                                                                                  /gene="rpoB"
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Best Local Similarity 87.5%;
Matches 182; Conservative
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                                         (bases 1 to 616)
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          and review
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2 (bases 1
Herrera,L.
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OPSQFMGQNNPLSGTTHKRRLSALGPGGLSRERAGLEVRDVHP"
                                                Herrera,L., Jimenez,M.S. and Saez,J.A.
Molecular analysis of rifampin-resistant Mycobacterium tuberculosis isolated in Spain (1996-2001). Description of new alleles into rpos gene and review
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Molecular analysis of rifampin-resistant Mycobacterium tuberculosis
isolated in Spain (1996-2001). Description of new alleles into rpob
                                                                                                                                                                  Direct Submission
Submitted (07-AUG-2001) Herrera L., Servicio Bacteriologia, Centro
Nacional Microbiologia., Ctra. Majadahonda-Pozuelo, Km 2.5,
Majadahonda. Madrid. 28220, SPAIN
Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium
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AJ318813.1 GI:22208402
RNA polymerase beta subunit; rpoB gene.
Mycobacterium tuberculosis.
Mycobacterium tuberculosis
Bacteria; Actinobacteria; Actinobacterium; Mycobacterium
Corynebacterium; Mycobacterium
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                                                                                                                                                                                                                                                                             tuberculosis"
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Pred. No. 3.8e-18;
0; Mismatches 26;
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Mycobacterium tuberculosis partial
beta subunit, isolate 1763-97.
                                                                                                                                                                                                                                                                           /organism="Mycobacterium
                                                                                                                                                                                                                                                                                                            /db_xref-"taxon:1773"
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                                                                                                                                                                                                                                                                                         /isolate="1417-97
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sal Similarity 87.5%;
182; Conservative
                  tuberculosis complex
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Matches 16
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Gaps

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tuberculosis
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Pred. No. 3.8e-18;
0; Mismatches 26;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        633 bp
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1. .618
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                                    /gene="rpoB"
<1. .>618
                                                                                                                                                                                                                                                                  Ouery Match
Best Local Similarity 87.5%;
Matches 182; Conservative
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<1. .>618

<1. .>618

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/gene="rpoB"

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FFGTSQLSQFMDONNPLSGLTHKRRLLALGPGGLSRERAGLEVRDV"
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gene for RNA polymerase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (07-AUG-2001) Herrera L., Servicio Bacteriologia, Centro
Nacional Microbiologia., Ctra. Majadahonda-Pozuelo, Km 2.5,
Majadahonda. Madrid. 28220, SPAIN
Location/Qualifiers
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RNA polymerase beta subunit; rpoB gene.
RNA polymerase beta subunit; rpoB gene.
Mycobacterium tuberculosis
Bacteria; Actinobacteria; Actinobacteria; Actinomycetales;
Corynebacterinese; Mycobacteriaceae; Mycobacterium; Mycobacterium
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Nacional Microbiologia., Ctra. Majadahonda-Pozuelo,
Majadahonda. Madrid. 28220, SPAIN
Location/Qualiflers
1. .618
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                                                                tuberculosis
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/isolate-"2348-98"
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                                                                                                                                                                                                                                                                                                                                                                                    26;
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                                              1. 618
/organism="Mycobacterium tu
/isolate="2540-97"
/db_xref="taxon:1773"
1. 618
                                                                                                                                                                                                                                                                                                                                                       Score 166.4;
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beta subunit, isolate 2348-98.
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llarity 87.5%;
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Matches 182;
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AUTHORS
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                              FEATURES
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RESULT LOCUS

g ò g ò q ò q

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FFGNRLRTVGELIONGIRVGASRMERVVRENTTQDVEATTPQTLINIRPVVAAIKE
FFGTSAPSFGGOONTLEGTHYRRLSALGPGGLSRERAGLEVRDV"
192 c 207 g 95 t
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Molecular analysis of rifampin-resistant Mycobacterium tuberculosis isolated in Spain (1996-2001). Description of new alleles into rpos gene and review
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (07-AUG-2001) Herrera L., Servicio Bacteriologia, Centro
Nacional Microbiologia., Ctra. Majadahonda-Pozuelo, Km 2.5,
Majadahonda. Madrid. 28220, SPAIN
Location/Qualifiers
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Gaps 9 180

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Herrera,L., Jimenez,M.S. and Saez,J.A.
Molecular analysis of rifampin-resistant Mycobacterium tuberculosis
isolated in Spain (1996-2001). Description of new alleles into rpob
gene and review
                    IDHFGNRRLRTVGELLQNQIRVGMSRMERVVRERMTTQDVEAITPQTLINIRPVVAAI
KEFFGTSQLSQFMDQNNPLSGLTHKRRMFALGPGGLSRERAGLEVRDVHPSH*
1 198 c 210 g 101 t
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gene for RNA polymerase
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AJ318821.1 GI:22208418
FNA polymerase beta subunit; rpoB gene.
RNA polymerese beta subunit; rpoB gene.
Mycobacterium tuberculosis.
Bacteria; Actinobacteria; Actinobacteria; Actinomycetales;
Corynebacterineae; Mycobacteria
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                                                                                                      Length
                                                                                                                                   Indels
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                                                                                                 Score 166.4; DB 1;
Pred. No. 3.7e-18;
0; Mismatches 26;
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beta subunit, isolate 1071-98.
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/organism="Mycobacterium
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llarity 87.5%;
Conservative
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Submitted (07-AUG-
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                                                                                                                               Matches 182;
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                                                  BASE COUNT
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MTU318821
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TITLE
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JOURNAL
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/procein_id="CAC87031.1"
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AAIKEFEGTSQLSQFMDONNPLSGLTYKRRLSALGPGGLSRERAGLEVRDV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                circular BCT 09-AUG-2002 gene for RNA polymerase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation-"VCTDEALLDIYRKLRPGEPPTKESAQTLLENLFFKEKRYDLARV
GRYKVNKKLGLHVGEPITSSTLTEEDVVATIEYLVRLHEGGTTMTVPGGVEVPVETDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Centro
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Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium
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Submitted (07-AUG-2001) Herrera L., Servicio Bacteriologia,
Nacional Microbiologia., Ctra. Majadahonda-Pozuelo, Km 2.5,
Majadahonda. Madrid. 28220, SPAIN
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                    121 CCATCGAGTACCTGGTGCGCCTGCACGAGGCCAGGACCACGATGACCGTCCCCGGCGGCG
                                                                                                                                                                                                                                                                                                                                                                                                  TCAAGGAGAAGCGCTACGACCTGGCCCGCGTGGGCCGCTACAAGAAGAAGCTGG
                                                                                                                                                                                            Length 633;
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                                                                                                                                                                                            DB 1;
                                                                                                                                                                                        Score 166.4; DB 1
Pred. No. 3.8e-18;
); Mismatches 26
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Mycobacterium tuberculosis partial
beta subunit, isolate 1255-98.
AJ318816
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Mycobacterium tuberculosis.
Mycobacterium tuberculosis.
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/trans1_table=11
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larity 87.5%;
Conservative (
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Matches 182; Conserv
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Query Match
Best Local Similarity 87.5%;
Matches 182; Conservative (
                                                                                                                                                 /strain="Rv"
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Imboden, P.
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Persing, D.H., Hunt, J.J., Young, K.K.Y., Felmlee, T.A., Roberts, G.D. and Whelan, A.Christian.
and Whelan, A.Christian.
Detection of a genetic locus encoding resistance to rifampin in mycobacterial cultures and in clinical specimens
Patent: US 5643723-A 1 01-JUL-1997;
Location/Qualifiers
                                                                               GCCTGAACGCCGGCCAGCCGATCACGTCGTCGACTCTGACCGAGGAAGACGTCGTCGCCA 120
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Mycobacterium tuberculosis
Bacteria; Firmicutes; Actinobacteridae;
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              Indels
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  Pred. No. 3.7e-18;
0; Mismatches 26;
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Sequence 1 from patent US 5643723.
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302 c 330 g
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Best Local Similarity 87.5%;
Matches 182; Conservative
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Best Local Similarity 87.5%;
Matches 182; Conservative C
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Bergeron, M.G., Boissinot, M., Huletsky, A., m Nard, C., Ouellette, M., Picard, F.J. and Roy, P.H.
Highly conserved genes and their use to generate probes and primers for detection of microorganisms
Patent: WO 0123604-A 2072 05-APR-2001;
Infectio Diagnostic (I.D.I.) INC. (CA)
Location/Qualifiers
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Microbiology, University of Berne, Friedbuehlstrasse 51, Berne,
3010, Switzerland
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Mycobacterium tuberculosis
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae;
Mycobacterium; Mycobacterium tuberculosis complex.
I (bases 1 to 3853)
Inhoden, P., Troller, R., Marchesi, F., Telenti, A., Bodmer, T.,
Cole, S., Schopfer, K. and Burkart, T.
The room gene of Mycobacterium tuberculosis
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Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium tuberculosis complex.
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Pred. No. 2.8e-18;
0; Mismatches 26;
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/organism-"Mycobacterium

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1081 c 1188 g
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RDTVGVRIDRKRROVTVLKALGGTWTVPGGVEVPVETDDIDHFGNRRLRYGELIONGIRG
RSTKENSTOPVATIETUROLENLFFRENTYATIONGRAPVETDE
INTRALSALGPGGLSRERAGLEVROVHSSYTGAMCYPETPGROSTETSTUR
MSRMENTTOOVEATTPOTALINIRPWAAIKEFRGTSGLSGPMDONNELSGLT
HKRELSALGPGGLSRERAGLEVROVHSSTTGAMCYANTREFRAGENTYRRKAG
EVEVYPSSEVDVANDVSSROWSVATAMIPFLEHDDARRALMGANMORAVPLVRSEAP
LVGTGMELRAAIDAATSSSQESGVIEEVSADYITVHHDNGTRRTYRMRKFARSNHGTC
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ILVGKVYTRGSTELTPEERLLRAIFGEKAREVROTSLKVPHGESGRVIGIRVSRED
BELPAGVNELVRYVAGRKRISDGNLAGGRAGKVDBMARLIDVEDELLEAHNAIVS
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KLHHLVDDKIHARSTGPPTVENTRINGENGRAPURDTSLKAMLFDGRSGEPFPYPVTVGYMYIN
KLHHLVDDKIHARSTGPPTVENTRINGENGRAPURDSLCLINEVLEDMPFLEDLL
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GLFCERIRGPREDWECYGKYKRVRFKGIICBRCGVEYTRAKVRRERMGHIELAAPVT
HWYFKGYPORT 1691.01 1990 t 1890 t 1534 c 1691.01 990 t
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Pred. No. 2.7e-18;
0; Mismatches 26; Indels 0;
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Mycobacterium tuberculosis CDC1551,
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/transl_table=11
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                                                                                                                                            REPLEYPGILLOUGUES RIABLA LAGARAN SEY SAN TAY CALGARY STARLY SEAL RALL REPLEYPGILLOUGUES RALL SERVICES AND SERVICE SERV
                                                                                                                      /translation-"MLEGCILADSRQSKTAASPSPSRPQSSSNNSVPGAPNRVSFAKL
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Mycobacterium tuberculosis (strain Rv) DNA.
Mycobacterium tuberculosis (strain Rv) DNA.
Mycobacterium tuberculosis
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium
tuberculosis complex.
1 (bases I to 5084)
Miller, L. P., Crawford, J. T. and Shinnick, T. M.
The rpoB gene of Mycobacterium tuberculosis
Antimicrob. Agents Chemother. 38 (4), 805-811 (1994)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
/product="RNA-polymerase beta subunit"
/protein_id="AAA20242.2"
/db_xref="G1:7144499"

    5084
    /organism="Mycobacterium tuberculosis"

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Whole genome comparison of Mycobacterium tuberculosis clinical and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished
(bases) to 19352)
Fleischmann, R.D., Alland, D., Elsen, J.A., Carpenter, L., White, O., Peterson, J., DeBoy, R., Dodson, R., Gwinn, M., Haft, D., Hickey, E., Kolonay, J.F., Nelson, W.C., Umayam, L.A., Ermolaeva, M., ealther, A., Utterback, T., Weldman, J., Khouri, H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (25-APR-2001) The Institute for Genomic Research, 9712 Medical Center Dr. Rockville, MD 20850, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="DNA-directed RNA polymerase, beta subunit"
/protein_id="AAK44921.1"
/db_xref="GI:13880218"
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/strain="CDC1551"
/db_xref="taxon:83331"
/fob_re="clinical strain"
                                                                                                                       Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae;
                                                                                                                                                                                            Mycobacterium; Mycobacterium tuberculosis complex.
1 (bases 1 to 19352)
Fleischmann, R.D., Alland, D., Eisen, J.A., Carpenter, L.,
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Mycobacterium tuberculosis CDC1551
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Gill, J., Mikula, A. and Bishai, W.
Direct Submission
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/gene="MT0695"
163. ?£^^
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/gene="MT0696"
3744. .7694
/gene="MT0696"
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/gene="MT0695"
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10167. .10925
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                                                                                                                                                                                                                                                                                                   /translation="MSDTHVVTNQVPPLENVNPASSPVLIEALIOEGGWGLDEVNEY
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PEGHAFVADAKIGFRDAVRRABEPFGDYGRAGASRYT
AFWREVNRCGALDTTTEGPVTTSGATCADNRRVVLLTVDDAGHRWPSFATQTLWRFFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ó
                                                                                                                                /note="similar to SP:P33224 GB:L20915 PID:457172
PID:457174 PID:537028; identified by sequence similarity;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1184 CCATCGAATATCTGGTCCGCTTGCACGAGGTCAGACCACGATGACCGTTCCGGGCGGCG 1243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FLATRLGGQWGGAYGTMPAGLDLAPILERALVKG"
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                                                                                                                                                                                                                                         /product="acyl-CoA dehydrogenase, putative"
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/db_xref="GI:13880223"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="MT0703"
/note="identified by Glimmer2; putative"
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les 26;
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/product="hypothetical protein"
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Pred. No. 2.2e-
0; Mismatches
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                                                                                                                                                                                                                         /transl_table=11
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                                                                                                         /gene="MT0701"
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Best Local Similarity 87.5%;
Matches 182; Conservative
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RESULT 15

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Bacteria; Firmicutes Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae;
Mycobacterium; Mycobacterium tuberculosis complex.
I (bases 1 to 1977).
I (bases 1 to 1977).
I (bases 1 to 1977).
I (bases 1 to 1970).
I (conor, R., Davies, R., Basham, D., Broomin, J., Rajandream, M.A., Rogers, J., Rutter, S., Seeger, K., Skelton, S., Squares, S., Squares, R., Sulston, J.E., Taylor, K., Whitehead, S. and Barrell, B.G.
Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence
L. Nature 393 (6685), 537-544 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Parkhill, J.
Direct Submission
Submitted (11-JUW-1998) Submitted on behalf of the Mycobacterium tuberculosis sequencing and mapping teams, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 15A Unite de Genetique Moleculaire Bacterienne, Institut Pasteur, 28 rue du bocteur Roux, 75724 Paris Cedex 15, France E-mail: parkhill@sanger.ac.uk
Mycobacterium tuberculosis H37Rv complete genome; segment 32/162.
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/note="Rv0654, (MTC1376.22), len: 501. unknown, FASTA
score: Q53353 LIGNOSTILBENE-ALPHA,BETA-DIOXYGENASE (485
aa) opt:280 z-score: 330.1 E(): 2.3e-11, (28.5% identity
in 523 aaoverlap). Also similar to M. tuberculosis protein
MTCY21C12.07c (29.5% identity in 522 aa overlap)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (URL, http://www.sanger.ac.uk/Projects/M_tuberculosis/) CDS have been renumbered from the original cosmid submissions but the old gene designations are in brackets after the new gene numbers. Gene prediction was based on a Hidden Markow Model of TB genes implemented in TBparse (Krogh) supplemented with visual inspection of positional base preference in codons, especially where there is an increase in the observed/expected third position G + C. CAUTION: In some cases we may not have predicted the correct initiation codon. Where possible we choose an initiation codon (atg, or ttg) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most upstream
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Details of M. tuberculosis sequencing at the Sanger Centre are available on the World Wide Web.
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68. .1573
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Mycobacterium tuberculosis H37Rv
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68. .1573
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1762. 1785
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//codon_start=1
//codon_start=1
//codon_start=1
//codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                     /note="RV0655, (MTC1376.21), len: 359, abc transporter, fasta score: YRBE_ECOLI P45393 hypothetical abc transporter atp-binding (269 aa) opt: 644 z-score: 721.8 E(): 3.4e-33 (38.5% identity in 244 aa overlap); contains ps00017 APP/GTP-binding site motif A, PS00211 ABC transporters family signature, highly similar to M. leprae MKL_WTCLE P30769 possible ribonucleotide transport atp- (347 aa) opt: 2021 z-score:2244.4 E(): 0, (92.2% identity tuberculosis ABC transporters eg. MTCY253.24 (33.6% identity in 241 aa overlap).
                                                                                                                          YVIYDLPVTFDPMQVVPASVPRWLQRPARLVIQSVLGRVRIPDPIALGNRWGGHSD
RYPAMNPSYPARKGVMPREGGNEDVRWFDIEDCYYYHPLNAYSECRNGAEVLVLDVV
RYSRNFDRDRRGPGGDSRFSLDRWTINLATGAYTAERDDRAADEPRINTNETLVGGPHR
FAYTVGIEGGFLVARGAALSTPLYKQDCVTGSSTVASLDPDLLIGEWYFVPNFSARAE
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AHPORDPHTGELHAVSYSFARGHRVQYSVIGTDGHARRTVDIEVAGSPMMHSFSLTDN
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Complement(3530. 3685)

Complement(3530. 3685)

Complement(3530. 3685)

Appere"Rv0657c.

(MTC1376.19), unknown, len: 51 aa; similar to several other M. tuberculosis hypothetical proteins eq. WM9_MTC17 U01848 hypothetical 8.9 kd protein cr39.08c (80 aa), fasta scores; opt: 107 z-score: 182.3 E(): 0.0038, 45.8% identity in 48 aa overlap. Also similar to MTC448_5 aa), 41.0% identity in 39 aa overlap. Also similar to MTC448_5 aa), 41.0% identity in 39 aa overlap."
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MSRWFGDVYPDVPVFKSVWRWIDSAQHRLARAGAVGALSVVDLLICDTAAARGLVVLH
COMPLEMENT(3530. 3685)
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1585. .2664
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complement(3691. 3696)
/note="possible RBS upstream of Rv0657c"
complement(371. .4477)
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complement(3761. .4477)
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ALARSRE"
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/gene="Rv0659c"
/note="Rv0659c"
/note="Rv0659c, (MTC1376.17), len: 102; unknown, similar
to YW28_MYCTU 010867 hypothetical 12.3 & protein cy39.28
(114 aa), fasta scores; opt: 144 z·score: 213.2 E():
7.3e-05, 30.8% identity in 107 aa overlap. Also similar to
MTCV09F9.22 (32.7% identity in 101 aa overlap)*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref-"SPTREMBL:006780"
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Anote-"possible RBS upstream of Rv0658c"
complement(4753...5061)
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Pred. No. 2.1e-18;
0; Mismatches 26;
db_xref-"SPTREMBL:006782
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complement(5048. .5293)
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Best Local Similarity 87.5%;
Matches 182; Conservative (
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BG349727 947030C07 ALB30B17 ALB30B17 BG577676 3524 1_39 BG579756 WHE2974_B

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1282 bp mRNA linear EST 24-JAN-2000 42 Wycobacterium anaerobic stationary phase library Mycobacterium Smegmatis cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Mycobacterium smegnatis
Bacteria: Actinobacteria: Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
1 (bases 1 to 1282)
Muruqasu-Coci, B., Tay, A. and Dick, T.
Upregulation of stress response genes and ABC transporters in anaerobic stationary-phase Mycobacterium smegmatis
MOI. Gen. Genet. 262 (4-5), 677-682 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Murugasu-Oei, B.
Mycobacterium Laboratory
Institute of Molecular and Cell Biology
30 Medical Drive, Singapore 117609, Republic of Singapore
Tel: 65 874 3011
Fax: 65 779 1117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: mcbbomēimcb.nus.edu.sg
Insert Length: 1282 Std Error: 0.00
Seq primer: T3 Forward; T7 Backward.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                           ALIGNMENTS
                                                                                       BQ246063
BM285614
BM285614
BB756092
CNS02NV2
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AW056150
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BG906999
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BI489596
BE196164
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AU070110
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AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                         ACCESSION
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KEYWORDS
SOURCE
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BG908023 TaLr1164F
BE418320 SCL024.FO
BF444643 262617 MA
BM190539 POSM01000
BG907534 TaLr1160G
                                                   ; Search time 1109.13 Seconds (without alignments) 3037.202 Million cell updates/sec
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                                                                                  US-09-697-123B-17
208
1 tcaaggagaagcgctacgac......ccggtggaaaccgacgacat 208
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                                                                                                                                                              32308132
     GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd
                                                                                                                                                           of hits satisfying chosen parameters:
                                                                                                                                            16154066 seqs, 8097743376 residues
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                                                    November 12, 2002, 16:59:42
                                   OM nucleic - nucleic search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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BE418320
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length: 2000000000
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em_gss_pln:*
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Maximum
                                                    Run on:
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source

Result Š. υ

BE196164 BJ470020 AW484285

ANDS6150 660004G09
AL236849 Terracodon
BQ246115 Tar15016A
BG906999 TarL11156D
BQ346063 Tar15016F
BW385614 524291 MA
BE756092 210134 MA
AL205895 Terracodon
BQ754171 EBCa01_SQ
BG36999 HVSNE1002
AV835256 BA4835256
BA469527 B478452 EBCO07_SQ
BF618921 HVSNE2001
AV8107010 Cas mays
AF107010 Cas mays
AF1070

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source
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BE418320
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            FEATURES
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                                                                                                                               Anotes Vector: Landar All Bardelli were disrupted using a Mini bead beater (Blospec). RNA was isolated using the RNeasy protocol (Olagen). Purified RNA was subjected to 2 rounds of digestion with RNase free DNase I (Promega). DNase I was heat-inactivated at 750c for 5 min. and removed by using RNeasy columns followed by phenol removed by using RNeasy columns followed by phenol preparations were confirmed to be free of genomic DNA contamination by carrying out PCR and RT-PCR using the Access kit (Promega) and primers specific for the histone-like protein gene hip (Lee et al., 1998). CDNA was synchesized using random hexamer primers (Promega) and Stratagene's cDNA synthesis kit. CDNA fragments were ligated into lambda App II vector and packaged in vitro using Stratagene reagents.
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Cloutier,S., Dong,G. and Walsh,A.
Wheat functional genomics - Thatcher Lrl cDNA library
Unpublished (2001)
Contact: Dr. Sylvie Cloutier
Cereal Research Centre, Agriculture and Agri-food Canada
195 Dafoe RA, Winnipeg, MB, Canada R3T 2M9
Fax: (204) 983-4604
Email: scloutier@em.agr.ca
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BG908023 649 bp mRNA linear EST 05-JUN-2001 TaLrl164F05R TaLrl Triticum aestivum cDNA clone TaLrl164F05 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 was cloned directionally, not all sequences generated with reverse primer were from the 5' end (same with forward primer and 3' end). Average inset size is >2.2 kb
Plate: 164 row: F column: 05
Seq primer: M13 Reverse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCCTGAACACCGCGTCCCCGATCACGACGACCACTCTGACCGAAGAGGACGTCGTCGCCA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="Mycobacterium anaerobic stationary phase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74.6%; Score 155.2; DB 9; Length 1282; 84.1%; Pred. No. 3.4e-25; 1ve 0; Mismatches 33; Indels 0;
/organism="Mycobacterium smegmatis"
/strain="mc2155"
                                                                                                              /lab_host="E. coli XL1-Blue MRF'"
                                                /db_xref~"taxon:1772"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 TCGAGGTGCCGGTGGAACCGACGACAT 208
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Matches 175; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   bread wheat.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BASE COUNT
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AUTHORS
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JOURNAL
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KEYWORDS
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/organism="Triticum aestivum"
/cultivar="Thatcher Lr1"
/db_xref="taxon:4565"
/clone="Talr1164F05"
/clone="Talr1164F05"
/clone="Talr1164F05"
/clone="Talr1164F05"
/clone="Talr1164F05"
/dev_stage="L4 Days old"
/dev_stage="L4 Days old"
/lab_host="E. col1 XLOLR"
/note="Vector: Lambda ZapII; mass excised in plasmid vector: DBK-CMV (Stratagene).; Site_1: EcoRI: Site_2: XhoI; mRNA obtained from wheat NIL Thatcher Lil 24 hours after inoculation with leaf rust pathogen Puccinia triticina race BBB carrying the avirulence gene Avrl."
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1 (bases 1 to 1013)

2 Anderson, O. A., Appels, R., Bailey, P., Blake, T., Close, T., Cloutier, S., Dubcovsky, J., Feulllet, C., Gale, M., Graner, A., Gustafson, P., Herrmann, R.G., Holton, T., Jacquemin, J. M., Jia, J., Joudrier, P., Pecchioni, N., Qualset, C., Schuch, W., Salvaraj, G., Shariflou, M., Sortells, M., Warburton, M. and Wenzel, G.

International Triticeae EST Cooperative (ITEC): Production of Expressed Sequence Tags for Species of the Triticeae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SCLÖ24.F08R990724 ITEC SCL Wheat Leaf Library Triticum aestivum cDNA clone SCL024.F08, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            190 CGCGGGTGGGCCCCTACGAGCTCGGCGTGGCGCGAGGCAGCTTCGCCAAGGTCA 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   85 CGACGACCACTCTGACCGAAGAGGACGTCGTCGCCACCATCGAGTACCTGGTCCGCCTGC 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       250 AGATCGCCAAGGACCGCAACGCCCCCTGCGCCATCAAGGTGCTCGACGCAACC 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25 CGCGGGTGGGCCGCTACAAGGTCAACAAGAAGCTCGGCCTGAACACCGCGTCCCCGATCA 84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 649;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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/cultivar="Thatcher Lr1"
/db_xref="taxon:4565"
/clone="SCLD24.F08"
/clone_lib="ITEC SCL Wheat Leaf Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23.2%; Score 48.2; DB 12;
57.7%; Pred. No. 0.28;
ive 0; Mismatches 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               145 ACGAGGCCACACCACGATGACCGTCCCG 173
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Location/Qualifiers
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Best Local Similarity 57.78
Matches 86; Conservative
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138
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AUTHORS
TITLE
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VERSION
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ORIGIN
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BM190539
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 487)
Stone R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.W.
Design and use of two pooled tissue normalized cDNA libraries for ET discovery in swine
Unpublished (2000)
Contact: Smith TPL
Unpublished (2000)
Contact: Smith TPL
UNDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
                                                                                                                                                                                                                                                                                                                                                                                        EST 01-DEC-2000
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/tissue_type="young leaf"
/dev_stage="after 24 hour challenge with LR-AVR1"
/note="Vector: Lambda ZAP; 1.0 Kbp average insert size."
237 c 271 g 223 t 36 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI; Library made from pooled tissue from testis, ovary, endometrium, hypothalamus, pituitary, and placenta."
                                                                                                                                                                  CGACGACCACTCTGACCGAAGAGGACGTCGTCGCCACCATCGAGTACCTGGTCCGCCTGC 144
                                                                                                                                                                                                                              11 111 1 111 1 246 AGATCGCCAACGCGCAACCACGCAACC 305
                                                                                                                             Gaps
                                                                                                                                                  25 CGCGGGTGGGCCGCTACAAGGTCAACAAGAAGCTCGGCCTGAACACCGCGTCCCCGATCA 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                             Length 1013;
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                                                                                                                                                                                                                                                                                                                                                                                      mRNA linear
5', mRNA sequence.
                                                                                                                          Indels
                                                                                        23.2%; Score 48.2; DB 10;
llarity 57.7%; Pred. No. 0.28;
Conservative 0; Mismatches 63;
                                                                                                                                                                                                                                                                                                                                                                                  487 bp
262617 MARC 2PIG Sus scrofa cDNA
BF444643
BF444643.1 GI:11504735
EST.
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/organism="Sus scrofa"
/db_xref="taxon:9823"
/clone_lib="WARC_2PIG"
/tissue_type="pooled"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                       145 ACGAGGCCACCACGATGACCGTCCCG 173
                                                                                                                                                                                                                                                                                          PCR PRIMETS
FORMARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTTCCCAGTCACGACG
Plate: 98 row: L column: 4
Seq primer: ATTTAGGTGACACTATAG.
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                                                                                                        Similarity
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es 108; Conserv
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Sus scrofa
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                                                                                             Local 5...
86;
                                                                                        Query Match
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LOCUS
                                          BASE COUNT
ORIGIN
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Matches
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                                                                                                                     Matches
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AUTHORS
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SOURCE
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1 TCAAGGAGAAGCGCTACGACCTCGCGGGTGGGCCGCTACAAGGTCAACAAGAAGCTCG 60

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ISM Sus scrofa

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1;

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1;

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1;

E losses 1 to 704)

IR Yao,1, Coussens,P., Ernst,C. and Saama,P.

Analysis of expressed sequence tags from a normalized porcine skeletal muscle cDNA library

INAL Unpublished (2002)

Contact: Jianbo Yao

Department of Animal Science
Michigan State University

Eat: 517-355-8443

Fax: 517-353-1699

Email: yaojemsu.edu

Seq primer: M13 reverse.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                   EST 11-DEC-2001
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BM190539 GI:17526502
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/db_xref="taxon:9823"
/clone_lib="porcine skeletal muscle cDNA library (PoSM)"
/sex="male and female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note-"Organ: hind limbs; Vector: pSPORT1; Site_1: NotI; Site_2: SalI" 253 c 207 q 106 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="skeletal muscles"
/dev_stage="45 d and 90 d of gestation, birth, 7 wk and
61 GCCTGAACACCGCGTCCCCGATCACGACGACCACTCTGACCGAAGAGGACGTCGTCGCCA 120
                                                                                                121 CCATCGAGTACCTGGTCCGCCTGCACGAGGCCCACACCACGATGACCGTCCCGGGCGGAG 180
                                                                                                                                        288 TCACGGACGGCCGCTCAGACACCCAGAGGGACACCACCCGGTGAGCGTGCTCTGCGGCC 229
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                                          348 TGCAGTACACCCGGAGCCAGCTGCTGCCCCCCACTCAGAACAACCGGATCGCCTGGTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23.1%; Score 48; DB 13; Length 70 51.9%; Pred. No. 0.31; 1ve 0; Mismatches 100; Indels
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                                                                                                                                                                                                     181 TCGAGGTGCCGGTGGAAACCGACGACAT 208
                                                                                                                                                                                                                                228 CCGACATCCAGGTGGTCTCCGTGGGCAT 201
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/lab_host-"DH10B"
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Best Local Similarity 51.9
Matches 108; Conservative
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/u.i.../
/cultivar="Chinese Spring"
/cultivar="Chinese Spring"
/db_xer="chinese Spring"
/db_xer="chinese Spring"
/clone="whe7920"
/clone="whe7920"
/clone="lib="Y. Ogihara unpublished cDNA library, Wh_e"
/tissue_type="seed DPA10"
/dev_stage="Feekes' scale lil.2"
/dote="Vector: Lambda Uni-ZAP XR, excised phagemid;
Site_1: EcoRi; Site_2: XhOi; Plants were grown under
hydroponic conditions at UC Davis, salt stressed for 12
hours, and for 7 days, then dissected and frozen (Akhunov
in J Dvorak Lab). Total RNA was prepared from the two
samples, polyA was purified from the pooled RNA, a cDNA
library was made, and the CDNA clones were in vivo
excised to give pBluescript phagemids in the TJ Close lab
at the University of California, Riverside (Akhunov, Chin
/ Close, Fenton, Kianian, Otto, Simons, Zhang).
Plasmid DNA preparations and DNA sequenching were
performed in the Ob Anderson lab (all other authors)."
                                                           bread wheat.
Triticum aestivum
Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta: Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
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                                                                                                                                                                                                                                                                  Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tat: 81-559-81-6856
                                                                                                                                                    Triticeae, Triticum.

( hases 1 to 517)
Ogihara,Y. and Murai,K.
Expressed genes in Triticum aestivum
Unpublished (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                      Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
1.517
                   BJ233830.1 GI:20050958
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BJ258518.1 GI:20081256
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Best Local Similarity 56.49
Matches 84; Conservative
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BJ258518
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Triticeae; Triticum.

( bases 1 to 363)

Cloutier, S., Dong, G. and Walsh, A.
Wheat functional genomics - Thatcher Lrl cDNA library
Wnpublished (2001)
Contact: Dr. Sylvie Cloutier
Cereal Research Centre, Agriculture and Agri-food Canada
195 Dafoe RG, Winnipeg, MB, Canada R3T 2M9
Fax: (204) 983-4604
                                                                                                                                        BG907534 363 bp mRNA linear EST 05-JUN-2001
Talr1160G09R Talr1 Triticum aestivum cDNA clone Talr1160G09 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="last tissue"
/dev_stage="14 Days old"
/dab_bost="E. coll xLOLR"
/note="Vector: Lambda ZapII; mass excised in plasmid
vector pBK-CMV (Stratagene).; Site_1: EcoRI; Site_2: XhoI:
mRNA obtained from wheat NIL Thatcher Lrl 24 hours after
incollation with leaf rust pathogen Puccinia triticina
race BBB carrying the avirulence gene Avrl."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       was cloned directionally, not all sequences generated with reverse primer were from the 5' end (same with forward primer and 3' end). Average inset size is >2.2 kb
Plate: 160 row: G column: 09
Seq primer: M13 Reverse.
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/db_xref="taxon:4565"
194 CCGACATCCAGGTGGTCTCCGTGGCGT 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             145 ACGAGGCCACACCACGATGACCGTCCCG 173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: scloutier@em.agr.ca
                                                                                                                                                                                                                              BG907534.1 GI:14315210
                                                                                                                                                                                                                                                                                                    Triticum aestivum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .363
                                                                                                                                                                                      mRNA sequence.
                                                                                                                                                                                                                                                                            bread wheat
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Best Local Similarity
Matches 85; Conserv
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BG907534
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/cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone_ib="wha607"
/clone_lib="Triticum aestivum"
/clone_lib="Triticum aestivum"
/clone_lib="Triticum aestivum"
/clone_lib="Triticum aestivum"
/clone_lib="Triticum aestivum"
/clone_lib="Triticum aestivum aestivum
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947030C07.y2 947 - 2 week shoot from Barkan lab Zea mays cDNA, mRNA
sequence.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Pantcoideae; Andropogoneae; Zea.
1 (bases 1 to 448)
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1.4;
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                                                                                                                                         Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Fat: 81-559-81-6856
Fax: 81-559-81-6855
                                                                                                                                                                                                                                                                                                                                                                            /organism="Triticum aestivum"
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21.6%; Score 45; DB 13
Best Local Similarity 56.4%; Pred. No. 1.4;
Matches 84; Conservative 0; Mismatches
1 (bases 1 to 684)
Ogihara,Y. and Mural,K.
Expressed genes in Triticum aestivum
Unpublished (2002)
Contact: Tadasu Shin-i
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Contact: Walbot V
Department of Biological Sciences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            300 ACGTCCTCCGCCACAAGATGGTCGAGCAG 328
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                                                                                                                                                                                                                                                                                      Email: tshini@genes.nig.ac.jp.
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BG349727.1
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BG349727
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticaeae; Triticum.
1 (bases I to 468)
Wilson,I., Beswick,R., Shepherd,S., Barker,G., Parker,J., Owen,P., Balanca,D., Coghill,J., Holdsworth,M., Lenton,J., Shewry,P. and
                                                                                                                                                                                                                                                                                                                                       /note-"Organ: shoot; Vector: Lambda ZAP (pBlueScript SK-); Site_1: ECORI; Site_2: XhoI; Directionally cloned using Stratagene's Unizap XR colona cloning Ait with the 5' end at the ECORI site. The library represents 8 x 10e5 independent recombinant phage. The plants were greenhouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      85 CGACGACCACTCTGACCGAAGAGGACGTCGCCACCATCGAGTACCTGGTCCGCCTGC 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            228 AGCACGCGCGACTCCCGCACCGCGCCCCTCAAGGTGCTCGACGCGAACC 287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A BBSRC-funded wheat EST resource for the academic community
                                                                                                                                                         1. .448.
/organism="zea mays"
/cultivar="sea"
/cultivar="sea"
/db_xref="taxon:4577"
/clone_lib="947 - 2 week shoot from Barkan lab"
/fissue_type="leaf and stem, including leaf base"
/dev_stage="z week old seedling (3 leaves)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 947030 row: C column: 07.
Location/Qualifiers
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Long Ashton, Bristol BS41 9AF United Kingdom.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 43.8; DB 12;
Pred. No. 2.6;
0; Mismatches 77;
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/clone_lib="q:242"
/tissue_type="egg cell"
/dev_stage="pre-fertilisation"
150 c 139 q 87 t
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/db_xref="taxon:4565"
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53.98;
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140 c
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Matches 90; Conservative
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Contact: Barker G
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84

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221 AGCACGCGCGCGCCCCCCCCCCCCCCCCTCAAGGCCCCAACCGCGCAACC 280
            CGCGGGTGGGCCGCTACAAGGTCAACAAGAAGCTCGGCCTGAACACGCGTCCCCGGATCA
                                                                           85 CGACGACCACTCTGACCGAAGAGGACGTCGTCGCCACCATCGAGTACCTGGTCCGCCTGC
                                                                                                                                               145 ACGAGGCCACACCACGATGACCGTCCCGGGCGGAGTCGAGGTGCCG 191
                                                                                                                                                                        bread wheat.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoldee; Andropogoneae; Zea.
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Site_1: ECORI (5-prime); Site_2: XhoI (3-prime);
Unamplified cDNA ilbrary directionally cloned by Rima Kulikauskas using Stratagene's Uni-Zap system. Insert Sizes ranged from 0.5kb to 2kb. 50 microliter aliquot had 338,000 pfu when it was made in Sept, 1995, from oligo dT-primed poly A+ RNA."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="2ea mays"
/cultivar="873"
/db_xref="taxon:4577"
/clone_llb="3524 - Mature pollen from Sheila McCormick's
                                                                                                                                                                                                                                                            260 GGACGTGGAGCTCGCCGAGAAGTTCGTCAGCGTGGACCAGGGGCTCGGCCTCCT 319
                                                                                                                         62 CCTGAACACCGGGTCCCCGATCACGACGACCACTCTGACCGAAGAGGACGTCGTCGCCAC 121
                                                                                                                                                                                          200 GGTGACCCCCATGTCCGCCATGTCTCCAGCATCACCTCATCAACGAGTTCAGCGTCTACAA 259
                                                                                                                                                                                                                                       122 CATCGAGTACCTGGTCCGCCTGCACGAGGCCACACCACGATGACCGTCCCGGGGGGGAGT 181
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Maize ESTs from various cDNA libraries sequenced at Stanford
                                                                                                  2 CAAGGAGAAGCGCTACGACCTCGCGGGGGGGCCGCTACAAGGTCAACAAGAAGCTCGG
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                                         Length 468;
                                                                       Indels
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                                   Score 43.8; DB 9;
Pred. No. 2.6;
0; Mismatches 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   column: 12
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/dev_stage="mature"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                           182 CGAGGTGCCGGTGGAACCGACGACAT 208
                                                                                                                                                                                                                                                                                                                                           320 CAAGGTGGCACTGCGCTCCGACACCGT 346
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Plate: 3524_1_39_1 row: H c
Location/Qualifiers
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                                                                    Matches 105; Conservative
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Unpublished (1999)
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Fax: 650 725 8221
                                                     Best Local Similarity
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Best Local Similarity
Matches 90; Conserv
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                                  Query Match
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DEFINITION
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/ultivar="Brevor"
/cultivar="Brevor"
/cultivar="Brevor"
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/cultivar="Brevor"
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/clone_"NHE2974_B09_D18"
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/clone_"Lype="Seed embryo"
/dev_stage="Mature seed"
/lab_host="E_col! Solk"
/lab_host="E_col! Solk"
/note="Vector: Lambda Uni-ZAP XR, excised phagemid;
Site_1: Econi; Site_2: XhOi; Plants were grown to seed maturity under conditions favoring seed dormancy (L.
Dohery at K. Walker_Simmons lab, Washington State University, Pullman, WA). Embryos were cut from mature dormant seed (Doherty). Total RNA was prepared from these embryos, polyA was purified, a cDNA library was made, and the CDNA clones were in vivo excised to give pBluescript phagemids in the TJ Close lab at the University of California, Riverside (Chin, Penton). Plasmid DNA Preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."
                                                                                                                                                                                                     Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Lillopsida; Poales; Poaceae; Pooldeae;
Triticeae; Triticum.
1 (bases 1 to 648)
Anderson, O.D., Chao, S., Chin, A., Close, T.J., Doherty, L., Fenton
A.R.D., Lazo, G.R., Rausch, C.J., Walker-Simmons, M.K. and Wilson, C.
The structure and function of the expressed portion of the wheat
      EST 19-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595818
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Sequences have been trimmed to remove vector sequence and low
quality sequence with phred score less than 20
Seq primer: SK primer.
                   WHE2974_B09_D182S Wheat dormant embryo cDNA library Triticum aestivum cDNA clone WHE2974_B09_D18, mRNA sequence.
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      linear
   mRNA
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                                                                                                               BQ579756.1 GI:21483073
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Best Local Similarity 52.57
Matches 94; Conservative
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 645)

2 (base ESTS from various cDNA libraries sequenced at Stanford University

2 (base ESTS from various cDNA libraries sequenced at Stanford University

3 (base ESTS from various cDNA libraries sequenced at Stanford University

4 (base ESTS from various cDNA libraries sequenced at Stanford University

5 (contact: Walbot V Belogical Sciences Stanford University B55 California Ave, Palo Alto, CA 94304, USA Tel: 507 723 2227

Fax: 650 725 8221

Fax: 650 725 8221
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note-"Organ: anthers; Vector: Lambda Zap; Site_1: ECORI; Site_2: XhOI; Anther and pollen cDNA library. Directionally sequenced with 5' end at the EcoRI site. Created by Amine Franklin."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml; Actinopterygii; Neopterygii; Teleostel; Euteleostel; Neoteleostel; Acanthopterygii; Teleostel; Euteleostel; Neoteleostel; Acanthopterygii; Teleostel; Euteleostel; Neoteleostel; Letraodontidae; Tetraodon.

I (bases 1 to 896)

Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Benot, A., Fizames, C., Wincker, P., Brottler, P., Quetler, F., Saurin, W. and Weissenbach, J.

Human gene number estimate provided by genome wide analysis using Tetraodon nigrcviridis DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /cultivar="Oblog"s / /cultivar="Oblog"s / /cultivar="Colored"s / /cu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          118 CCACCATCGAGTACCTGGTCCGCCTGCACGAGGGCCACCACCACGATGACCGTCCCGGGCG 177
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/organism="Zea mays"
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Tetraodon nigroviridis
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1 (bases 1 to 413)
Wilson, I., Beswick, R., Shepherd, S., Barker, G., Parker, J., Owen, P., Palanta, J., Coghill, J., Holdsworth, M., Lenton, J., Shewry, P. and
                                                                                                                                                                                                                                                                                                                                                                                                        ALB30932 A:242 Triticum aestivum cDNA clone C04_q242_plate_15, mRNA
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196 GCGGCGCGCGGGGAGGTCCTGCACCAGCGAGGCGGCCGCCTGCCGTACGGGCCCGGGA 255
                                                            88 CGACCACTCTGACCGAAGAGGACGTCGCCCACCATCGAGTACCTGGTCCGCCTGCACG 147
                                                                                               86 GACGACCACTCTGACCGAAGGACGTCGTCGCCACCATCGAGTACCTGGTCCGCCTGCA 145
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                                                                                                                                                                                  148 AGGGCCACACCACGATGACCGTCCCGGGCGGAGTCGAGGTGCCGGTGGAAACCGACGAC 206
                                                                                                                                                                                                                      26 GCGGGTGGGCCGCTACAAGGTCAACAAGAAGCTCGGCCTGAACACCGGGTCCCCGATCAC 85
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A BBSRC funded wheat EST resource for the academic community
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Contact: Barker G
Institute of Arable Crop Research
Long Askhron, Bristol BS41 9AF United Kingdom.
Location/Qualifiers
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/clone_lib="9:242"
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/dev_stage="pre-fertilisation"
129 c 123 f 77 t
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/cultivar="florida"
/db_xref="taxon:4565"
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Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J.
Mensterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
                                                                                                                                                                                                                                                                                                                                                        83 CACGACGACCACTCTGACCGAAGAGGACGTCGTCGCCACCATCGAGTACCTGGTCCGCCT 142
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Sequence 9522, Ap
Sequence 9, Appli
Sequence 7788, Ap
Sequence 7788, Ap
Sequence 7939, Ap
Sequence 29, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 7692, Appli
                                                                                     November 12, 2002, 16:05:40 ; Search time 21.1607 Seconds (without alignments) 3487.380 Million cell updates/sec
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1 tcaaggagaagcgctacgac......ccggtggaaaccgacgacat 208
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GenCore version 5.1.3 Copyright (c) 1993 2002 Compugen Ltd.
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Perfect score:
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Sequence 7, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 1738, Appli Sequence 1759, Appli Sequence 1759, Appli Sequence 1759, Appli Sequence 1259, Appli Sequence 1259, Appli Sequence 1176, Appli Sequence 1176, Appli Sequence 1176, Appli Sequence 1176, Appli Sequence 1176, Appli Sequence 1174, Appli Sequen	Sequence 04, Appli Sequence 1, Appli Sequence 7925, Ap
US-09-733-383-7 US-09-999-745-19 US-09-916-709-2 US-09-816-707-2 US-09-811-077-2 US-09-815-944-2 US-09-815-944-2 US-09-815-242-7738 US-09-915-242-7696 US-09-915-242-7696 US-09-915-242-7696 US-09-915-242-7696 US-09-915-242-7696 US-09-960-352-11569 US-09-960-352-11569 US-09-960-352-1176 US-09-960-352-1176 US-09-960-352-1474 US-09-999-745-12	US-09-920-922-1 US-09-815-242-7925
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ALIGNMENTS

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Sequence 5, Application US/09984711
Sequence 5, Application US/09984711
Sequence 5, Application US/09984711
Sequence 5, Application US/09984711
Septent No. US20020119549A1
SPETCANT: MEDEREL, Bettina
APPLICANT: STEPHAN, Hans
APPLICANT: REUTZER, Caroline
APPLICANT: PFEFFERLE, Walter
APPLICANT: PFEFFERLE, Walter
APPLICANT: PFEFFERLE, Walter
APPLICANT: BINDER, Michael
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE rpsL GENE
FILE REFERENCE: 20420920,
CURRENT APPLICATION NUMBER: DS.001-10-31
PRIOR FILING DATE: 2001-10-31
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin version 3.1
SEQ ID NO 5
LENGTH: 5096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 69 ACCGCGTCCCCGATCACGACGACCACTCTGACCGAAGAGGACGTCGTCGCCACCATCGAG 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Corynebacterium glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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; OTHER INFORMATION:
US-09-984-711-5
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Best Local Simi
Matches 133;
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FILE REFERENCE: 204212USOX
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GENERAL INFORMATION:
APPLICANT: MCKEL, BETTINA
APPLICANT: BATHE, BRIGITTE
APPLICANT: HANNS, STEAM
APPLICANT: HERMANN, THOMAS
APPLICANT: HERMANN, THOMAS
APPLICANT: HERMANN, THOMAS
APPLICANT: HERMANN, THOMAS
APPLICANT: BINDER, MCHAEL
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE FPSL GENE
FILE REPERBANCE: 21847200X
CURRENT FILING DATE: 2002-02-15
FRIOR PLICATION NUMBER: DE 10107230.9
FRIOR FILING DATE: 2001-02-16
FRIOR FILING DATE: 2001-12-19
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 5
LENGTH: 5099
                      129 TACCTGGTCCGCCTGCACGAGGCCACACACGATGACCGTCCCGGGCGGAGTCGAGGTG 188
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APPLICANT: HERMANN, Thomas
APPLICANT: HERMANN, Thomas
APPLICANT: HERMANN, MICHAE
APPLICANT: BINDER, MAICHE
TITLE OF INVENTION: NUCLEOTIDE SEEQUENCES WHICH CODE FOR THE rPOB GENE
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Pred. No. 1.6e-12;
0; Mismatches 64; Indels
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                                                                                                                                                                                                      Sequence 5, Application US/10075460 Patent No. US20020155557A1
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Patent No. US20020119537A1
GENERAL INFORMATION:
APPLICANT: MOECKEL, Bettina
                                                                                             1755 CCAGTCGAGACCGATGACAT 1774
                                                                        189 CCGGTGGAAACCGACGACAT 208
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39.2%;
Best Local Similarity 66.5%;
Matches 133; Conservative
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; LOCATION: (702)..(4196)
; OTHER INFORMATION:
US-10-075-460-5
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US-09-887-052-1
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Sequence 3, Application US/09887052
Sequence 3, Application US/09887052
Patent No. US20020119537A1
GENERAL INFORMATION:
APPLICANT: MATHE, Brighte
APPLICANT: HERMANN, Thomas
APPLICANT: HERMANN, Thomas
APPLICANT: BINDER, Michael
TITLE OF INVENTION: NUCLEOTIDE SEEQUENCES WHICH CODE FOR THE rpoB GENE
FILE REFERENCE: 204212050X
CURRENT PELLING DATE: 2001-06-25
PRIOR FILING DATE: 2001-06-25
PRIOR APPLICATION NUMBER: DE10107229:5
PRIOR PELLING DATE: 2001-02-16
NUMBER: DE10107229:5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1578 AAGCGCTACGACCTGGCTTGGTCGTTACAAGATCAACCGCAAGCTCGGCTTGGT 1637
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Pred. No. 1.6e-12;
0; Mismatches 64;
                                                                                                                                                                                                                                                                                                           39.2%; Score 81.6; DB 10
66.5%; Pred. NO. 1.6e-12;
tive 0; Mismatches 64
CURRENT APPLICATION NUMBER: US/09/887,052
CURRENT FILING DATE: 2001-06-25
PRIOR APPLICATION NUMBER: DE10107229.5
PRIOR FILING DATE: 2001-02-16
                                                                                                                                                             TYPE: DNA ORGANISM: Corynebacterium glutamicum
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                                                                             NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin version 3.0
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin version 3.0
SEQ ID NO 3
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Best Local Similarity 66.5%;
Matches 133; Conservative (
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NAME/KEY: CDS

LOCATION: (702)..(4196)

US-09-887-052-1
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Best Local Similarity
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                                                                                                                                                                                                                              Sequence 5, Application US/09887052
| Patent No. US20020119537A1
| GENERAL INFORMATION |
| APPLICANT: BATHE, Brigitte |
| APPLICANT: BATHE, Brigitte |
| APPLICANT: BATHE, Brigitte |
| APPLICANT: BATHE, Michael |
| TITLE OF INVENTION: WUCLECTIDE SEEQUENCES WHICH CODE FOR THE rpob GENE |
| FILE REFERENCE: 204212450x |
| CURRENT APPLICATION NUMBER: US/09/887,052 |
| CURRENT FILING DATE: 2001-06-25 |
| PRIOR FILING DATE: 2001-0-16 |
| NUMBER OF SEQ ID NOS: 8 |
| SOFTWARR: PATENTIN VERSION 3.0 |
| SEQ ID NO 5.00
TACCTGGTCCGCCTGCACGAGGCCACACCACGATGACCGTCCCGGGCGGAGTCGAGGTG 188
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APPLICANT: Taien, Roger Y.
APPLICANT: Taien, Roger Y.
APPLICANT: Baird, Geoffrey
TITLE OF INVENTION CIRCULARRY PERMUTED FLUORESCENT PROTEIN INDICATORS
FILE REFERENCE: REGENIA70-1
CURRENT APPLICATION NUMBER: US/09/999,745
CURRENT FILING DATE: 2001-10-23
PRIOR APPLICATION NUMBER: 09/316,920
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Pred. No. 1.6e-12;
0; Mismatches 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Corynebacterium glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 14, Application US/0999745
Patent No. US20020157120A1
GENERAL INFORMATION:
                                                                                                                                  1755 CCAGTCGAGACCGATGACAT 1774
                                                                                                                  189 CCGGTGGAAACCGACGAT 208
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Matches 133; Conservative
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; LOCATION: (702)...(4196)
US-09-887-052-5
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US-09-999-745-14
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Sequence 7, Application US/09205448
Patent No. US20020137661A1
GENERAL INFORMATION:
APPLICANT: Arnold, Frances
APPLICANT: Shao, Zhixin
APPLICANT: Shao, Zhixin
APPLICANT: Volkov, Alexander
APPLICANT: Volkov, Alexander
APPLICANT: Volkov, Mexander
TITLE OF INVENTION: Sequences
FILE REFERENCE: 018097-025710PC
CURRENT FILING DATE: 1998-12-04
PRIOR FILING DATE: 1998-12-04
PRIOR PRILIG DATE: 1999-12-08
NUMBER: US 60/067,908
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                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Description of Artificial Sequence:Actinoplanes OTHER INFORMATION: utahensis echinocandin B (ECB) deacylase gene OTHER INFORMATION: mutant M-15 created by in vitro heteroduplex OTHER INFORMATION: formation followed by in vivo repair
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                                                                                                                                                                                DB 9; Length 720;
                                                                                                                                                                            Score 38; DB 9; Le
Pred. No. 0.16;
0; Mismatches 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 TCGAGGTGCCGGTGGAAACCGACGAC 206
                                                                                                                                                                                                                  ő
PRIOR FILING DATE: 1999-05-21
NUMBER OF SEQ ID NOS: 67
SOFTWARE: PATENTIN VERSION 3.0
SEQ ID NO 14
LENGTH: 720
                                                                                                                                                                          18.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence
                                                                                                                       Aequorea victoria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 7
                                                                                                                                                                                                                Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: CDS
LOCATION: (1196)..(3559)
                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                     US-09-999-745-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 4039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Simi
Matches 82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-205-448-7
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                                                                                                   TYPE: DNA
                                                                                                                     ORGANISM:
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Sequence 95.22, Application US/09960352

Sequence 95.22, Application US/09960352

Patent No. US20020137139A1

GENERAL INFORMATION:
APPLICANT: Warren, Weslay C.
APPLICANT: Byatt John C.
APPLICANT: Mathalagan, Nagappan
APPLICANT: Mathalagan, NacLEIC ACID AND CTHER MOLECULES ASSOCIATED WITH LACTATION AND TITLE OF INVENTION: NUCLEIC AND FAT DEPOSITION
FILLE REPRENCE: 1631.006/37.21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
LENGTH: 394
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                    103 AGTTCATCTCCACCTCATCTTCGTCTTCGCCGGCCAGGGCTCCGGCATGGCCTTCAGCA 162
                                                                                                                             43 TCGCCCTGGGGAGCCACCAGGAGGTGTACCACCCGGGCGCCCTCAAGGCGGCGTTCGCTG 102
                                                                                                                                                                                82 TCACGACGACCACTCTGACCGAAGAGGGACGTCGTCGCCACCATCGAGTACCTGGTCCGCC 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           82 TCACGACGACCACTGACCGAAGAGGACGTCGTCGCCACCATCGAGTACCTGGTCGGC 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             118 AGTICATCICCACCCTCATCTTCGTCTTCGCCGGCCAGGGCTCCGGCATGGCCTTCAGCA 177
                          Gaps
                                                                       22 TCGCGCGCGGTGGGCCGCTACAAGGTCAACAAGAAGCTCGGCCTGAACACCGCGTCCCCGA 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22 TCGCGCGGGTGGGCCGCTACAAGGTCAACAAGAAGCTCGGCCTGAACACGCGGTCCCCGA 81
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Sequen
                       86; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Bos taurus
OTHER INFORMATION: Clone ID: 41-LIB3058-002-01-K1-C2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17.5%; Score 36.4; DB 10;
50.6%; Pred. No. 0.38;
tive 0; Mismatches 86;
                       Mismatches
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Best Local Similarity 50.6%
Matches 88; Conservative
              Conservative
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US-09-960-352-9522
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US-09-815-242-7935
                 88;
                 Matches
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                                                                                                                                                                                         Sequence 7.4 Application US/09799514

Batent No. US2002006522041

GENERAL INFORMATION:

TITLE OF INVERTION: Immunoglobulin Superfamily Polynucleotides, Polypeptides, and An TITLE OF INVERTION UNMBER: US/09/799,514

CURRENT APPLICATION NUMBER: US/09/799,514

PRIOR FILING DATE: 2000-03-07

PRIOR FILING DATE: 2000-08-29

PRIOR FILING DATE: 1999-03

NUMBER OF SEQ ID NOS: 19

SOFTWARE: Patentin Ver. 2.0
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Sequence 3629, Application US/09923876

GENERAL INFORMATION:
APPLICANT: Lalgudi, Radhunath V.
APPLICANT: Alengudi, Radhunath V.
APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING
FILE REPERENCE: PL-0012-1 CON
CURRENT APPLICATION NUMBER: US/09/923,876
CURRENT FILING DATE: 2001-08-06
FRIOR PRICATION NUMBER: 09/298,329
PRIOR FILING DATE: 1999-04-21
PRIOR APPLICATION NUMBER: 60/085,331
PRIOR FILING DATE: 1998-05-05
NUMBER OF SED ID NOS: 6332
SOFTWARE: PERL Program
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10 AGCGCTACGACCTCGCGGGGGGGGCGGCTACAAGGTCAACAAGAAGCTCGGCCTGAACA 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                130 ACCTGGTCCGCCTGCACGAGGGCCACACCACGATGACCGTCCCGGGGGGGAGTCGAG 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1182;
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: OTHER INFORMATION: Incyte ID No. US20020013958A1 700405343H1
US-09-923-876-3629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 36.8; DB 10;
Pred. No. 0.33;
0; Mismatches 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 36.4; DB 10;
Pred. No. 0.37;
                                140 CCTGCACGAGGCCACACCACGATGACCGTCCCGGGC 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17.7%;
54.5%;
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50.6%;
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Matches 96; Conservative
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US-09-799-514-7
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Best Local Similarity
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ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 9
US-09-923-876-3629
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LENGTH: 1182
                                                                                                                                         RESULT 8
US-09-799-514-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 3629
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1984 ATGCCCAACGCCGTGGCGCACGTGCGCAACGCCGTGTCCGCCCTGAGCGAC 2043
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                                                                                                                                                                                                                                                                                                                                                                                                111 GTCGTCGCCACCATCGAGTACCTGGTCCGCCTGCACGAGGGCCACACCACGATGACCGTC 170
                                                                                                                                                                                                                                 Length 2329;
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TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Identification NUMBER: US/09/815,242
CURRENT APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR PAPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
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                                                                                                                                                                                                                      Ouery Match
Best Local Similarity 51.9%; Pred. No. 0.44;
Matches 82; Conservative 0; Mismatches 76;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2044 CTGCACGCGCACAAGCTTCGGGTGGACCCGGTCAACTT 2081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      171 CCGGCGGAGTCGAGGTGCCGGTGGAAACCGACGACAT 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 7788, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Pseudomonas aeruginosa
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Zyskind, Judith W.
Wall, Daniel
Trawick, John D.
Carr, Grant J.
Yamamoto, Robert T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Haselbeck, Robert
                                                                                                                                ; NAME/KEY: CDS
; LOCATION: (1612)..(2211)
US-09-816-828-9
                                                                 TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; LOCATION: (1)...(1704)
US-09-815-242-7788
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US-09-815-242-7788
                       SEQ ID NO 9
                                                                                                               FEATURE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                242 ACCCGCAGGCCACCGTGCGCACATCGTCGAAGAGGCCGTCGGCCAGATCAAGCAGGCCC 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17.5%; Score 36.4; DB 10; Length 1665; 49.5%; Pred. No. 0.43; ative 0; Mismatches 96; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Wang, Jian-Rui
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: NO. US20020150898A1el Nucleic Acids and
TITLE OF INVENTION: PolyPeptides
FILE REFERENCE: 791C1P2E
CURRENT APPLICATION NUMBER: US/09/816,828
CURRENT FILING DATE: 2001-03-22
PRIOR APPLICATION NUMBER: 09/770,160
PRIOR FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 09/750,160
PRIOR FILING DATE: 2000-04-18
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PL.FL_genes Version 2.0
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-27
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-62
STORING DATE: 2001-02-6
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FESISEQ for Windows Version 4.0
SEQ ID NO 7935
LENTH: 1665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 9, Application US/09816828
Patent No. US20020150898Al
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 17.5
Best Local Similarity 49.5
Matches 94; Conservative
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Goodrich, Ryle
Asundi, Vinod
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Xue, Aidong J.
Ma, Yunqing
Wang, Zhiwei
Zhao, Qing A.
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Wang, Jian-Rui
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; LOCATION: (1)...(1665)
US-09-815-242-7935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      193 TGGAAACCGA 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: CDS
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APPLICANT:
APPLICANT:
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APPLICANT:
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APPLICANT:
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APPLICANT:
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450 cagcaaggaaarccgcgccarggrgcrggrgcccccccgagggarcgagggracg 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62 CCTGAACACCGCGTCCCCGATCACGACGACTCTGACCGAAGAGGACGTCGTCGCCAC 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 CAAGGAGAAGCGCTACGACCTCGCGCGGGGGGCCGCTACAAGGTCAACAAGAAGCTCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 639;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      122 CATCGAGTACCTGGTCCACTTGCACGAGGGCCACACCACGATGACCG 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        570 CGGCTACATCCTTCCGGGCCTGGGCGGCCGCCGCCAAGATCTTCG 616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 35.8; DB 10;
Pred. No. 0.56;
0; Mismatches 82;
                              CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-24
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-27
PRIOR FILING DATE: 2000-10-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
PRIOR PILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SEQ ID NOS: 14110
SECTION OF 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Search completed: November 12, 2002, 16:58:30 Job time: 35.1607 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17.2%;
50.9%;
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Best Local Similarity 50.9
Matches 85; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; LOCATION: (1)...
US-09-815-242-7939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: CDS
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                                                                                                                                                                                                                                                                                                                                                                                      DEFICEANT: Smit, John APPLICANT: Smit, John APPLICANT: Bingle, Wade H. To USZODO009792Alellini, John F. TITLE OF INVERTION: EXPRESSION AND SECRETION OF HETEROLOGOUS POLYPEPTIDES FROM CAULG CURRENT APPLICATION NUMBER: US/09/379,931
CURRENT FILING DATE: 1996-08-24
PRIOR APPLICATION NUMBER: US 08/194,377
PRIOR APPLICATION NUMBER: US 08/194,290
PRIOR APPLICATION NUMBER: US 08/194,290
PRIOR FILING DATE: 1994-02-09
PRIOR FILING DATE: 1992-06-09
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FASTSEQ for Windows Version 4.0
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                                                                                                                 92 CACTCTGACCGAAGAGGACGTCGTCGCCACCATCGAGTACCTGGTCCGGCCTGCACGAGGG 151
32 GGGCGGTACAAGATCAACAAGAAGCTCGAACACCGGGTCCCCGATCACGACGAC 91
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                                                                                                                                                                           152 CCACACCACGATGACCGTCCCGGGCGGAGTCGAGGTGCCGGTGGAAACCGACGACAT 208
                                                                                                                                                                                                           Length 3300;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17.4%; Score 36.2; DB 10;
50.9%; Pred. No. 0.51;
tive 0; Mismatches 83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 7939, Application US/09815242
Patent No. US20020061569A1
                                                                                                                                                                                                                                                                                                        US-09-379-931-6
; Sequence 6, Application US/09379931
; Patent No. US2002009792A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Caulobacter crescentus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Oblsen, Karl L.
APPLICANT: Oblsen, Karl L.
APPLICANT: Wall, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Travick, John D.
APPLICANT: Travick, John D.
APPLICANT: Tramick, John D.
APPLICANT: Yamamoto, Robert T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 50.99
Matches 86; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; NAME/KEY: CDS
; LOCATION: (101)...(3178)
US-09-379-931-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-815-242-7939
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LENGTH: 3300
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GenCore version 5.1.3

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OM nucleic - nucleic search, using sw model

Run on: November 12, 2002, 15:56:36; Search time 27.8936 Seconds

(without alignments)
2286.857 Million cell updates/sec

Title:

US-09-697-1238-17

Perfect score: 208
Sequence: 1 tcaaggagaaggctacgac......ccggtggaaaccgacgacat 208
Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 10%
Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/Packfiles1.seq:*

Database

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	ID	US-08-250-030-1	PCT-US95-06790-1	US-08-313-185-57	US-09-082-614A-57	US-07-988-260B-2	US-09-029-603-1	US-08-804-227C-7	US-08-804-198-1	US-09-513-783A-49	US-09-094-359-7	US-09-172-063-13	US-09-316-919-14	US-09-094-359-11	US-09-172-063-27	US-09-513-783A-33	US-09-232-468A-1	5196516-7	US-08-732-412-1	US-09-543-084A-31	US-09-543-084A-30	-60	US-09-543-084A-26	US-09-543-084A-28		- 1	US-09-329-350-32	US-08-194-290-6	
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æ	Query	76.9	76.9		69.2	18.6	18.4	18.4	18.4	18.3	18.3	18.3	18.3	18.3	18.3	18.3	18.3	18.3	17.9	17.8	17.8	17.8	17.8	17.8	17.8	17.5	17.4	17.4	
	Score	160	160	144	144	38.6	38.2	38.2	38.2	38	38	38	38	38	38	38		m	37.2	37	37	37	37	37	37	36.4	36.2	36.2	
	Result No.	1	7	e	4	5	9	7	æ	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	

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sednence sed		0; 0; IIIIII
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-5488-6 -6488-6 -3-440A-7 -53-440A-7 -534-7 -537-5 -63-4 -088-3 -755A-1 -755A-1 -755A-1 -755A-1 -754-1 -754-1 -791-4	enetic enetic empin s sessne: rsion	5e-30 ches GCCGCT GTCGCT GTCGCT
US-08-614-377A-6 US-09-142-648B-6 US-09-103-840A-2 US-09-103-840A-1 US-08-105-537-30 US-09-105-537-30 US-09-105-537-30 US-09-105-537-5 US-09-029-603-4 US-08-089-755A-1 US-08-089-755A-1 US-08-421-754-4 US-08-421-754-4 US-08-421-791-4 US-08-421-791-4 US-08-421-791-4 US-08-421-791-4 US-08-421-791-4 US-08-421-791-4 US-08-421-791-4 US-08-421-791-4 US-08-421-791-4	ALIGNMENT 1.0030 1.0030 1. Specimens 4. Specimens 4. Specimens 4. Specimens 4. Specimens 5. Specimens 7. Specimens	Score 160; DB 1 Pred. No. 5e-30; ; Mismatches CGGGGGGGCGCTA
2 US- 1	11: 11: 11: 11: 11: 11: 11: 11: 11: 11:	Score Pred. O; Mi Street Stree
3300 3300 3300 4411529 4411529 138728 38778 38708 5835 5835 5835 5835 5835 5835 5835 58	tion us/08 ting, bavid ng, bavid NN: Detect NN: Detect NN: Clinis ES: 15 DORES: 15 DORES: 15 DORES: 15 NN: Clinis Lisc compatible NC compatible	76.9%; 85.6%; Itive ACGACCTO
7.17.7.7.7.7.7.7.7.7.7.7.7.7.7.7.7.7.7.	THIS THIS TO THE PROPERTY OF T	tch 76.9%; Score 160; DB 1; Length 970; 12.1 Similarity 85.6%; Pred. No. 5e-30; Indels 0; G. 178; Conservative 0; Mismatches 30; Indels 0; G. TCAAGGAGAAGCGCTGCGGGGGGGGCGCTACAACAACAAGAAGCTCG
9339 3439 3439 3499 3499 3499 3499 3499	THE PERSONNEL STREET OF THE PROPERTY OF THE PR	ch 11 Similarity 178; Conser CAAGGAGAAGCG
800044440678004444 	RESULT 1 US-08-250-030-1 Sequence 1, As Fatent No. 564 GENERAL INFOS GENERAL INFOS APPLICANT: TITLE OF INTITLE	Y Ma Loc hes 1
ਜ਼	RESULT US-08-1: Sequence of the control of the cont	Query M Best Lo Matches Qy 1 Db 26

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US-09-082-614A-57
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CCATCGAGTACCTGGTCCGCCTGCACGAGGGCCACACCACGATGACCGTCCCGGGCGGAG 180
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                                                                                                                                                                                                                                                                 Sequence 1, Application PC/TUS9506790
GENERAL INFORMATION:
APPLICANT: Mayo Foundation for Medical Education and Research
APPLICANT: and Hoffmann-La Roche Inc.
TITLE OF INVENTION: Detection of a Genetic Locus Encoding
TITLE OF INVENTION: Resistance to Rifampin
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 160; DB 5; Length 970;
Pred. No. 5e-30;
0; Mismatches 30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: DATORIN PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06790
FILING DATE: 26-MAY-1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Schwegman, Lundberg & Woessner
STREET: 3500 IDS Center
CITY: Minneapolis
                                                                                                                                          181 TCGAGGTGCCGGTGGAAACCGACGAT 208
                                                                                                                                                                TCGAGGTGCCGGTGGAAACCGACGACAT 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCGAGGTGCCGGTGGAAACCGACGACAT 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Reacach, Kevin W.
REGISTRATION NUMBER: 35.651
REFERENCE/DOCKET NUMBER: 150.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-339-3061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 85.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 970 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 178; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: MN
COUNTRY: U
                                                                                                                                                                                                                                RESULT 2
PCT-US95-06790-1
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61 GCCTGAACACCGCGTCCCCGATCACGACGACCACTCTGACCGAAGAGGACGTCGTCGCCA 120
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                                                                                                                                    APPLICANT: Cole, Stewart
APPLICANT: Cole, Stewart
APPLICANT: Zhang, Ying
APPLICANT: Telenti, Amalio
APPLICANT: Telenti, Amalio
APPLICANT: Bodmer, Thomas
TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
NUMBER OF SEQUENCES: 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 3447;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OVERMINDS STSTEM: rc-LUDS,rbs-LUDS
SOFFWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/313,185
FILING DATE: 12-0CT-1994
FILING DATE: 12-0CT-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MA-9CTS, Kenneth J.
REGISTRATION NUMBER: 02356.0068-00000
TELECOMMUNICATION INFORMATION:
TELEPAX: (202) 408-4400
TELEPAX: (202) 408-4400
TELEPAX: (202) 408-4400
TELEPAX: (202) 408-4600
                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Finnegan, Henderson, Farabow, Garrett ADDRESSEE: Dunner STREET: 1300 I Street, N.W. STATE: D.C. COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 144; DB 2;
Pred. No. 3.6e-26;
0; Mismatches 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                  Sequence 57, Application US/08313185 Patent No. 5851763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; MOLECULE TYPE: DNA (genomic)
US-08-313-185-57
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80.8%;
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Best Local Similarity 80.8'
Matches 168; Conservative
                                                                                GENERAL INFORMATION:
APPLICANT: Heym, Beate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 20005-3315
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
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US-08-313-185-57
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linear
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                     GENERAL INFORMATION:
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                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 6
US-09-029-603-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 CCATCGAGTACCTGGTCCGCCTGCACGAGGGCCACCACGATGACCGTCCCGGGGGGGAG 180
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                                                                    APPLICANT: Cole, Stewart
APPLICANT: Cole, Stewart
APPLICANT: Young, Douglas
APPLICANT: Anny Ying
APPLICANT: Honore, Nadine
APPLICANT: Honore, Thomas
TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
TITLE OF INVENTION: In Mycobacterium Tuberculosis
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69.2%; Score 144; DB 3; Length 3447; 80.8%; Pred. No. 3.6e-26; 1ive 0; Mismatches 40; Indels
                                                                                                                                                                                                                                                          ADDRESSEE: Finnegan, Henderson, Farabow, Garrett ADDRESSEE: Dunner STREET: 1300 I Street, N.W.
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/082,614A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Meyers, Kenneth J.
RECISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 02356.0068-00000
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 TCGAGGTGCCGGTGGAAACCGACGAT 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/313,185
FILING DATE: 12-OCT-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                    ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
Sequence 57, Application US/09082614A
Patent No. 6124098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 2, Application US/07988260B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                    Heym, Beate
Cole, Stewart
Young, Douglas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 80.8'
Matches 168; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nucleic acid
EDNESS: single
                                    GENERAL INFORMATION:
APPLICANT: Heym, 1
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PARTICIANT: BREAZINSKI, RYSZAND

TITLE OF YNEWTION:
RINGHOUS:
NUMBERSON SENGERS:
ADDRESSER: CUSHANN

STREET: ADDRESSER:
ADDRESSER: CUSHANN

STREET: BIN PACA, MORELOR

COMPUTED: BAS ADDRESSER:
ADDRESSER: CUSHANN

STREET: BIN PACA, MORELOR

COMPUTED: BAS ADDRESSER:
ADDRESSER:
ADDRESSER: CUSHANN

STREET: BIN PACA, MORELOR

COMPUTED: BAS ADDRESSER:
ADD
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Db 20997 GGTGCGGGCAGCGCGGTCAACCAGGACGGTGCCAGCAACGGCCTCACCGCACCCAGCGG 21056
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                                                                                                                                                                                                                                                                                                                                                     5 GGAGAAGCGCTACGACCTCGCGGGGGGGGCGGCTACAAGGTCAACAAGAAGCTCGGCCT 64
                                                                                                                                                                                                                                                                                 Length 44377;
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                                                                                                                                                                                                                                                                       Query Match 18.4%; Score 38.2; DB 2; I Best Local Similarity 49.3%; Pred. No. 0.69; Matches 100; Conservative 0; Mismatches 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/08804198
Patent No. 5945320
GENERAL INFOMATION:
GENERAL INFOMATION:
APPLICANT: Burgett, Stanley G.
APPLICANT: Rao, Nagaraja R.
APPLICANT: Rao, Nagaraja R.
APPLICANT: Rosteck, Paul R., Jr.
TITLE OF INVENTION: PLATENOLIDE SYNTHASE GENE NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: PAUL R. CANTRELL 1138
STREET: LILLY CORPORATE CENTER
CTITY: INDIANAPOLIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 46285
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: Macintosh 7.0
SOFTWARE: Microsoft Word 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/804,198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          185 GGTGCCGGTGGAAACCGACGACA 207
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NAME: CARTRELL, PAUL R.
REGISTRATION NUMBER: 36,470
REFERENCE/DOCKET NUMBER: P911:
TELEPHONE: 317.276-3885
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH 444377 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                CDS
14046..20036
                                                                       CDS
20110..31284
                                                                                                                                    CDS
31329..36071
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CLASSIFICATION: 435
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                                                                                                             FEATURE:
NAME/KEY:
LOCATION:
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              NAME/KEY:
LOCATION:
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LOCATION:
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US-08-804-227C-7
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US-08-804-198-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     128 GTACCTGGTCCGCCTGCACGAGGGCCACACGATGACCGTCCCGGGCGGAGTCGAGG 186
                                                                                                                                                                                                                                                                                                                           8 GAAGCGCTACGACCTCGCGCGGGGGCCGCTACAAGGTCAACAAGAAGCTCGGCCTGAA 67
                                                                                                                                                                                                                                         / Match 18.4%; Score 38.2; DB 4; Length 2122; Local Similarity 50.8%; Pred. No. 0.52; les 91; Conservative 0; Mismatches 88; Indels 0
                                                                                                                                                                                                                                                                                     88; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: DeHOFF, Bradley S.
APPLICANT: Kubstoss, Stuart A.
APPLICANT: Rosteck, Paul R., Jr.
APPLICANT: SULTON, Kimberly L.
TITLE OF INVENTION: POLYKETIDE SYNTHASE GENES
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: THOMAS G. PLANT 1501
STREET: LILLY CORPORATE CENTER
                                                                                                                                      NAME.KEY: misc_RNA
LOCATION: (1)..(2122)
OTHER INFORMATION: product = 2.1 kb region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: ASCI(DOS) Text only
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/804,227C
FILING DATE: FEBRUARY 21, 1997
                                                                                TYPE: DNA ORGANISM: Streptomyces longisporoflavus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Plant, Thomas, G.
REGISTRATION NUMBER: 35,784
REFERENCE/DOCKET NUMBER: X-8231
TELEPROMENICATION INFORMATION:
TELEPHONE: 317-276-2459
INFORMATION FOR SEO ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 7, Application US/08804227C Patent No. 5876991 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: DNA (genomic)
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LENGTH: 44377 base pairs
TYPE: nucleic acid
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver, 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: single
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LOCATION: 350..14002
FEATURE:
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ZIP: 46285
                                        SEQ ID NO 1
LENGTH: 2122
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Matches
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121 CCATCGAGTACCTGGTCCGCCTGCACGAGGCCCACACCACGATGACCGTCCCGGGCGGAG 180
            452 TCTATATCACCGCCGACAAGCAGAAGAACGGCATCAAGGCCAACTTCAAGATCCGCCACA 511
                                                                          61 GCCTGAACACCGCGTCCCCGGATCACGACCACTCTGACCGAAGAGGACGTCGTCGCCA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 CCATCGAGTACCTGGTCCGCCTGCACGAGGCCACCACGATGACCGTCCCGGGCGGAG 180
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Fatent No. 6150176
GENERAL INFORMATION:
APPLICANT: Miyawaki, Atsushi
APPLICANT: Miyawaki, Atsushi
APPLICANT: Miyawaki, Atsushi
APPLICANT: Morher, Robekka M.
APPLICANT: Memington, S. James
TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
TITLE OF INVENTION: MEASURING THE PH OF A BIOLOGICAL SAMPLE
FILE REFERENCE: 07257/071001
CURRENT APPLICATION NUMBER: US/09/172,063
CURRENT FILING DATE: 1998-10-13
EARLIER APPLICATION NUMBER: 09/094,359
                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Tsien, Roger Y.
APPLICANT: Hyawaki, Atsushi
APPLICANT: Llopis, Juan
TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
TITLE OF INVENTION: MEASURING THE PH OF A BIOLOGICAL SAMPLE
FILE REFERENCE: 07257/067001
CURRENT APPLICATION NUMBER: US/09/094,359
CURRENT APPLICATION NUMBER: US/09/094,359
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18.3%; Score 38; DB 3; Length 720;
49.0%; Pred. No. 0.53;
tive 0; Mismatches 105; Indels
                                                                                                                                                               572 ACGCCCCGTCTCCTCCCCAAC 597
                                                                                                                              181 TCGAGGTGCCGGTGGAACCGACGAC 206
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Patent No. 6140132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Aequorea victoria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 18.3
Best Local Similarity 49.0
Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: (1)...(717)
OTHER INFORMATION: ECFP
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                                                                                                                                                                                                                                                  US-09-094-359-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 GGAGAAGCGCTACGACCTCGCGCGGTGGGCCGCTACAAGAGGTCAACAAGAAGCTCGGCCT 64
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: LOCATION: (1)..(717)
: OTHER INFORMATION: Description of Artificial Sequence: ECFP
US-09-513-783A-49
                                                                                                                                                                                                                                                                                                                                                                          Ouery Match
18.4%; Score 38.2; DB 2; Length 4
Best Local Similarity 49.3%; Pred. No. 0.69;
Matches 100; Conservative 0; Mismatches 103; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18.3%; Score 38; DB 4; Length 717, 49.0%; Pred. No. 0.53; ive 0; Mismatches 105; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Gluliano, Kenneth A.
APPLICANT: Gluliano, Kenneth A.
APPLICANT: Gluliano, Kenneth A.
TITLE OF INVENTION: A System for Cell Based Screening
FILE REFERENCE: 97-022-L1
CURRENT APPLICATION VIBBER: US/09/513,783A
CURRENT FILING DATE: 2000-02-25
NUMBER OF SEQ ID NOS: 180
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21177 CGCGCTGATGCCCACCTACGGCA 21199
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Patent No. 6416959
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TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
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ORGANISM: Artificial Sequence
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14046..20036
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36155..41830
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31329..36071
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350..14002
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US-09-513-783A-49
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US-08-804-198-1
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Pred. No. 0.53;
0; Mismatches 105; Indels
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US-09-316-919-14
Sequence 14, Application US/09316919
Sequence 14, Application US/09316919
Retent No. 6469154
GENERAL INFORMATION:
APPLICAMT: Taien, Roger Y.
APPLICAMT: Baird, Geoffrey
TITLE OF INVENTION: FLUORESCENT PROTEIN INDICATORS
FILE REFERENCE: 07257/073001
CURRENT APPLICATION NUMBER: US/09/316,919
CURRENT FILING DATE: 1999-05-21
NUMBER OF SEQ ID NOS: 63
SOFTWARE: FastSEQ for Windows Version 4.0
EARLIER FILING DATE: 1998-06-09
NUMBER OF SEQ ID NOS: 38
SOFTWARE: PASTSEQ for Windows Version 4.0
SEQ ID NO 13
LENGTH: 720
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Best Local Similarity 49.0%;
                                                                                   TYPE: DNA
ORGANISM: Aequorea victoria
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US-09-316-919-14
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OTHER INFORMATION: ECFP
                                                                                                                                      NAME/KEY: misc_feature
LOCATION: (0)...(0)
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LENGTH: 720
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61 GCCTGAACACCGGGTCCCCGATCACGACGACCACTCTGACCGAAGAGGACGTCGTCGCCA 120
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                                                                  GENERAL INFORMATION:
APPLICANT: Tsien, Roger Y.
APPLICANT: Tsien, Atsushi
APPLICANT: Liopis, Juan
TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
TITLE OF INVENTION: MEASUBING THE PH OF A BIOLOGICAL SAMPLE
FILE REFERENCE: 07257/06/7001
CURRENT APPLICATION NUMBER: US/09/094,359
CURRENT FILING DATE: 1998-06-09
NUMBER OF SEQ ID NOS: 18
SOTWARR: FASTSEQ for Windows Version 4.0
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APPLICANT: Tsien, Roger Y.
APPLICANT: Miyawaki, Atsushi
APPLICANT: Liopis, Juan
APPLICANT: Hopis, Juan
APPLICANT: Rediditor, S. James
TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
TITLE OF INVENTION: MEASURING THE PH OF A BIOLOGICAL SAMPLE
FILE REFERENCE: 0727/071001 The PH OF A BIOLOGICAL SAMPLE
FILE REFERENCE: 1998-10-13
CURRENT FILIUG DATE: 1998-10-13
EARLIER FILING DATE: 1998-06-09
NUMBER OF SEQ ID NOS: 38
SOFTWARE: FastSEQ for Windows Version 4.0
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Best Local Similarity 49.0%; Pred. No. 0.53;
Matches 101; Conservative 0; Mismatches 105; Indels
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                            Sequence 11, Application US/09094359
Patent No. 6140132
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Patent No. 6150176
GENERAL INFORMATION:
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CTHER INFORMATION: ECFP-mito
US-09-094-359-11
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ORGANISM: Aequorea victoria
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ORGANISM: Aequorea victoria
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LOCATION: (0)...(0)
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JS-09-094-359-11
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LENGTH: 972
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LOCATION: (1)..(1623)

OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: YFP-NLS-CP3-multiple DEVD-CFP-Annexin II construct US-09-513-783A-33
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Best Local Similarity 49.0%; Pred. No. 0.54;
Matches 101; Conservative 0; Mismatches 105; Indels
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Sequence 33. Application US/09513783A
Sequence 33. Application US/09513783A
GENERAL NNOPMATION:
APPLICANT: Giuliano, Kenneth A.
TITLE NEFERENCE: 97-022-L1
CURRENT APPLICATION NUMBER: US/09/513,783A
CURRENT FILING DATE: 2000-02-25
NUMBER OF SEQ ID NOS: 180
SEQ ID NO 33
LENGTH: 1623
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; OTHER INFORMATION: GT-ECFP US-09-172-063-27
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Best Local Similarity
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Non-tuberculous mycobacteria; rpoB gene fragment; NTM; HIV; PRA; RFLP; PCR-restriction fragment length polymorphism analysis; ds.
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  AAS05217 standard; DNA; 208
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 WO200131061-A1.
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3438.621 Million cell updates/sec
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2. SIDSZ/gcgdata/geneseqf.embl/NA1981.DAT:*
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15. /SIDSZ/gcgdata/geneseqf.embl/NA1993.DAT:*
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18. /SIDSZ/gcgdata/geneseqf.embl/NA1999.DAT:*
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Mycobacterium a
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                                                                   2002, 15:44:35; Search time 136.222 Seconds
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      GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                    2185239 seqs, 1125999159 residues
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                                              nucleic - nucleic search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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AAS05215
AAS05219
AAS05201
AAS05211
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AAS05203
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Gapop 10.0 , Gapext 1.0
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Human Rapla, c-Raf Human Rapla, c-Raf

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3 Park

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27-OCT-2000; 2000WO-KR01223.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Non-tuberculous mycobacteria; rpoB gene fragment; NTM; HIV; PRA; RFLP; PCR-restriction fragment length polymorphism analysis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                              CCATCGAGTACCTGGTCCGCCTGCACGAGGGCCACCACGATGACCGTCCCGGGGGGAG 180
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                                                                                                                                                                                                                                                                                                            Length 208;
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                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                               Sequence 208 BP; 48 A; 71 C; 64 G; 25 T; 0 other;
                                                                                                                                                                                                                                                                                                      Query Match 100.0%; Score 208; DB 22; Best Local Similarity 100.0%; Pred, No. 5.4e-38; Matches 208; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mycobacterium kansasii rpoB gene fragment.
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           Claim 1; Page 45; 50pp; English.
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The present sequence for Mycobacterium kansasii rpoB gene fragment is 1 of 24 rpoB gene fragments (AAS05201-AAS05224) from various Mycobacterial species. These rpoB gene fragments can be used in the diagnosis and identification of Mycobacterium species using a novel PCR-restriction fragment length polymorphism analysis (PRA) (method. The method comprises obtaining a restriction fragment length polymorphism (RFLP) pattern of the 24 rpoB gene fragments; isolating, amplifying and digesting the DNA fragment from the microorganism to be identified and comparing the RFLP patterns from the known rpoB gene fragments with the unidentified fragment. The rpoB gene fragments comparing the RFLP patterns from the known rpoB gene fragments with the unidentified fragment. The rpoB gene fragments of are useful to identify a wide range of Mycobacterium species, e.g. for diagnosis or to obtain epidemiological and pathogenesis information for selection of appropriate therapies, including W. tuberculosis, M. leprae and non-tuberculosis mycobacteria (NTM) encountered in subjects infected with human immunodeficiency virus (HTV). Analysis of the rpoB gene fragments is rapid, precise, simple and cost effective (only 1 PCR required), and can differentiate between many species in a single experiment, including those difficult to distinguish by usual blochemical districtive proving analysis of the rests. Also described are oligonuclectide probes (AAS05227-AAS05242) for darentian analysis of the rests.
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                                                                  New DNA fragments from the rpoB gene of mycobacteria, useful idiagnosis and identification of many mycobacterial species by restriction fragment length polymorphism
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Pred. No. 1.9e-30;
0; Mismatches 21; Indels
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PCR-restriction fragment length polymorphism analysis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 208 BP; 51 A; 65 C; 65 G; 27 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    detecting specific Mycobacterial species.
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Best Local Similarity 89.9%;
Matches 187; Conservative
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WPI; 2001-300520/31.
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Park HJ

Kim Y,

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Park YK, Bai G, Kim

99KR-0046795.

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(ERUM-) ERUME BIOTECH CO LTD.
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                  WO200131061-A1.
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fragment is 1 of 24 rpoB gene fragments (AASO5201-AASO5224) from
various Mycobacterial species. These rpoB gene fragments can be used
in the diagnosis and identification of Mycobacterium species using a
novel PCR-restriction fragment length polymorphism analysis (PRA)

cc method. The method comparises obtaining a restriction fragment length

cc method. The method comparing the DNA fragment from the microorganism to

bolymorphism (RFLP) pattern of the 24 rpoB gene fragments; isolating,

amplifying and digesting the DNA fragment from the microorganism to

cc be identified and comparing the RFLP patterns from the known rpoB gene

cc fragments with the unidentified fragment. The rpoB gene fragments

cc fragments with the unidentified fragment. The rpoB gene fragments

cc diagnosis or to obtain epidemalological and pathogenesis information for

cs election of appropriate therapies, including M. tuberculosis, M. leprae

and non-tuberculous mycobacteria (MTM) encountered in subjects infected

cc with human immunodeficiency virus (HIV). Analysis of the rpoB gene

cc with human immodeficiency virus (HIV). Analysis of the rpoB gene

cr required, and can differentiate between many species in a single

cc experiment, including those difficult to distinguish by usual blochemical

cc rests. Also described are oligonucleotide probes (AASO5227-AASO5227) for
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                                                                                                                              for
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                                                                                                                      New DNA fragments from the rpoB gene of mycobacteria, useful idiaynosis and identification of many mycobacterial species by restriction fragment length polymorphism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 208;
                                                                        Park HJ;
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                                                                       Kim Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 208 BP; 44 A; 69 C; 69 G; 26 T; 0 other;
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Pred. No. 5.1e-29;
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                                                                                                                                                                               Claim 1; Page 44; 50pp; English.
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                                        (ERUM-) ERUME BIOTECH CO LTD.
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88.0%;
             99KR-0046795.
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                                                                     Park YK,
             27-OCT-1999;
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Best Local 3
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The present sequence for Mycobacterium fortuitum rpoB gene fragment is 1 of 24 rpoB gene fragments (AASO5201-AASO524) from various Mycobacterial species. These rpoB gene fragments can be used in the diagnosis and identification of Mycobacterium species using a novel PCR-restriction fragment length polymorphism analysis (PRA) method comprises obtaining a restriction fragment length polymorphism (RFLP) pattern of the 24 rpoB gene fragments; isolating, amplifying and digesting the DNA fragment from the microorganism to comparing the RFLP patterns from the microorganism to comparing the RFLP patterns from the known rpoB gene fragments with the unidentified fragment. The rpoB gene fragments with the unidentified fragment. The rpoB gene fragments or to obtain epidemiological and pathogenesis information for selection of appropriate therapies, including Mycobacterium species, e.g. for diagnosis or to obtain epidemiological and pathogenesis information for selection of appropriate therapies, including N. tuberculosis, M. leprae and non-tuberculous mycobacteria (NFM) encountered in subjects infected fragments is rapid, precise, simple and cost effective (only 1 PCR required), and can differentiate between many species in a single experiment, including those difficult to distinguish by usual blochemical detecting shorific Mycobacterial generates (ABSO5227-AASO5242) for detecting shorific Mycobacterial are oliginated per observed.
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New DNA fragments from the rpoB gene of mycobacteria, useful diagnosis and identification of many mycobacterial species by
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Pred. No. 5.1e-29;
0; Mismatches 25; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25; Indels
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                                                                               restriction fragment length polymorphism
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                                                                                                                                               Claim 1; Page 46; 50pp; English
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Best Local Similarity 88.07
Matches 183; Conservative
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BP

AAS05211 standard; DNA; 208

(first entry)

07-SEP-2001

AAS05211;

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The present sequence for Mycobacterium gordonae type I rpoB gene fragment is 1 of 24 rpoB gene fragments (AASO5201-AASO5224) from 20 various Mycobacterial species. These rpoB gene fragments can be used in the diagnosis and identification of Mycobacterium species using a novel PCR-restriction fragment length polymorphism analysis (PRA) method. The method comprises obtaining a restriction fragment length comprises obtaining a restriction fragment length amplifying and digesting the DNA fragment from the microorganism to be identified and comparing the RPLP patterns from the known rpoB gene fragments with the unidentified fragment. The rpoB gene fragments with the unidentified fragment. The rpoB gene fragments of diagnosis or to obtain epidemiological and pathogenesis information for selection of appropriate therapies, including M. tuberculosis, M. leprae cand non-tuberculosus mycobacteria (NTM) encountered in subjects infected the brown views (NTM) and manifered to the control of the
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                                                           Non-tuberculous mycobacteria; rpoB gene fragment; NTM; HIV; PRA; RFLP; PCR-restriction fragment length polymorphism analysis; ds.
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  Mycobacterium gordonae type I rpoB gene fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kim Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26;
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                                                                                                                                             Mycobacterium gordonae type I.
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The present sequence for Mycobacterium marinum rpoB gene fragment is 1 of 24 rpoB gene fragments (AASO5201-AASO5204) from various Mycobacterial species. These rpoB gene fragments can be used to the diagnosis and identification of Mycobacterium species using a novel PCR-restriction fragment length polymorphism analysis (PRA) method comprises obtaining a restriction fragment length colymorphism (RFLP) pattern of the 24 rpoB gene fragments length polymorphism (RFLP) pattern of the 24 rpoB gene fragments is isolating, amplifying and digesting the DNA fragment from the microorganism to be identified and comparing the RFLP patterns from the known rpoB gene fragments with the unidentified fragment. The rpoB gene fragments con a useful to identified and comparing the RFLP patterns from the known rpoB gene fragments with the unidentify a wide range of Mycobacterium species, e.g. for a selection of appropriate therapies, including M. tubberculosis, M. leprae and non-tuberculous mycobacteria (NTM) encountered in subjects infected tagments is rapid, precise, simple and cost effective (only 1 PCR required), and can differentiate between many species in a single capteriant should are oligonuclectide probes (AASO5227-AASO5242) for cherent and sometian energial and searched are oligonuclectide probes (AASO5227-AASO5242) for cherent in a service continual and cost from the service of the propes of the probes (ABSO5227-AASO5242) for cherent in a service continual and cost from the service of the probes (ABSO5227-AASO5242) for cherent in the service of the probes of the probes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New DNA fragments from the rpoB gene of mycobacteria, useful f
diagnosis and identification of many mycobacterial species by
restriction fragment length polymorphism
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                                                                                                                                                                                    Non-tuberculous mycobacteria; rpoB gene fragment; NTM; HIN PCR-restriction fragment length polymorphism analysis; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Park HJ;
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87.0%; Pred. No. 2.6e-28;
1ve 0; Mismatches 27;
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                                                                                                                                      Mycobacterium marinum rpoB gene fragment.
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                                                                                                                                                                                                                                                           Mycobacterium marinum.
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RESULT 6 AAS05211

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181 TCGAGGTGCCGGTCGAGACCGACGACAT 208
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The present sequence for Mycobacterium xenopi rpoB gene fragment is 1 of 24 rpoB gene fragments (AASO5201-AASO5224) from various Mycobacterial species. These rpoB gene fragments can be used to the diagnosis and identification of Mycobacterium species using a novel PCR-restriction fragment length polymorphism analysis (PRA) comprises obtaining a restriction fragment length polymorphism (RFLP) pattern of the 24 rpoB gene fragments; Isolating, amplifying and digesting the DNA fragment from the microorganism to De identified and comparing the RFLP patterns from the known rpoB gene fragments with the unidentified fragment. The rpoB gene fragments come serial to identify a wide range of Mycobacterium species, e.g. for diagnosis or to obtain epidemiological and pathogenesis information for selection of appropriate therapies, including M. tuberculosis, M. leprae and non-tuberculous mycobacteria (MTM) analysis of the rpoB gene continued to a precise, simple and cost effective (only 1 pcR required), and can differentiate between many species in a single experiment, including those difficult to distinguish by usual biochemical correction of escribed are oligonuclectide probes (AASO5227-AASO5242) for deferring analysis of the ropes (estering analysis of the ropes). Non-tuberculous mycobacteria; rpoB gene fragment; NTM; HIV; PRA; RFLP; PCR-restriction fragment length polymorphism analysis; ds. New DNA fragments from the rpoB gene of mycobacteria, useful f diagnosis and identification of many mycobacterial species by restriction fragment length polymorphism Park HJ; Kim Y, s, detecting specific Mycobacterial species. Mycobacterium xenopi rpoB gene fragment. Cho Park YK, Bai G, Kim S, Claim 1; Page 47; 50pp; English BP. (ERUM-) ERUME BIOTECH CO LTD. AASO5224 standard; DNA; 208 27-OCT-2000; 2000WO-KR01223. 99KR-0046795. 07-SEP-2001 (first entry) Mycobacterium xenopi WPI; 2001-300520/31. WO200131061-A1. 27-OCT-1999; 03-MAY-2001 AAS05224; Ŧ, Lee RESULT 7 AAS05224

Sequence 208 BP; 51 A; 65 C; 67 G; 25 T; 0 other;

ö Gaps ; 0 DB 22; Length 208; Score 164.8; DB 22; Length Pred. No. 2.6e-28; 0; Mismatches 27; Indels 79.2%; 87.0%; Best Local Similarity 87.09 Matches 181; Conservative Query Match

1 TCAAGGAGAAGCGCTACGACCTCGCGCGGGTGGGCCGCTACAAGGTCAACAAGAAGCTCG 60

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- 61 GCCTGAACACCGCGTCCCCGATCACGACGACCACTCTGACCGAAGAGGACGTCGTCGCCA 120 a
- ò qq

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HIV; PRA; RFLP;
CCATCGAGTACCTGGTCCGCCTGCACGAGGCCACCACGATGACCGTCCCGGGCGGAG 180
      Non-tuberculous mycobacteria; rpoB gene fragment; NTM;
PCR-restriction fragment length polymorphism analysis;
                                                                                             Mycobacterium gordonae type III rpoB gene fragment.
                           TCGAGGTGCCGGTGGAAACCGACGACAT
                                                                                                                        Mycobacterium gordonae type III.
                                                             BP.
                                                                                                                                                         27-OCT-2000; 2000WO-KR01223.
                                                                                                                                                                     99KR-0046795.
                                                            AAS05203 standard; DNA; 208
                                                                                  (first entry)
                                                                                                                                   WO200131061-A1.
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                                                                       AAS05203;
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121
                      181
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                                                 RESULT 8
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Park Kim Y, Š Cho ŝ Park YK, Bai G, Kim WPI; 2001-300520/31. Lee H,

(ERUM-) ERUME BIOTECH CO LTD.

for

ΗÜ;

New DNA fragments from the rpoB gene of mycobacteria, useful for diagnosis and identification of many mycobacterial species by restriction fragment length polymorphism

Claim 1; Page 41; 50pp; English.

The present sequence for Mycobacterium gordonae type III rpoB gene fragment is 1 of 24 rpoB gene fragments (AAS05201-AAS05204) from various Mycobacterial species. These rpoB gene fragments can be used in the diagnosis and identification of Mycobacterium species using a novel PCR-restriction fragment length polymorphism analysis (PRA) method comprises obtaining a restriction fragment length polymorphism (RFLP) pattern of the 24 rpoB gene fragments; isolating, amplifying and digesting the DNA fragment from the microorganism to be identified and comparing the RFLP patterns from the known rpoB gene fragments with the unidentified fragment. The rpoB gene fragments are useful to identify a wide range of Mycobacterium species, e.g. for diagnosis or to obtain epidemiological and pathogenesis information for selection of appropriate therapies, including withberculosis, M. leprec and non-tuberculous mycobacteria (NTM) encountered in subjects infected fragments is rapid, precise, simple and cost effective (only 1 PCR required), and can differentiate between many species in a single experiment, including those difficult to distinguish by usual blochemical deferentian encountered are oligonuclectide probes (AAS05227-AAS05242) for deferentian encountered are oligonuclectide probes (AAS05227-AAS05242) for detecting specific Mycobacterial species.

Sequence 208 BP; 46 A; 69 C; 63 G; 30 T; 0 other;

Gaps ö Length 208; 29; Indels 77.7%; Score 161.6; DB 22; 86.1%; Pred. No. 1.4e-27; 0; Mismatches Conservative Best Local Similarity Matches 179; Conserv Query Match

1 TCAAGGAGAAGCGCTACGACCTCGCGGGTGGGCCGCTACAAGGTCAACAAGAAGCTCG 60

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Non-tuberculous mycobacteria; rpoB gene fragment; NTM; HIV; PRA; RFLP; PCR-restriction fragment length polymorphism analysis; ds.
                                                                       121 CCATCGAGTACCTGGTCCGTCTGCACGAGGGTCAGCACCATGACCGTTCCGGGCGGCA 180
                                                                                                                          CCATCGAGTACCTGGTCCGCCTGCACGAGGCCCACACCACGATGACCGTCCCGGGCGGAG 180
                    9
GCCTGAACACCGCGTCCCCGATCACGACGACTCTGACCGAAGAGGACGTCGTCGCCA
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                                                                                                                                                                                                                     TCGAGGTGCCGGTGGAAACCGACGACAT 208
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The present sequence for Mycobacterium tuberculosis rpoB gene fragment is 1 of 24 rpoB gene fragments (AAS05201-AAS05224) from fragment is 1 of 24 rpoB gene fragments can be used in the diagnosis and identification of Mycobacterium species using a novel PCR-restriction fragment length polymorphism analysis (PRA) method comprises obtaining a restriction fragment length polymorphism (RFLP) pattern of the 24 rpoB gene fragments; isolating, amplifying and digesting the DNA fragment from the microorganism to be identified and comparing the RFLP patterns from the known rpoB gene fragments with the unidentified fragment. The rpoB gene fragments are useful to identify a wide range of Mycobacterium species, e.g. for diagnosis or to obtain epidemiological and pathogenesis information for selection of appropriate therapies, including M. tuberculosis, M. leprae and non-tuberculous mycobacteria (NTM) encountered in subjects infected with human immunodeficiency virus (HIV). Analysis of the rpoB gene fragments is rapid, precise, simple and cost effective (only 1 PCR
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                                                                                                                                                                                                                                   121 CCATGGAATACCTGGTCCGCTTGCACGAGGCCAGAACGCGCGATGACCGGGCGGTG 180
                                                                                                                                             61 GCCTGAACACCGCGTCCCCGATCACGACGACCACTCTGACCGAAGAGGACGTCGTCGCCA 120
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                                                                       1 TCAAGGAGAAGCGCTACGACCTCGCGGGGGGGCCGCTACAAGAGGTCAACAAGAAGCTCG
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   Length 208;
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diagnosis and identification of many mycobacterial species by
restriction fragment length polymorphism
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                                     Indels
   DB 22;
                                     29;
                      Pred. No. 1.4e-27
0; Mismatches 2
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   Score 161.6;
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77.78;
86.18;
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 Query Match 77.7
Best Local Similarity 86.1
Matches 179; Conservative
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required), and can differentiate between many species in a single experiment, including those difficult to distinguish by usual blochemical tests. Also described are oligonucleotide probes (AASO5227-AASO5242) for detecting specific Mycobacterial species.
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                                                                                                                                                                                                                                                                                                                121 CCATCGAGTACCTGGTCCGCCTGCACGAGGCCACACCACGATGACCGTCCCGGGCGGAG 180
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                                                                                                                Score 160; DB 22; Length 208;
Pred. No. 3.2e-27;
0; Mismatches 30; Indels
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                                                                                   Sequence 208 BP; 46 A; 62 C; 67 G; 33 T; 0 other;
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85.6%;
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                                                                                                                                Best Local Similarity 85.6
Matches 178; Conservative
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are useful to identify a wide range of Mycobacterium species, e.g. for diagnosis or to obtain epidemiological and pathogenesis information for selection of appropriate therapies, including M. tuberculosis, M. leprae and non-tuberculous mycobacteria (MTM) encountered in subjects infected with human immunodeficiency vitus (HTM). Analysis of the rpoB gene fragments is rapid, precise, simple and cost effective (only 1 PCR required), and can differentiate between many species in a single experiment, including those difficult to distinguish by usual biochemical tests. Also described are oligonucleotide probes (AASO5227-AASO5242) for detecting specific Mycobacterial species.
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                                                                                                                                                                                         Sequence 208 BP; 46 A; 62 C; 67 G; 33 T; 0 other;
                                                                                                                                                                                                                           76.9%; Score 160; DB 22; larity 85.6%; Pred. No. 3.2e-27, Conservative 0; Mismatches 3(
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Matches 178; Conserv
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novel PCR-restriction fragment length polymorphism analysis (PRA)
method. The method comprises obtaining a restriction fragment length
polymorphism (RFLP) pattern of the 24 rpoB gene fragments; isolating,
amplitying and digesting the DNA fragment from the microorganism to
be identified and comparing the RFLP patterns from the known rpoB gene
fragments with the unidentified fragment. The rpoB gene fragments
crangeness with the unidentified fragment. The rpoB gene fragments
can useful to identify a wide range of Mycobacterium species, e.g. for
diagnosis or to obtain epidemiological and pathogenesis information for
selection of appropriate theraphes, including M. tuberculosis, M. Leprae
and non-tuberculous mycobacteria (MTM) encountered in subjects infected
with human immunodeficiency virus (MTW). Analysis of the rpoB gene
fragments is rapid, precise, simple and cost effective (only 1 PCR
required), and can differentiate between many species in a single
experiment, including those difficult to distinguish by usual biochemical
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                                                                                                                                                                             Sequence 208 BP; 46 A; 62 C; 67 G; 33 T; 0 other;
                                                                                                                                                                                                Query Match 76.9%; Score 160; DB 22; Best Local Similarity 85.6%; Pred. No. 3.2e-27; Matches 178; Conservative 0; Mismatches 30;
                                                                                                                                                         detecting specific Mycobacterial species.
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This oligonucleotide DNA primer is specific for Mycobacterium tuberculosis, and may be used to amplify a sample DNA by targeting a portion of the gene encoding rope. The lst several bases comprise a nonhybridizing tail consisting of filler bases followed by a restriction site incorporated to facilitate cloning using the amplicon at a later date, if desired. The remaining bases hybridize to bacterial rope DNA. The method provides for the detection of M. tuberculosis and the concurrent determination of its drug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Detection of Mycobacterium tuberculosis - by amplifying sample DNA with a primer set that targets portions of the gene encoding rpoB.
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/note= "M. tuberculosis signature nucleotide"
/sig= n
/note= "primer rpo273"
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/note= "M. tuberculosis signature nucleotide"
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/note= "M. tuberculosis signature nucleotide"
                                                        tuberculosis signature nucleotide*
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/note= "primer NMQRQ-1"
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/note= "primer NMQRQ-2"
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/note= "primer rpo293"
640..666
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/note= "primer rpo397'
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/note= "primer KY292"
"primer KY290'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HOFF ) HOFFMANN LA ROCHE INC (MAYO-) MAYO FOUNDATION.
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/note= "M. i
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                      misc_feature
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                                                             an organism
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Identifying nucleotide or polypeptide sequence for use as drug target, involves providing algorithm that analyzes a functional relationship between nucleotide or polypeptide sequences, and comparing the
                                                                                                                                                                                                                 GCCTGAACACCGCGTCCCCGATCACGACGACCACTCTGACCGAAGAGGACGTCGTCGCCA 120
                                                                                                                                                                                                                                                                                           86 GCCTGCATGTCGGCGAGCCCATCACGTCGACGACGTGACGAAGAAGACGTCGTGGCCA 145
                                                                                                                                                                                                                                                                             CCATCGAGTACCTGGTCCGCCTGCACGAGGGCCACACCACGATGACCGTCCCGGGCGGAG 180
                                                                                                                           Gaps
                                                                                                                                                     1 TCAAGGAGAAGCGCTACGACCTCGCGGGGGGGGCCGCTACAAGGTCAAGAAGCTCG 60
                                                                                                                                                                                  26 TCAAGGAGAAGCGCTACGACCTGGCCCGCGTCGGTCGTATAAGGTCAACAAGAAGCTCG 85
susceptibility, particularly to rifamycin. The method can provide often greater than 95% sensitivity and 100% specificity. The biological sample is a fluid or tissue sample from a human.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mycobacterium tuberculosis potential drug target gene SEQ
                                                                                                                           30; Indels
                                                                                            Length
                                                             Seguence 970 BP; 182 A; 302 C; 330 G; 156 T; 0 other;
                                                                                          Score 160; DB 17;
Pred. No. 3.2e-27;
0; Mismatches 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Marcotte EM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 68-69; 207pp; English.
                                                                                                                                                                                                                                                                                                                                                            206 TCGAGGTGCCGGTGGAAACCGACGACAT 233
                                                                                                                                                                                                                                                                                                                                            181 TCGAGGTGCCGGTGGAAACCGACGACAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                      BP.
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99US-0165124.
2000US-0179531.
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                                                                                              76.9%;
85.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                              al Similarity 85.6
178; Conservative
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P-PSDB; AAG81125.
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                                                                                               Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                used to identify and detect the presence of algal, fungal and parasitical species in a test sample -
algorithm capable of analysing a functional relationship between nucleotide and polypeptide sequences. The method is useful for characterising the function of nucleic acids and polypeptides that may useful as a target for \epsilon drug or essential for the growth or viability
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 GCCTGAACACCGCGTCCCCGATCACGACGACCACTCTGACCGAAGAGGACGTCGTCGCCA 120
                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Species specific; genus specific; family specific; probe; detection identification; algal; archaeal; bacterial; fungal; parasitical; microorganism; diagnosis; translation elongation factor Tu; toxin; translation elongation factor G; RecA recombinase; resistance; catalytic subunit of proton-translocating ATPase; antimicrobial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCATCGAGTACCTGGTCCGCCTGCACGAGGCCCACACCACGATGACCGTCCCGGGCGGAG
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                                                                                                                                                                                                        Length 3519;
                                                                                                                                                                                                                                                                Indels
                                                                                                                                                         Sequence 3519 BP; 675 A; 1081 C; 1183 G; 580 T; 0 other;
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                                                                                                                                                                                                                                                                30;
                                                                                                                                                                                                        Score 160; DB 22;
Pred. No. 3.2e-27;
0; Mismatches 30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1064 TCGAGGTGCCGGTGGAAACCGACGACAT 1091
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 TCGAGGTGCCGGTGGAAACCGACGACAT 208
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                                                                                                                                                                                                                 76.9%;
85.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mycobacterium tuberculosis.
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                                                                                                                                                                                                                                                                   Matches 178; Conservative
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                                                                                                                                                                                                              Query Match
Best Local Similarity
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cc species with a combination of defined primer pairs. The method can be species with a combination of defined primers for detecting one or more related microorganisms e.g. algae, archaea, bacteria, fungi and parasites, for universal detection and for specific and ubiquitous contained using the method of an algal, archaeal, bacterial, fungal and parasitical species, genus, family and group. A nucleic acid (I) and parasitical species, genus, family and group. A nucleic acid (I) cobtained using the method of the invention can be used for the universal detection of at least one antimicrobial agent resistance gene or at least one toxin gene. hexa nucleic acids are used for the specific and upduitous detection and for identification of Streptococcus pneumoniae. (I) can be used to design a therapeutic agent which is effective against microorganisms. Microbial species or genus or family or phylum or group control and be detected include Abhiotrophia adiacens, Bordetella sp., CC (I) can be used to design a therapeutic agent which is effective against microorganisms. Microbial species or genus or family or phylum or group convices faster results than substrate specificity tests as results can be determined in an hour and improved accuracy is also achieved.

CC MAH00010 to AAH002304 represent nucleotide sequences and primers/probes convices faster results than substrate specificity tests as results can be determined in an hour and improved accuracy is also achieved.

AAH00010 to AAH002304 represent nucleotide sequences and primers/probes convices faster results than substrate specificity tests as results can be determined are given in the exemplification of the present invention.

So sequence 3334 BP; 679 A; 1081 C; 1188 G; 586 T; 0 other;
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ö 962 GCCTGCATGTCGGCGAGCCCATCACGTCGACGCTGACCGAAGAAGACGTCGTGGCCA 1021 1022 CCATCGAATATCTGGTCCGCTTGCACGAGGGTCAGACCACATGACCGTTCCGGGCGCG 1081 61 GCCTGAACACCGCGTCCCCGATCACGACGACCACTCTGACCGAAGAGGACGTCGTCGCCA 120 Gaps 1 TCAAGGAGAAGCGCTACGACCTCGCGGGTGGGCCGCTACAAGGTCAACAAGAAGCTCG 60 121 CCATCGAGTACCTGGTCCGCCTGCACGAGGCCCACACCACGATGACCGTCCCGGGCGGAG ; Indels Ouery Match 76.9%; Score 160; DB 22; Best Local Similarity 85.6%; Pred. No. 3.2e-27; Matches 178; Conservative 0; Mismatches 30; 1082 TCGAGGTGCCGGTGGAAACCGACGACAT 1109 181 TCGAGGTGCCGGTGGAAACCGACGACAT 208 q q ò q ò ò

Search completed: November 12, 2002, 16:50:16 Job time : 140.222 secs

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208
1 tcaaggagaagcgctacgac......ccggtggaaaccgacgacat 208
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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Listing first 45 summaries
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1: 9b_ba:*

2: 9b_btg;*

3: 9b_ow:*

1: 9b_ow:*

9b_pt:*

9b_pt:*

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/db_xref-"d1:2208413"
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RLRTVGELIONOIRVGMSRMERVYREMTTQDVEAITPQTLINIRPVVAAIKEFFGTS
OPSOFWAGNNPLSGTTHKRRLSALGFGGLSRERAGLEVRDVHP"
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Molecular analysis of rifampin-resistant Mycobacterium tuberculosis isolated in Spain (1996-2001). Description of new alleles into rpoB
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                                                         Therera, L.

Herrera, L.

Herrera Submission

Submitted (07-AUG-2001) Herrera L., Servicio Bacteriologia, Centro
Nacional Microbiologia., Ctra. Majadahonda-Pozuelo, Km 2.5,

Majadahonda. Madrid. 28220, SPAIN
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AJ318819.1 GI:22208414
RNA polymerase beta subunit; rpoB gene.
Mycobacterium tuberculosis.
Mycobacterium tuberculosis.
Bacteria; Actinobacteria; Actinobacterium; Mycobacterium
Corynebacterium; Mycobacterium; Mycobacterium
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Pred. No. 1e-17;
0; Mismatches 30; Indels
                                                                                                                                                                                     /organism="Mycobacterium tuberculosis"
/isolate="1415-97"
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Mycobacterium tuberculosis partial
beta subunit, isolate 1417-97.
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                                                                                                                                                                                                                                                                                /gene="rpoB"
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Local Similarity 85.6%;
hes 178; Conservative
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/translation-"LDIYRKLRPGEPPTKESAQTLLENLFFKEKRYDLARVGRYKVNK
KLGHYGEPTISSTLTEEDVATIELTKLHEGGTTMTVPGGVEVPVETDDIDHFGNR
KLRTVGELLQONGTSGARRENVERMITQDVEAITPQTLINIRPVVAAIKEFFGTS
QPSQFMGQNNPLSGLTHKRRLSALGPGGLSRERAGLEVRDVHP"
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Direct Submission
Submitted (07-AUG-2001) Herrera L., Servicio Bacteriologia, Centro
Nacional Microbiologia., Ctra. Majadahonda-Pozuelo, Km 2.5,
Majadahonda. Madrid. 28220, SPAIN
Location/Qualifiers
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Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium
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Mycobacterium tuberculosis partial rpoB gene for RNA polymerase
beta subunit, isolate 1763-97.
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                                                                                                                                                                       tuberculosis"
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0; Mismatches 30;
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AJ318813.1 GI:22208402
RNA POlymerase beta subunit; rpoB gene.
Mycobacterium tuberculosis.
Mycobacterium tuberculosis

    610
    /organism="Mycobacterium/isolate="1417-97"

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/gene="rpoB"
/codon_start=1
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AJ318815.
RN3 BOLVMARAS.
                                                                                                   Herrera,L., Jimenez,M.S. and Saez,J.A.
Molecular analysis of rifampin-resistant Mycobacterium tuberculosis
isolated in Spain (1996-2001). Description of new alleles into rpob
gene and review
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Pred. No. 1e+17;
0; Mismatches 30; Indels
/organism="Mycobacterium tuberculosis"
/isolate="1763-97"
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/isolate="2540-97"
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                          /db_xref="taxon:1773"
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                                                                             /gene="rpoB"
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                                                     /gene="rpoB"
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/product="RNA polymerase beta subunit"
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Molecular analysis of rifampin-resistant Mycobacterium tuberculosis
isolated in Spain (1996-2001). Description of new alleles into rpob
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Mycobacterium tuberculosis partial rpoB gene for RNA polymerase beta subunit, isolate 2348-98.

AJ318817

AJ318817

AJ318817.1 GI:22208410

RNA polymerase beta subunit; rpoB gene.

Mycobacterium tuberculosis.

Bacteria; Actinobacteria; Actinobacterians Actinomycetales;

Colymbacterium; Mycobacterium; Mycobacterium; Mycobacterium

Colymbacterium; Mycobacterium; Mycobacterium; Mycobacterium
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Submitted (07-AUG-2001) Herrera L., Servicio Bacteriologia,
Nacional Microbiologia., Ctra. Majadahonda-Pozuelo, Km 2.5,
Majadahonda. Madrid. 28220, SPAIN
Location/Oualifiers
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/protein.id="CAC87034.1"
/db_xref="G1:22208411"

    618
    /organism="Mycobacterium tuberculosis"
/isolate="2348-98"

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Pred. No. 1e-17;
0; Mismatches 3
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Best Local Similarity
Matches 178; Conserv
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Herrera, L.
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/translation="TDEALLDIYRKLRPGEPPTKESAQTLLENLFFKEKRYDLARVGR
YKVNKKLGLHVGEPITSSTLTEEDVVATIEYLVRLHEGGTTWTVPGGVEVPVETDDID
HFGNRRLRTYVGELIQNQIRVGMSRMERVYRERWTTQDVEATTPQTLINIRPVVAAIKE
FFGTSQPSGFWGQNNPLSGLTHKRRLSALGPGGLSRERAGLEVRDV"
192 c 207 g 95 t
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/product="RNA polymerase beta subunit"
/protein_id="CAC87031.1"
/db_xref="G1:22208405"
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AAIKEFEGTSQLSQFMDONNPLSGLYKRRLSALGPGGLSRERAGLEVRDV"
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Submitted (07-AUG-2001) Herrera L., Servicio Bacteriologia,
Nacional Microbiologia, Ctra. Majadahonda-Pozuelo, Km 2.5,
Majadahonda. Madrid. 28220, SPAIN
Location/Qualifiers
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                                                                                                               Length 618;
                                                                                                            Score 160, DB 1; Length 61
Pred. No. 1e-17;
0; Mismatches 30; Indels

    633
    /organism="Mycobacterium tuberculosis"

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Mycobacterium tuberculosis.
Mycobacterium tuberculosis
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ilarity 85.6%;
Conservative
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/codon_stai.-...
/transl_teable-11
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/product="RNA polymerase beta subunit"
/product="RNA polymerase beta subunit"
/db_xref="G1:2208400"
/db_xref="G1:2208400"
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IDHFGNRRLYTVGELIONGINTVGMSRMERVYREMTTODVEATTPOTLINIRPVVAAI
KEFFGTSGLSGFMONVPLSGITHRRAFALGFGGLSRERAGLEVRDVHPSH"
'08 C 210 g 101 t
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Molecular analysis of rifampin-resistant Mycobacterlum tuberculosis
isolated in Spain (1996-2001). Description of new alleles into rpob
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gene for RNA polymerase
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Submitted (07-AUG-2001) Herrera L., Servicio Bacteriologia, Centro
Nacional Microbiologia., Ctra. Majadahonda-Pozuelo, Km 2.5,
Majadahonda. Madrid. 28220, SPAIN
Location/Qualifiers
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AJ318816.

AJ318816.1 GI:22208408

RNA polymerase beta subunit; rpoB gene.

Mycobacterium tuberculosis.

Mycobacterium tuberculosis.

Mycobacterium tuberculosis.

Corynebacteria: Actinobacteria: Actinobacteria: Actinobacteria: Actinobacteria: Actinobacteria: Luberculosis complex.
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  Length 633;
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                                              Indels
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/isolate="1255-98"
                                              30;
    DB 1;
                       Pred. No. 1e-17;
0; Mismatches
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    Score 160;
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85.6%;
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VERSION
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150706
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/product="RNA polymerase beta subunit"
/product="RNA polymerase beta subunit"
/protein_id="CaC87038.1"
/db_xref="Gi:2208419"
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GRYKVNKRLAGLHYGEPTSSTLTEEDVATIETLURLHEGOTTMTVPGGVEVPVETDD
IDHFGRRRLRRYGELIONOIRVGMSRMERVVRERMTTQDVEAITPOTLINIRPAVAII
KEFFGTSQLSQFMVQNNPLSGLTQKRRLSALGPGGLSRERAGLEVRDVHPSHS"
a 202 c 212 g 99 t
                                                                                                                                                                                                                                                    DNA circular BCT 09-AUG-2002 rpoB gene for RNA polymerase
                                                                                                                                                                                                                                                                                                                                                                                                                 Herrera,L., Jimenez,M.S. and Saez,J.A. Molecular analysis of rifampin-resistant Mycobacterium tuberculosis isolated in Spain (1996-2001). Description of new alleles into rpos gene and review
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (07-AUG-2001) Herrera L., Servicio Bacteriologia, Centro Nacional Microbiologia., Ctra. Majadahonda-Pozuelo, Km 2.5, Majadahonda. Madrid. 28220, SPAIN Location/Oualifiers
                                                                                                                                                                                                                                                                                                                                                         Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium
                                                        120
                                                                                            CCATCGAGTACCTGGTCCGCCTGCACGAGGGCCACACCACGATGACCGTCCCGGGCGGAG 180
                                                                                                          Gaps
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                                        GCCTGAACACCGCGTCCCCGATCACGACGACTCTGACCGAAGAGGACGTCGTCGCCA
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Pred. No. 1e-17;
0; Mismatches 30; Indels

    639
    /organism="Mycobacterium tuberculosis"

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Mycobacterium tuberculosis partial
beta subunit, isolate 1071-98.
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Mycobacterium tuberculosis.
Mycobacterium tuberculosis
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AJ318821.1 GI:22208418
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Best Local Similarity 85.6%;
Matches 178; Conservative
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Herrera, L.
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Actinobacteridae;
Actinobacteridae;
Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteridaeae;
Mycobacterium; Mycobacterium tuberculosis complex.

Mycobacterium; Mycobacterium tuberculosis complex.

I (bases It 0 354)
Bergeron, M.G., Boissinot, M., Huletsky, A., m Nard, C., Ouellette, M.,
Picard, F.J. and Roy, P.H.
Highly conserved genes and their use to generate probes and primers
for detection of microorganisms
Patent: WO 0123604-A 2072 05-APR-2001;
Infectio Diagnostic (I.D.I.) INC. (CA)
Location/Qualifiers
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Persing, D. H., Hunt, J. J., Young, K. K. Y., Felmlee, T. A., Roberts, G. D. and Whelm, A. Christian.
Detection of a genetic locus encoding resistance to rifampin in mycobacterial cultures and in clinical specimens
Patent: US 5643723.A 1 01-JUL-1997:
Location/Qualifiers
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Pred. No. 9.7e-18;
0; Mismatches 30
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Sequence 2072 from Patent W00123604.
AX111339
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Sequence 1 from patent US 5643723.
150706
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// FURDALE=1
// PEOGLE=1
// PACALOJOH=2.2
// AD_xref="G1:7144499"
// CTATESTATE=1
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MSLSFSDPRFDDVAAPVDECKDKDMTAAPLEVTAEFINNWTGEIKSOTVFMGDFPMM
TEKGFFIINGTERNVVSQLVRSPGVYFDSTIDKSTDKTLHSVKVIPSRGAWLEFDVDK
RDTVGVRIDRKRROPVTVLLKALGYTSGQTVERFEFSEIMRSTLEKDNTVGTDEALLD
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EEDVVATIEYLUKGGTTMTVPGGVEVPVETDDIDHFGNRRLYVGELIQNOIRVG
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Submitted (11-100-1994) Paul Imboden, Institute for Medical
Microbiology, University of Berne, Friedbuehlstrasse 51, Berne,
3010, Switzerland
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/organism="Mycobacterium tuberculosis"
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                                                                                  76.9%; Score 160; DB 6;
85.6%; Pred. No. 7.7e-18;
iive 0; Mismatches 30
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         /strain="Rv"
/db_xref="taxon:1773"
1 1081 c 1188 g
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/gene="rpoB"
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576. .>3853
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Matches 178; Conservative
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U12205
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                                                                                     Query Match
                                         BASE COUNT
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DEFINITION
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MTU12205
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Miller, L. P., Crawford, J. T. and Shinnick, T.M.
Antimicrob. Agents Chemother. 38 (4), 805-811 (1994)
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    5084
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/strain="Rv"

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85.6%; Pred. No. 7.5e-18;
11ve 0; Mismatches 30
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1065. 4598
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HIWYFKGVPSRLGYLLDLAFKDLEKIIYFAAYVITSVDEEMRHNEL"
REPLEVPGLLDVQTDSFEWLIGSPRWRESAAERGDVNPVGGLEEVLYELSPIEDFSGS
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Mycobacterium tuberculosis CDC1551, section 50 of 280 of the
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1 (bases 1 to 1935)
Fleischmann, R.D., Alland, D., Eisen, J.A., Carpenter, L., White, O., Peterson, J., DeBoy, R., Dodson, R., Gwinn, M., Haft, D., Hickey, E., Kolonay, J.F., Nelson, W.C., Umayam, L.A., Ermolaeva, M.,
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Mycobacterium tuberculosis CDC1551
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/gene="rpoC"
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KEYWORDS
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TEKGTETINGTERVVYSQLVREPGYTEDETINKSTDETTHSVKVIEGRGAWLEFDUNK
RDTVGYRIDRKRRQPYTVLLKALGWTSEQIVERFGFSEIMRSTLEKDNTVGTDEALLD
IYRLRDGEPPTKESAQTILENLEFKERRYDLARVGRYKVNKKLGLHGEPTTSSTLT
EEDVANTIEVLUNLEHEGGTTWYPGGVEVPPTDDIPHFGNRRLGTWGELIONGIRVG
MSRMERVVRERMTTGDVEAITPQTLINIRPVYAAJIREFGTSQLSGPHÖUNDIRVG
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FGFIETPYRKVVDGVYSDEJIVLTADBEDRHVYAAANSTDAGGRFEPERTLURRKAG
EVETVPSSEVDYMDYSPROWYSYATAMIPFELHDDANRALMGANMORQAVPLVRSEAF
LVGTGMELRAAIDAGDRVVAEESGVIEEVSADYITVAHDNGTRRTYRNRFRESSHUGT
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GDILVGKYPYPKGETELTPEBELLAAIFGEKAREVROTSLKYPHGESGKVIGTRYFSRE
DEDELPAGVNELVRYVAQKRISDGDKLAGFRHGNKGVIGKILDVEDMPFLADGTPVD
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MKLHHLVDDKK HARSTGPYSAITYOPHGKAQFGGQRRGEMECWAMQAYGARYTLQEL
LTIKSDDTVGRYVKYRAIVKGENIEPPGIPPSFFWLLKELQSLCLNVEVLSSDGAAIE
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VEOCROEELERACKALAELEAEGAKADARRKVROGGEREMGIISTEAAYER
LEDIWSTFRILAEAOKLEADLAELEAEGAKADARRKVROGGEREMGIISTEADLAELEAEGAKADARRKVROGGEREMGIISTENDIDAEAEB
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IQAFEPMLVEGKAIOLHPLYCEAFNADFDGDQMAVHLPLSAEAQAEARILMLSSNNIL
Salzberg, S.L., Delcher, A., Utterback, T., Weidman, J., Khouri, H., Gill, J., Mikula, A. and Bishai, W. Whole genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="similar to GB:L27989 GB:L05910 GB:U12205 SP:P47766 PID:149992; identified by sequence similarity; putative="/codon_start=1/transl_table=11
                                                                                                                    Uppublished

2 (bases 1 to 1935)

Peterson,J., Daland,D., Elsen,J.A., Carpenter,L., White,O., Peterson,J., DeBoy,R., Dodson,R., Gwinn,M., Haft,D., Hickey,E., Kolonay,J.F., Nelson,W.C., Unmayam,L.A., Ermolaeva,M., Khouri,H., Salzberg,S.L., Delcher,A., Utterback,T., Weidman,J., Khouri,H., Direct Submisson,Mikula,A. and Bishal,W.

Submitted (25-APR-2001) The Institute for Genomic Research, 9712 Medical Center Dr. Rockville, MD 20850, USA
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3744. .7694
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163. .3699
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REGLADTALETADSGTONETOR TO STANDARD THE STAND
SPASGRPLAMPRLDMVTGLYYLTTEVPEDTGEYQPASGDHPETGVYSSPAEAIMAADR
GVLSVRAKTKVLTQLRPPVELEAELEGHSGWOPGDAWMAFYATTLGRYMFNELLPLGYP
FVNKOMHKKVQARI TNDLAPKPRI VVAGTYVDKLKABATSGYTVSMADVLYVPP
RKKEILDHYEERADKVEKQFORGALNHDERNBALVETWKEATDEVGGALREHYPDDNP
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/transl_table=11
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/protein_id="AR44994.1"
/db_xref="G1:13880221"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="WFDSAAAITNPCHAWASAMERSGLLECVAGLDEOPFGEFTADKL
NPDRGSSRRVPRRQADGGIATHVERGGGQRQSGGQAGVVPQRMHGFPALAMQDRLIHH
GEOTONRIAQAFRVRFCVCSPT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SYRLYKPVGLPSSAPLVVMLHGGFGSAKQAERSYGWDELADSEKFLVAYPDGYHRAWN
MGGGCGRPRARGYDDIGFYRAVVADAIANNVSIDPARVYTGHSNGAIMSYTLACNT
SIFAALGVVGSTQULDPDCQSPRPVSVJ HIHGTADPLYRYHGGPGGFRIDGPPVDLN
AFWREVNRCGALDTTTEGPVTTSGATCADNRRVVLLTVDDAGHRWPSFATQTLMRFFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALKAATLPIYVHAPYLINLASANNRVRIPSRKILQETCAAADIGAAAVIVHGGHYAD
DIDIDTGGGGWRKALDRLETEVPYVLENTAGGDHAMARREDITARLWDVIGDGGIGC
LDTCHTWAAGEALTDAVDRIKAJIGRIDLYHCNDSRDEAGSGRDRHANLGSGQIDPDL
LVAAVKAAGAPVICETAADGGRKDDIAPLRERTGS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   //orce-"This region contains an authentic frame shift and is not the result of a sequencing artifact; identified by Glimmer2; putative; conserved hypothetical protein, authentic frameshift"

10167...10925

/gene-WTH0699*
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protein_id-"aAK44921."
/db_xref="GI:\B80122"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /hote="similar to SP:P33224 GB:L20915 PID:457172
PID:457174 PID:537028; identified by sequence similarity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note-"identified by match to PFAM protein family HMM
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/gene="MT0700"
/note="similar to GB:U00012 PID:466863; identified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="identified by Glimmer2; putative"
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/product_hypothetical protein"
/protein.id="AAK44923.1"
/db_xref="GI:13880220"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(7691. .8065)
/gene="MT0697"
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/gene="MT0701"
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11859. .13487
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/brotein_id="An44927.1"
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VIAAADAKIGYPPTRVWGVPAAGLWAHRLGDQRAKRLLFTGDCITGAQAEWGLAVEA
PEGHAFVADAVEHGFRDAVRRDEPFGDYGRQARRLLTFGDGITGAQAEWGLAVEA
PEGHAFVADAVEHGFRDAVRRDEPFGDYGRQASRV*
                                                                                                TEALIOE AND THE TOTAL TO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product-"enoy1-CoA hydratase/isomerase family protein"
/protein_id-"AAK44927.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1184 CCATCGAATATCTGGTCCGCTTGCACGAGGTCAGACCACGATGACCGTTCCGGGCGGC 1243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1064 TCAAGGAGAAGCGCTACGACCTGGCCGCGTCGTATAAGGTCAACAAGAAGTCG 1123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1124 GGCTGCATGTCGGCGAGCCCATCACGTCGTCGACGAGAAAAACGTCGTGGCCA 1183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 GCCTGAACACCGCGTCCCCGATCACGACGACCACTGACCGAAGAGGACGTCGTCGCCA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 CCATCGAGTACCTGGTCCGCCTGCACGAGGCCCACACCACGATGACCGTCCCGGGCGGAG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Mycobacterium tuberculosis H37Rv
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae;
Mycobacterium; Mycobacterium tuberculosis complex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 19352;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="similar to GP:3885480; identified by similarity; putative"
/codon_start=1
/transl_table=11
       dehydrogenase, putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1
/transl_table=11
/product="hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 160; DB 1;
Pred. No. 5.6e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
/product-"acyl-CoA dehyd:
/protein_id-"AAK44926.1"
/db_xref-"GI:13880223*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCGAGGTGCCGGTGGAAACCGACGACAT 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="MT0703"
14439. .15161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene-"MT0702"
13498. .14436
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/gene="MT0702"
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/gene="MT0703"
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85.6%;
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Best Local S:
Matches 178
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KEYWORDS
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complement(3530..3685)
/gene="Rv0657c"
complement(3530..3685)
/gene="Rv0657c"

                                                                                                                                  /note="Rv0655, (MTC1376.21), len: 359, abc transporter, FASTA score: YRBF_ECOLI P45393 hypothetical abc transporter atp-binding (269 aa) opt: 644 z-score: 721.8 E(): 3.4e-33 (38.5% identity in 244 aa overlap); contains PS00017 ATP/GTP-binding site motif A, PS00211 ABC HARL_MYCLE P30769 possible ribonucleotide transport atp-MKL_MYCLE P30769 possible ribonucleotide transport atp-in 335 aa overlap). Also similar to many otherw. tuberculosis ABC transporters eg. MTCY253.24 (33.6% identity tuberculosis ABC transporters eg. MTCY253.24 (33.6%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /transl_table=11
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/product="hypothetical protein Rv0656c"
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/db_xref="GI: 2143305"
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/gene="Rv0656c"
/note="Rv0656c, (MTC1376.20, unknown), len: 127 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="PS00211 ABC transporters family signature" complement(3052, .3435)
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/gene="Rv0658c"
/note="Rv0658c, (MTCI376.18), len: 238, unknown,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="PS00017 ATP/GTP-binding site motif A" 2074. .118 /gene="Rv0655"
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/protein_id="CAB09377.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  identity in 241 as overlap)
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                                                             1585. .2664
/gene="Rv0655"
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/gene="Rv0655"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Details of M. tuberculosis sequencing at the Sanger Centre are available on the World Wide Web.

(URL, http://www.sanger.ac.uk/Projects/M_tuberculosis/) CDS have been renumbered from the original cosmid submissions but the old gene designations are in brackets after the new gene numbers. Gene prediction was based on a Hidden Markov Model of TB genes implemented in TBparese (Krogh) supplemented with visual inspection of positional base preference in codons, especially where there is an increase in the Observed/expected third position G + C. CAUTION: In some cases we may not have predicted the correct initiation codon. Where possible we choose an initiation codon (atg., gtg., or ttg) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most upstream
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tuberculosis sequencing and mapping teams, Sanger Centre, Wellcoursers Trust Genome Campus, Hinxton, Cambridge CBIO 1SA Unite de Genetique Moleculaire Bacterienne, Institut Pasteur, 28 rue du Docteur Roux, 75724 Paris Cedex 15, France E-mail: parkhill@sanger.ac.uk On Jun 27, 1998 this sequence version replaced gi:2143285.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="Rv0654" (MTC1376.22), len: 501. unknown, FASTA
/note="Rv0654, (MTC1376.22), len: 501. unknown, FASTA
score: Q53353 LIGNOSTILBENE-ALPHA, BETA-DIOXYGENASE (485
aa) opt:280 z-score: 310.1 E(): 2.3e-11, (28.5% identity
in 523 aaoverlap). Also similar to M. tuberculosis protein
MTCY21C12.07c (29.5% identity in 522 aa overlap)"
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YVVIYDLPVTFDPMQVVPASVPRWLQRPARLVIQSVLGRVRIPDPIAALGNRMQGHSD
REPYAANNFSYPARVGYMPREGONEDVRWFDIEDFCYYVHPLMAYSECRNGAEVLVUDVV
RYSRNFDRDRGGGDSRPSLDRWTINLATGAVTAECRDDRAQEFPRINTLVUGPHR
FAYTVGIEGGFLVGAGAALSTPLYKQDCVTGSSTVASLDPDLLIGEWYFVPRNSARAE
DDGILMGYGWHRGRDEGQLLLLDAQTLESIATVHLPQRVPMGFHGNWAPTT"
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LRNGPNPVAEVDPATYHWFTGDAMVHGVALRDGKARWYRNRWVRTPAVCAALGEPISA
RPHPRTGIIEGGPNTNVLTHAGRTLALVEAGVVNYELTDELDTVGPCDFDGTLHGGYT
                                Cole, S.T., Brosch, R., Parkhill, J., Garnier, T., Churcher, C., Harris, D., Gordon, S.V., Eiglmeier, K., Gas, S., Barry III, C.E., Hexaia, F., Badcock, K., Basham, D., Brown, D., Chillingworth, T., Connor, R., Davies, R., Devlin, K., Feltwell, T., Gentles, S., Hamlin, N., Holroyd, S., Hornsby, T., Jagels, K., Krogh, A., McLean, J., Moule, S., Murphy, L., Oliver, S., Osborne, J., Quail, M.A., Sqares, S., Sqares, S., Sulston, J.E., Taylor, K., Whitehead, S. and Barrell, B.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission Submitted on behalf of the Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                   Deciphering the biology of Mycobacterium tuberculosis from the
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68. .1573

    19770
/organism="Mycobacterium tuberculosis H37Rv"
/strain="H37Rv"

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/product="hypothetical protein Rv0654"
/protein_id="CAB09380.1"
/db_xref="G1:2143307"
/db_xref="SPTREMBL:006785"
                                                                                                                                                                                                                                                                                                                                                                                                                                complete genome sequence
Nature 393 (6685), 537-544 (1998)
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/clone="1376"
57. .61
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68. .1573
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(bases 1 to 19770)
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                                                                                                                                                                                                                   /translation="MEAGRADTVAPSHRWGLGAFLVVELVFLVASTSLAVVLTCHGPV
SAGVLALALAAPTVVAAGLAILITRLRGNGLRTDLRLRWSWRGLRLGLMFGFGGMLVT
TPASLVYTAIVGPEANSAVVRIFGGVRASWPALVVFLVAPFLCEEIIYRCLLWG
AVDRRWGRRAALVYTTVVFELAHLEFARAFLLVVVAIPIALRFYSGGLLASIVTHQV
TNLLHGIVLLGLTGAISLP"
                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="R00659c, (MTC1376.17), len: 102; unknown, similar to YW28_MYCTU Q10867 hypothetical 12.3 kd protein cY39.28 (14 aa), fasta scores; opt: 144 z-score: 213.2 E(): 7.3e-05, 30.8% identity in 107 aa overlap. Also similar to MTCY09F9.22 (32.7% identity in 101 aa overlap)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation-"MRRGELWFAATPGGDRPVLVLTRDPVADRIGAVVVVALTRTRRG
LVSELELTAVENRVPSDCVVNFDNIHTLPRTAFRRRITRLSPARLHEACQTLRASTGC
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Mycobacterium smegmatis DNA polymerase (rpoB) gene, complete cds.
U24494
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81, some similarity to
probablemembrane protein, similar to YPRB_ECOLI P33774 hypothetical24.3 kd protein (urf 1) (217 aa), fasta scores; opt: 174 z-score: 215.8 E(): 5.3e-05, (25.6% identity in 223 aa overlap). Also similar to MTCY359:10 (28.7% identity in 178 aa overlap)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCCTGAACACCGCGTCCCCGGATCACGACGACCACTCTGACCGAAGAGGACGTCGTCGCCA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Rv0660c, (MTC1376.16), len: 81, some similarit
har016488_130 Halobacterium sp; NRC-1 plasm (100 aa),
32.4%identity in 74 aa overlap"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 TCAAGGAGAAGCGCTACGACCTCGCGCGGGTGGGCCGCTACAAGGTCAACAAGAAGCTCG 60
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                                                                                                                                                                                                                                                                                                                       complement(4480. .4483)
/note="possible RBS upstream of Rv0658c"
complement(4753. .5061)
/gene="Rv0659c"
complement(4753. .5061)
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                                                                                                 /codon_start=1
/transl_table=11
/product="hypothetical protein Rv0658c"
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/db_xref="GI:2143303"
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/transl_table=11
/product=hppothetical protein Rv0659c"
/protein_id="CAB09387.1"
/db_xref="G1:2143302"
/db_xref="SPTREMBL:006780"
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/gene="Rv0660c"
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/gene="Rv0660c"
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85.6%;
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Best Local Similarity
Matches 178; Conserv
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Direct Submission
Submitted (11-APR-1995) Seth V. Hetherington, Infectious Diseases, St. Jude Children's Research Hospital, 332 N. Lauderdale, Memphis, TN 38101, USA
                                                                   1 (bases 1 to 3752)
Hetherington,S.V., Watson,A.S. and Patrick,C.C.
Sequence and analysis of the rpoB gene of Mycobacterium smegmatis
Antimicrob. Agents Chemother. 39 (9), 2164-2166 (1995)
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                                            Actinomycetales; Corynebacterineae; Mycobacteriaceae;
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/db_xref="taxon:1772"
194. .3703
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83.2%; Pred. No. 1.7e-16;
11ve 0; Mismatches 35,
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194. .3703
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Matches 173; Conservative
                                                          Mycobacterium.
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Search completed: November 13, 2002, 01:26:47 Job time : 660.723 secs

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Copyright (c) 1993 2002 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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			Description	AI770311 42 Mycoba	BI097733 949017G04	BI096671 949019B12	BM348454 MEST291-B	BM340507 MEST323-P	BG842655 MEST34-E0
SUMMARIES			ID	 AL770311	BI097733	BI096671	BM348454	BM340507	12 BG842655
			DB	0	13	13	13	13	12
			Match Length DB ID	 1282	431	202	531	579	586
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			Score	 123.8	42.4	42.4	42.4	42.4	42.4
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BM079854 MEST100-E BM333485 MEST166-D BM33756 MEST209-B BM073467 MEST209-B BM07346 MEST28-C BM33755 MEST209-C BM33755 MEST209-C BM33756 MEST209-H BM349198 MEST310-C BM075264 MEST32-E BM037564 MEST34-C AV631497 AV631497 AV631497 AV631497 AV631497 AV631497 BM36777 MEST198-G BM36777 MEST198-G BM36777 MEST198-G BM36777 MEST34-EO AV679799 WSL_31_AO BM766031 MEST386-F BM766031 MEST386-F BM076409 TEET-AOB BJ317721 BJ317721 BJ313305 BJ323305 BF345788 GO2017858 AX109418 Zea mays	ALIGNMENTS ALIGNMENTS 1282 bp mRNA linear EST 24-JAN-2000 42 Mycobacterium anaerobic stationary phase library Mycobacterium AI770311 42 Mycobacterium smegmatis cDNA, mRNA sequence. AI770311.1 GI:6742680 EST. Mycobacterium smegmatis. Mycobacterium laboratory I (bases) Mycobacterium laboratory Institute of Molecular and Cell Biology Appliant mcbbomdimcb.nus.edu.sg Location/Qualifiers Lucation/Qualifiers Lucation/Qualifiers Lucation/Qualifiers
BM079854 BM333485 BM333465 BM33756 BM337556 BM337556 BM337566 BM337566 BM337566 BM337566 BM337566 BM337567 BM337567 BM336777 BM336777 BM336777 BM336777 BM336777 BM336777 BM336777 BM336777 BM336777 BM3366 BJ118566 BJ118566 BJ118566 BJ118566 BJ118566 BJ118566 BJ118566 BJ118566 BJ118566 BJ11859 BM170926 BM266831 BM266831 BM266831 BM266831 BM266831 BM266831 BM266831 BM266831 BM266831 BM266831 BM327215 BM332305 BM3323305 BM3333305 BM3333305 BM33333305 BM333333333	ALIGNMENTS 1282 bp nrobbc stational sequence. 15. 15. 15. 18. A. and Dick,T. s response gene phase Mycobacte (4-5), 677-682 r and Cell Biol gapore 117609, r and Cell Biol gapore 117609, 3.edu.sg Std Error: 0.0 31. T7 Backward.
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949017G04.yl 949 - Juvenile leaf and shoot CDNA from Steve Moose
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                                                                                /clone_lib="Mycobacterium anaerobic stationary phase
library"
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Fax: 650 728 8221
Email: walbot@stanford.edu
Plate: 949017 row: G column: 04.
organism="Mycobacterium smegmatis"
                                                                                                                                         /lab_host="E. coli XL1-Blue MRF'"
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                                                     /db_xref-"taxon:1772"
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Contact: Walbot V
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/de__stage="4 stages from 3-13 days after imbibing"
/lab_host="E. coli XLOLR"
/lab_host="E. coli XLOLR"
/note="0rgan: juvenile vegetative shoots; Vector:
pAb-GA14-2.1: Site_1: ECORI; Site_2: Xhoi; Equal amounts
of total RNA by weight from 4 tissue sources (see below)
were pooled, polyA+ RNA isolated, and cDNA synthesized for
ECORI (5') and Xhoi (3') directional cloning into lambda
Hybrizap vector from Stratagene. Tissue Sources: 1. Whole
shoots 3 days after sowing/imbibing in wet soil: 2. Basal
1.5 cm shoots 6 days after sowing - includes yellow
portions of developing leaves 1-5, primordia from 6-8, and
the vegetative apex. 3. Non-green portions of developing
leaves 4-5 and the vegetative apex, including adult leaf
primordia, 9 days after sowing. 4. Partially expanded and
greening leaves 4-5 at 13 days after sowing."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         507 bp mRNA linear EST 22-JUN-2001 949019812.y1 949 - Juvenile leaf and shoot cDNA from Steve Moose BIO96671
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                           /clone_lib-*949 - Juvenile leaf and shoot cDNA from Steve
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( Dases 1 to 507)
Walbot,V.
Walbot,V.
                                                                            /tissue_type="immature leaf primordium and vegetative meristem"
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Best Local Similarity 58.9%; Pred. No. 2.4;
Matches 73; Conservative 0; Mismatches 51; Indels 0.
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University
L Unpublished (1999)
Contact: Walbot V
Contact: Walbot V
Contact: Walbot V
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 227
Fax: 650 728 8221
Email: walbotestanford.edu
Plate: 949019 row: B column: 12.
Location/Qualifiers
. .507
/db_xref-"taxon:4577"
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/cultivar="W64A"
/db_xref="taxon:4577"
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EST
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BM340507/c
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                                                                                               /dev_stage="4" stages from 3-13 days after imbibing"
/lab_host="E. coli XLOLR"
/lab_host="E. coli XLOLR"
/note="Organ: juvenile vegetative shoots; Vector:
pAb-GAL4-2.1; Site_1: EcoRI; Site_2: XhoI; Equal amounts
of total RNA by weight from 4 tissue sources (see below)
were pooled, polyA+ RNA isolated, and CDNA synthesized for
EcoRI (5') and XhoI (3') directional cloning into lambda
Hybrizap vector from Stratagene Tissue Sources: 1. Whole
shoots 3 days after sowing/imbibing in wet soil: 2. Basal
1.5 cm shoots 6 days after sowing - includes yellow
portions of developing leaves 1-5, primordia from 6.8, and
the vegetative apex. 3. Non-green portions of developing
leaves 4.5 and the vegetative apex, including adult leaf
primordia, 9 days after sowing. 4. Partially expanded and
greening leaves 4-5 at 13 days after sowing."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rt). Overall sequence quality assessment and vector trimming were conducted using the Lucy software (<a href="http://www.tigr.org/softlab/">http://www.tigr.org/softlab/</a>). Lucy parameters were set to ensure an overall trimmed quality of 97.5% or better without any vector fragments in the chosen high-quality region of each sequence. Low-quality bases between the poly-T and the high-quality region were replaced with N's to serve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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'clone_lib "949 - Juvenile leaf and shoot cDNA from Steve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wen,T.J., Olu,F., Guo,L., Ashlock,D.A and Schnable,P.S. Expressed Sequence Tags from B73 Maize: various stages and tissues including seedlings treated with a variety of hormones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoldeae; Andropogoneae; 2ea.
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                                                      'tissue_type="immature leaf primordium and vegetative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64 TGAACACCGATCATCACCACCACCACGACGCTGACCGAAGAAGACGTCGTCGCCACCA 123
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G405 Agronomy, Iowa State University, Ames, IA 50011-1010, USA
Tel: 515-294-0975
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Pred. No. 2.5;
0; Mismatches 51; Indels 0
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Contact: Patrick S. Schnable
Schnable Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       schnable@iastate.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BM348454.1 GI:18173066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 19.0%;
Best Local Similarity 58.9%;
Matches 73; Conservative
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BM348454/C
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TITLE
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Another John Part Part J. Site_1: EcoRI; Site_2: NotI; Tissues: Germinated seed and seedlings (1, 2, 8, 11 DAG), Mixed mature tissures (17, 21, 38, 69, 77 DAG), Kernels (3, 5, 10, 15, 20, 25, 30, DAP), Adventious roots (65 DAG), Tassel (3-39 cm, 53 and 56 DAG), Immature ear (0.2-3.0 cm, 53, 56, 59 DAG), Husk (73 DAG), Silk, unpollinated first ear, ear shank, etiolated seedlings, callus, Cycloheximide-treated callus, Anaerobic treated seedlings, NAA (a-Naphthalene acetic acid)-treated seedlings, Kinetin-treated seedlings, ACPC
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MEST323-F04.T3 ISUM5-RN Zea mays CDNA clone MEST323-F04 3', mRNA
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
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as spacers.

PCR PRImers

FORWARD: primer T7-1 (AA TAC GAC TCA CTA TAG)

BACKWARD: primer T3 (ATT AAC CCT CAC TAA AG)

Seq primer: primer T3 (ATT AAC CCT CAC TAA AG).

Location/Oualifiers
                                                                                                                                                         /cultivar="B73" "77"
/db_xref="taxon:4577"
/clone="MEST291-B06"
                                                                                                                                                                                                                        /clone_lib="ISUM5-RN"
                                                                                                                                        /organism≈"Zea mays"
                                                                                                                                                                                                                                           /tissue_type="mixed"
/lab_host="DH10B"
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Best Local Similarity 58.99
Matches 73; Conservative
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BM340507.1
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344 TCGA 341
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BG842655 586 bp mRNA linear EST 29-MAY-2001
MEST34-E06.T7-1 ISUM3-TL Zea mays CDNA clone MEST34-E06 5', mRNA
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                      Olu, F., Cui, F., Guo, L., Ashlock, D.A, Wen, T.J. and Schnable, P.S. Expressed Sequence Tags from B73 Maize Seedlings and Sliks
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Iowa State University
G405 Agronomy, Iowa State University, Ames, IA 50011-1010, USA
Tel: 515-294-0975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (2001)
On May 25, 2001 this sequence version replaced g1:14208977
Contact: Patrick S. Schnable
Schnable Laboratory
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Email: schnable@lastate.edu
PCR PKimers
FORWARD: T7-1 (AA TAC GAC TCA CTA TAG)
BACKWARD: T3 (ATT AAC CCT CAC TAA AG)
Seq primer: primer T7-1 (AA TAC GAC TCA TAG).
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Zea mays
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                                                                                                                                                   389
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TITLE
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BG842655
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KEYWORDS
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                                                                                                                                                                                                                                                                                                              (*http://depts.washington.edu/ventures/collabtr/direct/index.htm>#b rt). Overall sequence quality assessment and vector trimming were conducted using the Lucy software (*http://www.tigr.org/softlab/>). Lucy parameters were set to ensure an overall trimmed quality of 97.5% or better without any vector fragments in the chosen high-quality region of each sequence. Low-quality bases between the poly-T and the high-quality region were replaced with N's to serve as spacers.

PCR PRIMERS
FORWARD: primer T7-1 (AA TAC GAC TCA CTA TAG)
BACKWARD: primer T3 (ATT AAC CCT CAC TAA AG).

Seq Primer: primer T3 (ATT AAC CCT CAC TAA AG).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   resulting DNA:RNA hybrid was treated with RNASE H and used as a template for DNA PolI-catalyzed second strand synthesis. After the addition of EcoRI adaptors, the ds-cDNAS were digested with NotI and size-selected. The resulting molecules were directionally cloned into the EcoRI and NotI sites of the pT/T3PAC vector. The library then went through one round of normalization to CoT value of 5 based on the methods of Marcelo Bento Soares (Genome Research 6: 791-806, 1966)."
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Wen,T.J., Qiu,F., Guo,L., Ashlock,D.A and Schnable,P.S.
Expressed Sequence Tags from B73 Maize: various stages and tissues including seedlings treated with a variety of hormones
                                                                                                                                                                                                                                                                      Individual basecall and confidence value were assigned using the
                                                                                                                                                   Iowa State University
G405 Agronomy, Iowa State University, Ames, IA 50011-1010, USA
Tel: 515-294-0975
Fax: 515-294-2095
Email: schnable@iastate.edu
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clade; Panicoideae; Andropogoneae; Zea.
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Pred. No. 2.5;
0; Mismatches
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145 c 147 g 163 t
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/clone_lib="ISUM5-RN"
/tissue_type="mixed"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Zea mays"/cultivar="B73"
                                                                                                    Unpublished (2001)
Contact: Patrick S. Schnable
Schnable Laboratory
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58.9%;
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ORIGIN
                                      AUTHORS
TITLE
                                                                                                    JOURNAL
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GI:14244717

(bases 1 to 586)

1. .586 /organism="2ea mays"

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                                                                                                                                                                                                                   64 TGAACACCGATCATCCGATCACCACCACGCTGACGAAGAAGACGTCGTCGCCACCA 123
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                                                                                                                                                                                          Gaps
                                                                                                                                                                                                        4 AGGAGAAGCGCTACGACCTGGCCCGCGTCGGCCGCTACAAGGTCAAGAAGCTGGGCC 63
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                                                                                                                                                                         Length 586;
                                                                                                                                                                                         Indels
                                                                                                                                                                                         51;
                                                                                                                                                                         DB 12;
                                                                                                                                                                       19.0%; Score 42.4; DB 58.9%; Pred. No. 2.5; Live 0; Mismatches
                                                                                                                                                                      Query Match
Best Local Similarity 58.9 Matches 73; Conservative
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Gaps

51; Indels

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Best Local Similarity

4 AGGAGAAGCGCTACGACCTGGCCCGCGTCGGCCGCTACAAGGTCAACAAGAAGCTGGGCC 63

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Gaps

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51; Indels

Pred. No. 2.5;); Mismatches

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58.98;
                      Conservative
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Best Local Similarity
Matches 73; Conserv
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BM333485.1
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Zea mays
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                                                                                                                                                                                                                                                                                   RESULT 8
BM333485/c
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TITLE
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KEYWORDS
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rt). Overall sequence quality assessment and vector trimming were
conducted using the Lucy software (<http://www.tigr.org/softlab/>).
Lucy parameters were set to ensure an overall trimmed quality of
97.5% or better without any vector fragments in the chosen
high-quality region of each sequence. Low-quality bases between the
poly-T and the high-quality region were replaced with N's to serve
                                                                                                                                    BM079854 593 bp mRNA linear EST 14-NOV-2001
MEST100-E07.T3 ISUM4-TN Zea mays CDNA clone MEST100-E07 3', mRNA
                                                                                                                                                                                                                                                                        Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panátooldeae; Andropogoneae; Zea. (pases 1 to 593) qiu.F., Cui.F., Guo.L., Ashlock, D.A, Wen.T.J. and Schnable, P.S. Expressed Sequence Tags from B73 Maize Seedlings and Silks
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FORWARD: Forward PCR primer sequence, primer 17-1 (AA TAC GAC TCA TAG)
BACKWARD: Backward PCR primer sequence, primer T3 (ATT AAC CCT CAC TAA AG)
Seq primer: primer T3 (ATT AAC CCT CAC TAA AG).
Location/Qualifiers
1. .593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fax: 515-294-2299
Email: schnable@lastate.edu
Individual basecall and confidence value were assigned using the
                                                                                                                                                                                                                                                                                                                                                                                                                                     Iowa State University
G405 Agronomy, Iowa State University, Ames, IA 50011-1010, USA
Tel: 515-294-0975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="Seedling and silk"
/lab_host="DH108"
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/db_xref="taxon:4577"
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/clone_lib="ISUM4-TN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Zea mays"
                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (2001)
Contact: Patrick S. Schnable
Schnable Laboratory
                                                                                                                                                                                      BMÓ79854
BMO79854.1 GI:16926786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Phred software,
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                                                                                                                                                                       sequence.
                                                                                                                                                                                                                                             Zea mays.
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                                            272 TCGA 275
           124 TCGA 127
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TITLE
JOURNAL
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KEYWORDS
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                                                                                                   RESULT 7
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Score 42.4; DB 13; Length 593;

19.08;

Query Match

ORIGIN

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/note="Vector: pr713PAC; Site_1: EcoR1; Site_2: Not1;
Tissues: Germinated seed and seedlings (1, 2, 8, 11 DAG),
Mixed mature tissures (17, 21, 38, 69, 77 DAG), Kernels
(3, 5, 10, 15, 20, 25, 30, DAP), Adventious roots (65 DAG),
Tassel (3-39 cm, 53 and 56 DAG), Immature ear (0.2-3.0
m, 53, 56, 59 DAG), Husk (73 DAG), Silk, unpollinated
first ear, ear shank, etiolated seedlings, callus,
Cycloheximide-treated callus, Anaerobic treated seedlings
NAA (a-Naphthalene acetic acid)-treated seedlings,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rt). Overall sequence quality assessment and vector trimming were conducted using the Lucy software (<a href="http://www.tigr.org/softlab/">http://www.tigr.org/softlab/</a>). Lucy parameters were set to ensure an overall trimmed quality of 97.5% or better without any vector fragments in the chosen high-quality region of each sequence. Low-quality bases between the poly-T and the high-quality region were replaced with N's to serve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BM333485 597 bp mRNA 11near EST 16-JAN-2002 MEST156-D03.T3 ISUM5-RN Zea mays cDNA clone MEST156-D03 3', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (<http://depts.washington.edu/ventures/collabtr/direct/index.htm>#b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 597)
When T.J., Olur F., Guo, L., Ashlock, D.A and Schnable, P.S.
Expressed Sequence Tags from B73 Maize: various stages and tissues including seedlings treated with a variety of hormones
Contact: Patrick S. Schnable
Schnable Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoldeae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Individual basecall and confidence value were assigned using the
                                      64 TGAACACCGATCATCACCACCACGACGCTGACCGAAGAAGACGTCGTCGCCACCA 123
                                                                                                                                                                                                  4 AGGAGAAGCGCTACGACCTGGCCCGCGTCGGCCGCTACAAGGTCAACAAGAAGCTGGGCC 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Towa State University G405 Agronomy, Iowa State University, Ames, IA 50011-1010, Tel: 515-224-0975 Fax: 515-294-2299 Email: schnablediastate.edu
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Location/Qualifiers
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BACKWARD: primer T3 (ATT AAC CCT CAC TAA AG)
Seg primer: primer T3 (ATT AAC CCT CAC TAA AG
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/clone="MEST156-D03"
/clone_lib="ISUMS-RN"
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/lab_host="DH108"
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BM073467/C
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MEST209-B07.T3 ISUM5-RN Zea mays CDNA clone MEST209-B07 3', mRNA
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                                        (1-aminocyclopropane-1-carboxylix acid)-treated seedlings,
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Spermatophyta; Magnoliophyta; Lillopsida; Poales; Poaceae; PACC
clade; Panicoldeae; Andropogoneae; 2ea.
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Individual basecall and confidence value were assigned using the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Iowa State University
6405 Agronomy, Iowa State University, Ames, IA 50011-1010, USA
TTE1: 515-294-0975
Fax: 515-294-2299
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Wen,T.J., Qiu,F., Guo,L., Ashlock,D.A and Schnable,P.S.
Expressed Sequence Tags from B73 Maize: various stages including seedlings treated with a variety of hormones Unpublished (2001)
Contact: Patrick S. Schnable
Schnable Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 19.0%; Score 42.4; DB 13; Length 597; Best Local Similarity 58.9%; Pred. No. 2.5; Matches 73; Conservative 0; Mismatches 51; Indels 0;
Kinetin-treated seedlings, ACPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BM337568.1 GI:18167728
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64 TGAACACCGATCATCCGATCACCACCACGACGTGACGAAGAAGACGTCGTCGCCACCA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 AGGAGAAGCGCTACGACCTGGCCCGCGTCGGCCGCTACAAGGACAAGAAGCTGGGCC 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 42.4; DB 13; Length 606; Pred. No. 2.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13 others
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PCR PRimers
FORWARD: primer T7-1 (AA TAC GAC TCA CTA TAG)
BACKWARD: primer T3 (ATT AAC CCT CAC TAA AG)
Seq primer: primer T3 (ATT AAC CCT CAC TAA AG).
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  158 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 2.5;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                /clone="MEST209-B07"
/clone_lib="ISUM5-RN"
                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:4577"
                                                                                                                                                                                                                                             /organism-"Zea mays"
                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="mixed"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  156 g
                                                                                                                                                                                                                                                                                  /cultivar-"B73"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GI:16917872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 58.9%;
Matches 73; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BM073467
BM073467.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sednence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           124 TCGA 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EST.
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// Tissues: Germinated seed and seedlings (1, 2, 8, 11 DAG), Mixed mature tissures (17, 21, 38, 69, 77 DAG), Kernels (17, 5, 10, 15, 20, 25, 30, DAP), Adventious roots (65 DAG), Tassel (3-39 Cm, 53 and 56 DAG), Immature ear (0, 2-3.0 Cm, 53, 56, 59 DAG), Husk (73 DAG), Immature ear (0, 2-3.0 Cm, 53, 56, 59 DAG), Husk (73 DAG), Immature ear (0, 2-3.0 Cm, 53, 56, 59 DAG), Husk (73 DAG), Immature ear (0, 2-3.0 Cm, 53, 56, 59 DAG), Husk (73 DAG), Silk, unpollinated first ear, ear shank, etiolated seedlings, Cycloheximide-treated callus, Anaerobic treated seedlings, Kinetin-treated seedlings, ARC (1-aminocyclopropane-1-carboxylix acid)-treated seedlings, Brassinolide-treated seedlings, ARG (Abberellic acid)-treated seedlings, GA (Gibberellic acid)-treated seedlings, GA (Gibberellic acid)-treated seedlings, GA (Gibberellic acid)-treated seedlings, GA (Gibberellic acid)-treated seedlings described from oligo-dT selected mRNA by priming with a Notiological primer (5)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (<http://depts.washington.edu/ventures/collabtr/direct/index.htm>#b rt). Overall sequence quality assessment and vector trimming were conducted using the Lucy software (<http://www.igto.org/softlab/>). Lucy parameters were set to ensure an overall trimmed quality of 97.5% or better without any vector fragments in the chosen high-quality region of each sequence. Low-quality bases between the poly-T and the high-quality region were replaced with N's to serve as spacers.
                                                                                                                                                       Lea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta: Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 613)

Wen,T.J., Oliu,F., Guo,L., Ashlock,D.A and Schnable,P.S.

Expressed Sequence Tags from B73 Maize: various stages and tissues
Including seedlings treated with a variety of hormones
Contact: Patrick S. Schnable
       MEST328-C11.T3 ISUM5-RN 2ea mays cDNA clone MEST328-C11 3', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Individual basecall and confidence value were assigned using the
                                                                                                                                                                                                                                                                                                                                                                                                       Schnable Laboratory
Iowa State University
G405 Agronomy, Iowa State University, Ames, IA 50011-1010, USA
G15-294-0975
Fax: 515-294-2299
Email: schnable@lastate.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FOWMARD: primer T7-1 (AA TAC GAC TCA CTA TAG)
BACKWARD: primer T3 (ATT AAC CCT CAC TAA AG)
Seg primer: primer T3 (ATT AAC CCT CAC TAA AG).
Location/Oualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:4577"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="ISUM5-RN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Zea mays"
/cultivar="B73"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="MEST328-C11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="mixed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /lab_host="DH10B
                                                                                   GI:18171116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Phred software,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PCR PRimers
                                                         BM340956
BM340956.1
                                                                                                                                       Zea mays.
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                                                                                                     KEYWORDS
SOURCE
ORGANISM
       DEFINITION
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                                                         ACCESSION
                                                                                                                                                                                                                                                                                    AUTHORS
                                                                                                                                                                                                                                                                                                                                                          JOURNAL
                                                                                                                                                                                                                                                          REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURES
                                                                                                                                                                                                                                                                                                           TITLE
                                                                                   VERSION
                                                                                                                                                                                                                                                                                                                                                     rt). Overall sequence quality assessment and vector trimming were conducted using the Lucy software (<http://www.tigr.org/softlab/>) Lucy parameters were set to ensure an overall trimmed quality of 97.5% or better without any vector fragments in the chosen high-quality region of each sequence. Low-quality bases between the poly-T and the high-quality region were replaced with N's to serve as spacers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         as a template for DNA PolI catalyzed second strand synthesis. After the addition of EccRI adaptors, the ds-cDNAs were digested with NotI and size-selected. The resulting molecules were directionally cloned into the EcoRI and NotI sites of the pT/T3PAC vector. The library then went through one round of normalization to CoT value of 5 based on the methods of Marcelo Bento Soares (Genome Research 6: 791-806, 1996).
                                                                                                                                                                                                                                                                                                                              (<http://depts.washington.edu/ventures/collabtr/direct/index.htm>#b
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BACKWARD: Backward PCR primer sequence, primer T3 (ATT AAC CCT CAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FORWARD: Forward PCR primer sequence, primer T7-1 (AA TAC GAC TCA
                                                                                                                                                                                                                                                                    Individual basecall and confidence value were assigned using the Phred software,
                    Qiu.F., Cui.F., Guo,L., Ashlock,D.A, Wen,T.J. and Schnable,P.S. Expressed Sequence Tags from B73 Malze Seedlings and Silks
                                                                                                                                                                                 USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64 TGAACACCGATCATCCGATCACCACCACGACGCTGACCGAAGAGGACGTCGTCGCCACCA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        512 AGCTGATGCGCCAGCACCTGGCCACCGATGCCGGCAAGGAGGTCACCAAGAAGGTCGGCC 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63
                                                                                                                                                  Iowa State University
G405 Agronomy, Iowa State University, Ames, IA 50011-1010,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 AGGAGAAGCGCTACGACCTGGCCCGCGTCGGCCTACAAGGTCAACAAGAAGCTGGGCC
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seq primer: primer T3 (ATT AAC CCT CAC TAA AG)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="Seedling and silk"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="ISUM4-TN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="2ea mays"
/cultivar="B73"
                                                                           Unpublished (2001)
Contact: Patrick S. Schnable
Schnable Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="MEST67-H11"
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                                                                                                                                                                                                                                                     Email: schnable@iastate.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19.0%;
58.9%;
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                                                                                                                                                                                                                             Fax: 515-294-2299
                                                                                                                                                                                                   rel: 515-294-0975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1..610
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TAA AG)
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Local Sa.
73;
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BM340956/c
LOCUS
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AUTHORS
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JOURNAL
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Swaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Sea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.

Expressed Sequence Tays from B73 Maize: Various stages and tissues including seedlings treated with a variety of hormones including seedlings treated with a variety of hormones

AD Tayles Sea Sequence Tays from B73 Maizes and tissues including seedlings treated with a variety of hormones

Town State University

Tayles 
                                                                                                                                                                                                                                                                                                                                                                                                         resulting DNA:RNA hybrid was treated with RNASe H and used as a template for DNA Poll-catalyzed second strand synthesis. After the addition of EcoRI adaptors, the ds-cDNAs were digested with NoII and size-selected. The resulting molecules were directionally cloned into the EcoRI and NoII sites of the pT773PAC vector. The library then went through one round of normalization to CoT value of 5 based on the methods of Marcelo Bento Soares (Genome Research 6: 791-806, 1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BM332944 651 bp mRNA linear EST 16-JAN-2002 MEST181-G09.T3 ISUM5-RN Zea mays cDNA clone MEST181-G09 3', mRNA
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                                                                                                                                rt). Overall sequence quality assessment and vector trimming were conducted using the Lucy software (ehttp://www.tlgr.org/softlab/>). Lucy parameters were set to ensure an overall trimmed quality of 97.5% or better without any vector fragments in the chosen
first ear, ear shank, etiolated seedlings, callus, Cycloheximide-treated callus, Anaerobic treated seedlings, NAA (a-Naphthalene acetic acid)-treated seedlings, Kinetin-treated seedlings, ACPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    429 TCGTCTACCAGCTCAACATCGCCCCCAAGAAGATCGGCGTTGATGAGGAGATCTTCGTGG 370
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 42.4; DB 13; Length 622;
Pred. No. 2.5;
0; Mismatches 51; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BM332944
BM332944.1 GI:18163105
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Best Local Similarity 58.9%;
Matches 73; Conservative
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (-http://depts.washington.edu/ventures/collabtr/direct/index.htm>#brt). Overall sequence quality assessment and vector trimming were conducted using the Lucy software (<http://www.tigr.org/softlab/>). Lucy parameters were set to ensure an overall trimmed quality of 97.5% or better without any vector fragments in the chosen high-quality region of each sequence. Low-quality bases between the poly-T and the high-quality region were replaced with N's to serve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BM337575 622 bp mRNA linear EST 16-JAN-2002 MEST209-C08.T3 ISUM5-RN Zea mays cDNA clone MEST209-C08 3', mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoldeae; Andropogoneae; Zea.

( (bases 1 to 62)

Wen.F.J., Qlu.F., Guo,L., Ashlock,D.A and Schnable,P.S.
Wenesed Sequence Treated with a variety of hormones including seedlings from B73 Maize: various stages and tissues including seedlings treated with a variety of hormones
Contact: Patrick S. Schnable
Schnable Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: schnable@iastate.edu
Individual basecall and confidence value were assigned using the
Phred software,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Iowa State University
G405 Agronomy, Iowa State University, Ames, IA 50011-1010, USA
Tel: 515-294-0975
Fax: 515-294-2299
                                                                                                                                                                                                                                                                                                                                                                                              471 TCGTCTACCAGCTCAACATCGCCCCCAAGAAGATCGGCGTTGATGAGGAGGACATCGTGG 412
                                                                                                                                                                                                                                                                                   531 AGCTGATGCGCCAGCACCTGGCCACCGATGCCGGCAAGGAGGTCAAGAAGGTCGGCC 472
                                                                                                                                                                                                                                                                                                                                                       64 TGAACACCGATCATCCGATCACCACCACGACGATGACGAAGAAGACGTCGTCGCCACCA 123
                                                                                                                                                      Gaps
                                                                                                                                                                                                                      4 AGGAGAAGCGCTACGACCTGGCCCGCGTCGGCCGCTACAAGAGGTCAACAAGAAGCTGGGCC 63
                                                                                                                                                  ;
                                                                                     Length
                                                                                                                                                  51; Indels
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FORWARD: primer T7-1 (AA TAC GAC TCA CTA TAG)
BACKWARD: primer T3 (ATT AAC CCT CAC TAA AG)
Seq primer: primer T3 (ATT AAC CCT CAC TAA AG).
Location/Qualifiers
                                                                                     DB 13;
                                                                              Score 42.4; DB Pred. No. 2.5; 0; Mismatches
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/clone="%BST209-C08"
/clone=11b="15UM5-RN"
/tlssue_type="mixed"
/lab_host="DH108"
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/cultivar="B73"
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                                                                                     19.0%;
58.9%;
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                                                                                            Ma.
Local Sim.
73;
                                                                                         Query Match
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LOCUS
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AUTHORS
TITLE
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COMMENT
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                                                                                                                                                                                                                        JOURNAL
                                                                                                    REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       //doce="Vector: pT773PAC: Site_I: ECORI: Site_2: NotI: Tissues: Germinated seed and seedlings (1, 2, 8, 11 DAG), Mixed mature Lissures (17, 21, 38, 69, 77 DAG), Kernels (3, 5, 10, 15, 20, 25, 30, DAP), Adventious roots (65 DAG), Tassel (3-39 Cm, 25, 30, DAP), Immature ear (0.2-3.0 Cm, 23, 56, 59 DAG), Husk (73 DAG), Immature ear (0.2-3.0 Cm, 23, 56, 59 DAG), Husk (73 DAG), Silk, unpollinated first ear. ear shank, etiolated seedlings, callus, Cycloheximide-treated callus, Anacrobic treated seedlings, Kinetin-treated seedlings, ACPC (1-aninocyclopropane-1-carboxylix acid)-treated seedlings, Kinetin-treated seedlings, ACPC (1-aninocyclopropane-1-carboxylix acid)-treated seedlings, Ditreated seedlings, ABA (Abscisic acid)-treated seedlings, ABA (Abscisic acid)-treated seedlings, JA (Jasmonic acid)-treated seedlings, ABA (Abscisic acid)-treated as a temptate for DAN POIL-catalyzed second strand as a temptate for DAN POIL-catalyzed second strand seedlings were directionally cloned into the resulting molecules were directionally cloned into the EcoRI and NotI sites of the pT713PAC vector. The library then went through one round of normalization to CoT value of 5 based on the methods of Marcelo Bento soares (Genome
high-quality region of each sequence. Low-quality bases between the poly-T and the high-quality region were replaced with N's to serve as spacers.
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MEST386-H10.T3 ISUM5-RN 2ea mays cDNA clone MEST386-H10 3', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64 TGAACACCGATCATCGCATCACCACCACGACGCTGACCGAAGAAGACGTCGTCGCCACCA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
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                                                                                 PCR PRIMERS
FORWARD: primer T7-1 (AA TAC GAC TCA CTA TAG)
BACKWARD: primer T3 (ATT AAC CCT CAC TAA AG)
Seq primer: primer T3 (ATT AAC CCT CAC TAA AG).
Location/Qualifiers
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156 c 171 g 175 t
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Pred. No. 2.5;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                   /db_xref*"taxon:4577"
/clone="MEST181-G09"
/clone_lib="ISUM5-RN"
                                                                                                                                                                                                                                                                          /organism="Zea mays"
/cultivar="B73"
                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="mixed"
/lab_host="DH10B"
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58.9%;
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Matches 73; Conservative
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Zea mays
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BM266851/C
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(<http://depts.washington.edu/ventures/collabtr/direct/index.htm>#b
rt). Overall sequence quality assessment and vector trimming were
conducted using the Lucy software (<http://www.tigr.org/softlab/>).
Lucy parameters were set to ensure an overall trimmed quality of
97.5% or better without any vector fragments in the chosen
high-quality region of each sequence. Low-quality bases between the
poly.T and the high-quality region were replaced with N's to serve
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 659)
Wen, T.J., Qlu, F., Guo, L., Ashlock, D.A and Schnable, P.S.
Wen, T.J., and Schnable, P.S.
Expressed Sequence Tags from B73 Maize; various stages and tissues including seedlings treated with a variety of hormones
                                                                                                                                                                                                                                                                                                                                                                                              Email: schnable@lastate.edu
Individual basecall and confidence value were assigned using the
                                                                                                                                                                                                                                                                                     Iowa State University
6405 Agronomy, Iowa State University, Ames, IA 50011-1010, USA
TTE: 515-294-0975
Fax: 515-294-2299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FORWARD: primer T7-1 (AA TAC GAC TCA CTA TAG)
BACKWARD: primer T3 (ATT AAC CCT CAC TAA AG)
Seg primer: primer T3 (ATT AAC CCT CAC TAA AG).
Location/Qualifiers
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/tissue_type="mixed"
/lab_host="DH10B"
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/clone="MEST386-H10"
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/cultivar="B73"
                                                                                                                                                                                                                                Contact: Patrick S. Schnable
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Best Local Similarity
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/note="Vector: pr773PAC; Site_1: ECORI: Site_2: NotI:
Tissues: Germinated seed and seedlings (1, 2, 8, 11 DAG),
Mixed mature tissures (17, 21, 38, 69, 77 DAG), Kernels
(3, 5, 10, 15, 20, 25, 30, DAP), Adventious roots (65 DAG),
Tassel (3-39 CM, 33 and 56 DAG), Immature ear (0.2-3.0 CM, 53, 56, 59 DAG), Husk (73 DAG), Immature ear (0.2-3.0 CM, 53, 56, 59 DAG), Husk (73 DAG), Silk, unpollinated first ear, ear shank, etiolated seedlings, cycloheximide-treated callus, Anaerobic treated seedlings
(Yaloheximide-treated seedlings, ACPC
(1-aminocyclopropane-1-carboxylix acid)-treated seedlings,
Brassinolide-treated seedlings, ABA (Abscisic acid)
)-treated seedlings, GA (Gibberellic acid)-treated
                                                                                                                                                                                                                                                                                                                                                                                                                BM337566 659 bp mRNA linear EST 16-JAN-2002
MEST209-H08.T3 ISUM5-RN Zea mays CDNA clone MEST209-H08 3', mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 659)
When,T.J., Qiu,E., Guo,L., Ashlock,D.A and Schnable,P.S.
Expressed Sequence Tags from B73 Maize: various stages and tissues including seedlings treated with a variety of hormones
Context: Patrick S. Schnable
Schnable Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoldeae; Andropogoneae; 2ea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fax: 515-294-2299
Email: schnable@iastate.edu
Individual basecall and confidence value were assigned using the
                                                                                   64 TGAACACCGATCATCGATCACCACCACGACGTGACCGAAGAAGACGTCGTCGCCACCA 123
Iowa State University
6405 Agronomy. Iowa State University, Ames, IA 50011-1010, USA
Tel: 515-294-0975
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BACKWARD: primer T3 (ATT AAC CCT CAC TAA AG)
Seq primer: primer T3 (ATT AAC CCT CAC TAA AG).
Location/Qualifiers
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/clone=lib="18UM5-RN"
/tissue=type="mixed"
/lab_host="DH108"
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/cultivar="B73"
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BM337566.1 GI:18167726
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ACTOCARA TOTAL (A) A STANDARD TOTAL TOTAL TOTAL TO THE TESULTING DNA:RNA hybrid was treated with RNase H and used as a template for DNA Poll-catalyzed second strand synthesis. After the addition of EcoRI adaptors, the GS-CDNAs were digested with NotI and size-selected. The resulting molecules were directionally cloned into the EcoRI and NotI sites of the pTT3PAC vector. The library then went through one round of normalization to CoT value of 5 based on the methods of Marcelo Bento Soares (Genome 157 c 181 90 f.) 178 t.
                       molecules were generated as follows. First-strand cDNA was prepared from oligo-dT selected mRNA by priming with a NotI oligo-dT primer (5'
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seedlings, JA (Jasmonic acid)-treated seedlings. ds-cDNA
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Best Local Similarity 58.9%; Pred. No. 2.5;
Matches 73; Conservative 0; Mismatches
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Search completed: November 13, 2002, 04:00:03 Job time : 1198.62 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compu
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Maximum Match 100%
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ALGAGOR Synechocyst ALGAGOR Ralstonia ALGAGOR Ralstonia ALGAGORS Ralstonia ARO1587 Drosophil ARV19444 Drosophil ARV13137 Drosophil ACO07929 Drosophil ACO08202 Drosophil ACO08202 Drosophil ACO08202 Drosophil ACO08202 Drosophil ALGAGORS Streptomy APO0303 Mesorhizo AFG6953 Streptomy ALGC397 Oryza sat ALGG4073 Ralstonia Y18574 Streptomyce AEO12929 Chlorobiu X54073 T.flavus sc E13276 Tamias si Mycobacterium tuberculosis partial rpoB gene for RNA polymerase beta subunit, isolate 1415-97.

AJ318818
AJ318818.1 G1:22208412
RNA polymerase beta subunit; rpoB gene.
Mycobacterium tuberculosis.
Mycobacterium tuberculosis.
Bacteria; Actinobacteria; Actinobacteria; Actinobacterium tuberculosis.
Corpubbacterium tuberculosis.
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Herrera, L., Jimenez, M.S. and Saez, J.A.

tuberculosis complex

the number of results predicted by chance to have a

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Unpublished
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Molecular analysis of rifampin-resistant Mycobacterium tuberculosis isolated in Spain (1996-2001). Description of new alleles into rpoB
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KLGLHYGEPITSSTLTEEDVVATIEYLVRLHEGQTTMTVPGGVEVPVETDDIDHFGNR
RLRTVGELIQNQIRVGMSRMERVYREBMTTQDVEAITPOTLINIRPVVAAIKEFFGTS
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Mycobacterium tuberculosis.
Mycobacterium tuberculosis
Bacteria; Actinobacteria; Actinobacteria; Actinomycetales;
Corynebacterineae; Mycobacteriameae; Mycobacterium
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                                                                               Direct Submission
Submitted (07-AUG-2001) Herrera L., Servicio Bacteriologia,
Nacional Microbiologia, Ctra. Majadahonda-Pozuelo, Km 2.5,
Majadahonda. Madrid. 28220, SPAIN
Location/Qualifiers
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                                                                                                                                                                        /organism-"Mycobacterium tuberculosis"
/isolate-"1415-97"
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                                                                                                                                                                                                                                                                                                     /product-"RNA polymerase beta subunit"
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/db_xref-"G1:22208413"
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AJ318819. GI:22208414
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Mycobacterium tuberculosis partial rpoB gene for RNA polymerase AJ318813. GI:22208402
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KLGLHVGEPITSSTLTEEDVVATIEYLVRLHEGGTTMTVPGGVEVPVETDDIDHFGNR
RLRTVGELIONOIRVGMSRMERVYREMTTQDVEAITPQTLINIRPVVAAIKEFFGTS
OPSOFWGONPLESORDENTSALCPGGLSRERAGLEVRDVHP"

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Molecular analysis of rifampin-resistant Mycobacterium tuberculosis
isolated in Spain (1996-2001). Description of new alleles into rpos
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Mycobacterium tuberculosis.
Mycobacterium tuberculosis additional suberculosis.
Bacteria; Actinobacteria; Actinobacteria; Actinomycetales; Corynebacterinese; Mycobacterium; Mycobacterium
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Direct Submission
Submitted (07-AUG-2001) Herrera L., Servicio Bacteriologia,
Nacional Microbiologia., Ctra. Majadahonda-Pozuelo, Km 2.5,
Majadahonda. Madrid. 28220, SPAIN
Location/Qualifiers
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/db_xref="G1:22208415"
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/isolate="1417-97"
/db_xref="taxon:1773"
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Pred. No. 1.1e-21;
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KLGHYGEPTTSSTLTBEDVATIEVLYRLHEGOTTWTVPGCVEVPVETDDIDHFGNR
RLRTVGELIONQIRVGERRENVEREMTTDDVEATIPQTLINIRPVVAAIKEFFGTS
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Molecular analysis of rifampin-resistant Mycobacterium tuberculosis
stolated in Spain (1996-2001). Description of new alleles into rpob
gene and review
Unpublished
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AJ318815
AJ318815.1 GI:22208406
RNA polymerase beta subunit; rpoB gene.
Mycobacterium tuberculosis.
Mycobacterium tuberculosis
Bacteria; Actinobacteria; Actinobacteria; Actinomycetales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
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/organism="Mycobacterium tuberculosis"
/isolate="1763-97"
                                                                                 /gene="rpob"
//codon_start=1
/transl_table=1
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/protein_id="CAC87030]"
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    618 — Action - Mycobacterium tuberculosis" /isolate=".5540-97" /db_xref="taxon:1773"

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                           /db_xref="taxon:1773"
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Molecular analysis of rifampin-resistant Mycobacterium tuberculosis
stolated in Spain (1996-2001). Description of new alleles into rpob
gene and review
Unpublished
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Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium
tuberculosis complex.
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    618
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/isolate="2348-98"

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llarity 87.5%; Pred. No. 1.1e-21;
Conservative 0; Mismatches 26;
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RNA polymerase beta subunit; rpoB gene.
Mycobacterium tuberculosis.
Mycobacterium tuberculosis
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Best_Local Sim
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AJ318814
AJ318814 GI:22208404
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AAIKEFEGTSQLSQFMQONNPLSGLTYRRLSALGPGGLSRERAGLEVRDV*
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Submitted (07-AUG-2001) Herrera L., Servicio Bacteriologia, Centro
Nacional Microbiologia., Ctra. Majadahonda-Pozuelo, Km 2.5,
Majadahonda. Madrid. 28220, SPAIN
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Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium
tuberculosis complex.
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Pred. No. 1.1e-21;
0; Mismatches 26
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                                                                                                          80.0%;
llarity 87.5%;
Conservative
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KEFGTSQLSQFMDQNNPLSGLTHKRRMFALGPGGLSRERAGLEVRDVHPSH"
108 c 210 g 101 t
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gene for RNA polymerase
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Molecular analysis of rifampin-resistant Mycobacterium tuberculosis
isolated in Spain (1996-2001). Description of new alleles into rpoB
gene and review
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Submitted (07-AUG-2001) Herrera L., Servicio Bacteriologia, Centro
Nacional Microbiologia., Ctra. Majadahonda-Pozuelo, Km 2.5,
Majadahonda. Madrid. 28220, SPAIN
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Mycobacterium tuberculosis.
Mycobacterium tuberculosis
Bacteria; Actinobacteria; Actinobacteria; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium
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/isolate="1255-98"
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87.5%; Pred. No. 1.1e-21;
live 0; Mismatches 26;
                                            56;
      DB 1;
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rpob
                      Pred. No. 1.1e-21
0: Mismatches 20
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AJ318816.1 GI:22208408
      Score 166.4;
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<1. .>637
/gene="rpoB"
80.0%;
87.5%;
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                                      Conservative
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                  Similarity
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182; Conserv
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Herrera, L.
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/db_xref="GI:22208419"
/db_xref="GI:2208419"
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Mycobacterium tuberculosis partial rpoB gene for RNA polymerase beta subunit, isolate 1071-98.
AJ318821
AJ31822.
RNA polymerase beta subunit; rpoB gene.
Mycobacterium tuberculosis.
Mycobacterium tuberculosis.
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Submitted (07-AUG-2001) Herrera L., Servicio Bacteriologia, Centro
Nacional Microbiologia., Ctra. Majadahonda-Pozuelo, Km 2.5,
Majadahonda. Maria, Sa220, SPAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium tuberculosis complex.
CCATCGAGTATCTGGTCCGCCTGCACGAGGCCCAGGCCACGATGACCGTGCCGGGGG 180
                                                                                120
                                                                                                 61 GCCTGAACACCAATCATCCGATCACCACGACGACGTGACCGAAGAAGACGTCGTCGCCA 120
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/isolate="1071-98"
/db_xref="taxon:1773"
                                                                                                                                                                                                                                                                                           Location/Qualifiers
1. .639
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<1. .>639
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Patent: Wo 0123604-A 2072 05-APR-2001;
Infectio Diagnostic (1.D.I.) INC. (CA)
Location/Qualifiers
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Mycobacterium tuberculosis
Mycobacteria: Firmicutes: Actinobacteria: Actinobacteridae;
Actinomycotales: Corynebacterineae: Mycobacterium: Mycobacterium: Mycobacterium: Mycobacterium: Mycobacterium: Mycobacterium: Mycobacterium tuberculosis complex.

1 (bases 1 to 3534)
Bergeron, M.G., Boissinot, M., Huletsky, A., m Nard, C., Ouellette, M., Picard, F.J. and Roy, P.H.
                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 970)
Persing, D.H., Hunt, J.J., Young, K.K.Y., Felmlee, T.A., Roberts, G.D. and Whelman, A.Christian.
Detection of a genetic locus encoding resistance to rifampin in mycobacterial cultures and in clinical specimens
Patent: US 5643723-A 1 01-JUL-1997;
61 GCCTGAACACCAATCATCCGATCACCACGACGCTGACCGAAGAAGACGTCGTCGCCA 120
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Pred. No. 1e-21;
0; Mismatches 26;
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Sequence 1 from patent US 5643723.
150706.1 GI:2472409
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Best Local Similarity 87.5%;
Matches 182; Conservative
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REPLEVPGLLDVQTDSFEWLIGSPRHRESAAERGDVNPVGGLEEVLYELSPIEDFSGS
MSLSFSDPRFDDVKAPVDECROKDWTYAAPLEVTAEFINNNTGEIKSQTVFWGDFPWM
TEKGTFIIINGTERVVSQLVRSPGVFPDFIDKSTDKTLHSVKVIPSRGAWLEFDVOK
RDTVGVRIDKRRAQPYTVLLALGATSEQIVERFGFSEIMSTLEKDNTVGTDEALLD
IYRKLRPGEPPTKESAQTLLENLFFKERRYDLARVGRYKVNKKLGLHVGEPTSSTLT
EEDVVATIEYLVKHEGQTTMTVPGGVEVPVETDDIDHFGNRRLRTVGELIQNQIRVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MTU12205 3853 bp DNA linear BCT 02-MAR-2000 Mycobacterium tuberculosis H37Rv RNA-polymerase beta subunit (rpoB)
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Microbiology, University of Berne, Friedbuehlstrasse 51, Berne,
3010, Switzerland
                                                                                                                                                                                                                    61 GCCTGAACACCAATCATCCGATCACCACGACGCTGACCGAAGAAGACGTCGTCGCCA 120
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1 (bases 1 to 383)
Imboden, P., Troller, R., Marchesi, F., Telenti, A., Bodmer, T., Cole, S., Schopfer, K. and Burkart, T.
The rpo8 gene of Mycobacterium tuberculosis
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                                                                                                                              Length 3534;
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               /organism="Mycobacterium tuberculosis"
/strain="Rv"
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/protein_id="AAA20242.2"
/db_xref="G1:7144499"
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1. .3853
/organism="Mycobacterium tuberculosis"
                                                                                                                            DB 6;
                                                                                                                      80.0%; Score 166.4; DB 6
87.5%; Pred. No. 8.9e-22;
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                                                 /db_xref="taxon:1773"
1081 c 1188 g
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/db_xref="taxon:1773"
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576. .>3853
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/gene="rpoB"
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U12205
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MTU12205
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DEFINITION
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HKRRLSALGEGGLSRERAGLEYBDYHPSHYGBNCPIETPEGPNIGLIGSLSYYARVWP
GYGT FETPEYRKVDGCYVSDGIYYLTADEDRHYGBNCPIETPEGPNIGLIGSLSYYARVWP
EYGT FETPEYRKVDGCYWSDGIYYLTADEDRHYYAQANSPIDADGRRYEPRYLYRRRAG
EYGT FETPEYRKYDGCYOWSVATANTEHDDANRALMGANMOROAYPLVRSEAP
LVGTGMELRAA IDAATSSSQESGYIEEVSADYITYWHINGTRRTYRWRKFRRSHHGTG
VGTGMELRAA IDAATSSSQESGYIEEVSADYITYWHINGTRRTYRWRKFRRSHHGTG
VGTGMELRAA IDAATSSSQESGYIEEVSADYITYWHINGTRRTYRWRGHYYEDAIILSRRL
VEEDVLTSIHIEHEHDANDTRUGGETTRDIPNISDEVADLDERGIYRTGAAFNDG
DILVGKYTPKGFDELTPERELLARIFCGRENGRGWGYJGKILDYDGHPFLADGTPVDI
ILVHTGVPRRHNIGQILETHLGWCAHSGHWYONAAKCYDDWAARLPDELLEAQPNAIVS
TVYFDGAQEAELQGLSGTLPRRGDYLVDAGKAALFBGRSGEPFYYWTVGYWITM
KLHHLVDDKIHARSTGPYSMITQQPLGGGRAQFGGRREGEMECWAMOAYGAAYTLOELL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RNA polymerase beta-subunit; rpoB gene.
Mycobacterium tuberculosis (strain Rv) DNA.
Mycobacterium tuberculosis
Bacteria: Actinobacteria: Actinobacteridae: Actinomycetales;
Corynebacterineae: Mycobacteriaceae: Mycobacterium: Mycobacterium
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                                                                                                                                                                                                                                                                                                                                     Gaps
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1 (Dases 1 to 5084)

Milatri.P. Crawford, J.T. and Shinnick, T.M.

The rpoB gene of Mycobacterium tuberculosis
Antimicrob. Agents Chemother. 38 (4), 805-811 (1994)
8031050
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/protein_id="AAA21416.1"
/db_xref="GI:468334"
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/strain="Rv"
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Pred. No. 8.8e-22;
0; Mismatches 26;
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/gene="rpoB"
1065. .4598
/gene="rpoB"
/codon_start=1
/evidence=experimental
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1065. .4598
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87.58;
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L27989.1 GI:468333
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1534 c 1691 g 890 t
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1 (bases 1 to 1932)
Fleischmann,R.D., Alland,D. Eisen,J.A., Carpenter,L., White,O., Peterson,J., DeBoy,R., Dodson,R., Gwinn,M., Haft,D., Hickey,E., Kolonay,J.F., Nelson,W.C., Umayam,L.A., Ermolaeva,M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1966 TCAAGGAGAAGCGTACGACCTGGCCGCGCTCGTATAAGGTCAACAAGAAGCTCG 2025
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Mycobacterium tuberculosis CDC1551
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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4641. .55084
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MSLSFSDPREDDVKAPVDECKDKDMTYAAPLEYTAEFINNNYGEIEEVLYELSPIEDFSGS
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LVEEDVLTSTHIEEBEILDARDTVLLGARGHGUNGVUNDLUSKLEVPEDMPFIELAGGTPVUD
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Direct Submission

L. Submitted (25-APR-2001) The Institute for Genomic Research, 9712
Medical Center Dr. Rockville, MD 20850, USA

Location/Qualifiers

L. 19352

//Arganism-Mycobacterium tuberculosis CDC1551*

//Arganism-Mycobacterium tuberculosis CDC1551*
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STPVFDGAQEAELQGLLSCTLPNRDGDVLVDAGKAMLPDGRSGBPFPYFVTVGYMYI
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Salzberg,S.L., Delcher,A., Utterback,T., Weidman,J., Khouri,H.,
Gill,J., Mikula,A. and Bishal,W.
Whole genome comparison of Mycobacterium tuberculosis clinical and
laboratory strains
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RKKETLDHYERRADINCHARPALHUERNBALVETWKEATDEVGGALREHYEDDNP
ITTIVDSGATGNFTQTRTLAGMKGLVTNPKGEFIPRPVKSSFREGLTVLEYFINTHGA
                                                                                                                                                              RKGLADTALRTADSCYLTRRLVDVSQDVI VREHDCQTERG INCALL VELLE LAINDON TETSAAV RRACKTATAL STATE LAINDON TETSAAV RRACKTATAL STATE LAINDON TETSAAV RRACKTATADAV DEAGNVI VERGODLGDPE IDALLAAGITQVKVRSVLTCATST VYCATCYGRSMATGKLVDI GEAVGI VAAGSIGEBGTQLTMRTPHGGGVED ITGGLPR VQELERARVPRGKAR TADVTGRVKLEDGERFK IT IV PDDGGEEVVYDK ISKRQRLR VERHDGSERVLSDGDHVEVGQQLMEGSADPHEVLRVQPRESVOIHLVREVQEVYRAQG VSIHDKHIEVI VRQMLRRVI ID DGGTFFLPGCI IDRAEFERANRRVVARGGEBAGR PVLMGI RTASLAADSMLSAASFQETFRVLTDAAINGRSDKLMGLKENVI IGKLI PAGTGINRY RNIANQPTEERRAANYTI IPSY EDQXY SPDFGAATGAAVPLDDYGY SDYR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="MFDSAAAITNPGHAWASAMERSGLLECVAGLDEQPFGEFTADKL
NPDRGSSRRVPRRQADGGIA/THVERGGGQRQSGGAGVVPQRMHGFPALAMQDRLIHH
GGPTQUNTIAGAFRVRFCVCSPT"
complement (8058...9972)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            '....- inis region contains an authentic frame shift and
Glimmer2: putative; conserved hypothetical protein,
authentic frameshift"
10167. .10925
/gene="MT0699"
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/protein_id="AAK44925.1"
/protein_id="A860225.1"
/db_xref-"GI:138860225.1"
/translation-"MLRRVAILLAAVLAFAGCSGGTRLAAGFCNGNSVHTLDVDGAGR
SYRLYKPVGLPSSAFLVVMLHGGFGSAKQAERSYGWDELADSEKFLVAYPDGYHRAWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ANGGGCCGRPAREGVDDIGFVRAVVADIANNVSIDPARVYYTGMSNGAIMSYTLACNT
SIFAAIGVVSGTOLDPCQSPRPVSVIHIHGTADPLVRYHGGPGAGFARIDGPPVPDLN
AFWREVNRCGALDTTTEGPVTTSGATCADNRRVVLLTVDDAGHRWPSFATQTLMRFFA
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PID:457174 PID:537028; identified by sequence similarity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PFAM protein family HMM
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/note="similar to GB:U00012 PID:466863; identified by
sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="MT0697"
/note="identified by Glimmer2; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="hypothetical protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(7691. .8065)
/gene="MT0697"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(7691, .8065)
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/gene="MT0701"
11859. .13487
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/product="acy1-CoA dehydrogenase, putative"
/product="acy1-CoA dehydrogenase, putative"
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GASSCOAGRWGELADRNRPILHTHDAYGYRVDEVEYDPAYHELMRTAITHGWHAAP
WADDRRGAHVYRAGTSWNTYPERHCPLRYNYAVPLAAPTRAATTSAAYUED
DPELKPATYKAGITAGWSWTEKOGGSDVRACTTQARWHAOHRKRETAAYVELLTSREY
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VLADLAVEREAATIYAAMRAGATDAWSTGATRAYHHAOHRKREGAYLIDOPLMRN
VLADLAVEREAATIYAAMRAGATDAWSKGATETALILRRIGLAAAKYWCKRSTAHAAE
ALECLGGNGYVEDSGWPRLYREAPLMGIWEGSGWVSALDTLARMATRRACVEVLEDEL
ARSAGODPRILOGHUPRILRPQUEDLITIGYRAKIJAEDICLALGGSLLVRHGHPAVAEA
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segment 32/162.
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                                                                                                                                                                                                                                           13498. 14436
/gene="MT0702"
13498. 14436
/gene="MT0702"
/note="similar to GP:3885480; identified by sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Mycobacterium tuberculosis H37Rv
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae;
Mycobacterium; Mycobacterium tuberculosis complex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80.0%; Score 166.4; DB 1; Length 87.5%; Pred. No. 7.3e-22; live 0; Mismatches 26; Indels
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295972 AL123456
295972.1 GI:3261790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    by Glimmer2; putative"
                                                                                                                                                                                                                              FLATRIGGOWGGAYGTMPAGLDLAPILERALVKG"
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/codon_start=1
/transl_table=11
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tes 182; Conserv
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Matches
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MTCI376
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KEYWORDS
SOURCE
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1585. .2664
/gene="RV0655, (MTC1376.21), len: 359, abc transporter,
/note="RV0655, (MTC1376.21), len: 359, abc transporter,
FASTA score: YRBF_ECOLI P45393 hypothetical abc
transporter arep-binding (169 aa) opt: 644 z. score: 721.8
E(): 3 4e-33 (38.58 identity in 244 aa overlap); contains
FS00017 ATP/GTP-binding site motif A, PS00211 ABC
transporters family signature, highly similar to M. leprae
MKL_MYCLE P30769 possible ribonucleotide transport atp-
(347 aa) opt: 2021 z-score:2244.4 E(): 0, (92.2% identity
in 335 aa overlap). Also similar to many otherM.
tuberculosis ABC transporters eg, MTCY253.24 (33.6%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /traislation-**MRYSDSYHTTGRWQPRASTEGFPMGVSIEVNGLTKSFGSSRIWE
DVTLTIPAGEVSVLIGPSGTGKSVFLKSLIGLLRPERGSIIDGTDIIECSAKELYEI
TELEVLEGOOGALFGSMULYDNTAFPLREHTKKESEIRDIVWEKLALVGLGGDEKKF
PGEISGGMRRRAGLARALVLDPQIILLDCDEPDSGLDPVRTAYLSQLIMDINAQIDATIL
IVTHNINIARTVPDANGMLFRHILVMEGPREVLLTSDEPVVRQFLNGRRIGFTGMSEE
KDEATWAEEQALLDAGHHAGGVEEIEGVPPOISATPGMPERRAVARRQARVREMLHTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /transl_table=11
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/db_xref="SPTREMBL:006783"
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/translation-"MSVTQIDLDDEALADVMRIAAVHTKKEAVNLAMRDYVERFRIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(3052. .3435)
/gene="Rv0656c"
/note="Rv0656c, (MTCI376.20, unknown), len: 127 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /hote="PS00211 ABC transporters family signature" complement(3052, .3435)
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/gene="Rv0658c"
/note="Rv0658c, (MTCI376.18), len: 238, unknown,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               //ord="PS0017 ATP/GTP-binding site motif A" /2014. 1118 /gene="Rv0655"
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/protein_id="CAB09377.1"
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/note="possible RBS upstream
complement(3761, 4477)
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/gene="P:v0657c"
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/gene="Rv0655"
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                                                   CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 available on the World Wide Web.

(URL, http://www.sanger.ac.uk/Projects/M_tuberculosis/) CDS have been renumbered from the Original cosmid submissions but the old gene designations are in brackets after the new gene numbers.

Gene prediction was based on a Hidden Markov Model of TB genes implemented in TBpares (Krogh) supplemented with visual inspection of positional base preference in codons, especially where there is an increase in the observed/axpected third position G + C CAUTION: In some cases we may not have predicted the correct initiation codon. Where possible we choose an initiation codon (atg, 9tg, or ttg) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most upstream initiation codon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tuberculosis sequencing and mapping teams, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA Unite de Genetique Moleculaire Bacterienne, Institut pasteur, 28 rue du Docteur Roux, 75724 Paris Cedex 15, France E-mail: parkhill@sanger.ac.uk On Jun 27, 1998 this sequence version replaced g1:2143285.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AHPQRDPHTGELHAVSYSFARGHRVQYSVIGTDGHARRTVDIEVAGSPMMHSFSLTDN
YVVIYDLPVTFDPMQVVPASVPRWLQRPARLVIQSVLGRVRIPDPIAALGNRMQGHSD
RLPYAWNPSYPARVGVMPREGGNEDVRWFDIEPCYVYHPLNAYSECRNGAEVLVLDVV
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FAYTVGIEGGFLVGAGAALSTPLYKQDCVTGSSTVASLDPDLLIGEMVFVPNPSARAE
DDGILMGYGWHRGRDEGQLLLLDAQTLESIATVHLPQRVPMGFHGNWAPTT*
                           Cole, S.T., Brosch, R., Parkhill, J., Garnier, T., Churcher, C., Harris, D., Gordon, S.V., Eiglmeier, K., Gas, S., Barry III, C.E., Fekafa, F., Badcock, K., Basham, D., Brown, D., Chillingworth, T., Connor, R., Davies, R., Devlin, K., Feltwell, T., Gentles, S., Hamlin, N., Holroyd, S., Hornsby, T., Jagels, K., Krogh, A., McLean, J., Murphy, L., Oliver, S., Osborne, J., Quail, M.A., Rajandream, M.A., Rogers, J., Rutter, S., Seeger, K., Skelton, S., Squres, S., Sqares, R., Sulston, J.E., Taylor, K., Whitehead, S. and Barrell, B.G.
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Lrngpnpvaevdpatyhwfygdamvhgvalrdgrarmyrnrwvrtpavcaalgepisa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (11-JUN-1998) Submitted on behalf of the Mycobacterlum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Notes: Details of M. tuberculosis sequencing at the Sanger Centre are
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    19770
/organism="Mycobacterium tuberculosis H37Rv"
/strain="H37Rv"

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/protein_id="CaB09380.1"
/db_xref="GI:2143307"
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Nature 393 (6685), 537-544 (1998)
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/clone="1376"
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/transl_table=11
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68. .1573
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Parkhill, J.
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AUTHORS
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JOURNAL
   REFERENCE
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Gene="Rv0659c"

Complement(4753. 5061)

Gene="Rv0659c"

Complement(4753. 5061)

Gene="Rv0659c"

(MTC1376.17), len: 102; unknown, similar to YW28_MYCTU 010867 hypothetical 12.3 kd protein cY39.28

(114 aa), fasta scores; opt: 144 z-score: 213.2 E():

7.3=05, 30.8% identity in 107 aa overlap, Also similar to Kodon_start=1

/ Codon_start=1

/ Transl_table=11

/ Product="hypothetical protein Rv0659c"

/ Ab_xref="General Protein Rv0659c"

/ Ab_xref="General Protein Rv0659c"
                                                                                                                                                                                      /db_xref="SPTREMBL:006781"
/translation="MEAGRADTVAPSHRWGLGAFLVVELVFLVASTSLAVVLTGHGPV
SAGVLALAAPTVVAAGLATLITRLRGNGLRTDLRLRRWSRRGLRLGLMFGFGGMLVT
IPASLVYTAIVGPEANSAVVRIFGGVRASWPMALVVFLVVVFVAPLCEEIIYRGLLMG
TWDRWGRWAALVYTVVFLAHLEFARAPLLVVVVAIPIALARFYSGGLLASIVTHQV
TNLLPGIVLLLGLTGAISLP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation-"mrrgelwFpATpGGDRPVLVLTRDPVADRIGAVVVVALTRTRG
LVSELELTAVENRVPSDCVVNFDNIHTLPRTAFRRITRLSPARLHEACGTLRASTGC
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probablemembrane protein, similar to YPRB_ECOLI P33774 hypothetical24.3 kd protein (urf 1) (217 aa), fasta scores; opt: 174 z-score: 215.8 E(): 5.3e-05, (25.6% identity in 123 aa overlap). Also similar to MTCY359.10 (28.7% identity in 178 aa overlap).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mycobacterium smegmatis DNA polymerase (rpoB) gene, complete cds.
U24494
U24494.1 GI:790347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ....e="RV0560c, (MTC1376.16), len: 81, some similarity
|AF016485_130 Halobacterium sp; NRC-1 plasm (100 aa),
32.4%identity in 74 aa overlap"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 GCCTGAACACCAATCATCCGATCACCACGACGACGCTGACCGAAGAAGACGTCGTCGCCA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80.0%; Score 166.4; DB 1; Length 19770; Ilarity 87.5%; Pred. NO. 7.3e-22; Conservative 0; Mismatches 26; Indels 0:
                                                                                                                                                                                                                                                                                                   complement(4480. .4483)
/note="possible RBS upstream of Rv0658c"
complement(4753. .5061)
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                                                                                                                                  /product="hypothetical protein Rv0658c"
/protein_id="CAB09376.1"
/db_xref="G1:2143303"
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complement(5048. .5293)
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                                                                                             /codon_start=1
/transl_table=11
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nes 182; Conserv
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/product="DNA polymerase"
/product="DNA polymerase"
/product="DNA polymerase"
/db_ref="C1:7144498"
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VANTGOILERHGIGERARAGNNI DVLAGVPDMASKLEPELYSAPADSTVAT PVFDGAQE
GELAGILGSTLPNRDGEVMVNADGKATLFDGRSSGEPPPY PVTVGYNIT LIKLHHLVDD
KIHARGIGSTGPYSMITOQPLGGRADGGORFGENECWANGAYGAAYTLOELLTIK SDDTV
GRVKVYEAIVKGENIPEPGIPESFKVLLKELQSLCLNVEVLSSDGRAIEMRDGDDEDL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 (bases 1 to 3752)
Hetherington,S.V.
Direct Submission
Submitted (11-APR-1995) Seth V. Hetherington, Infectious Diseases, St. Jude Children's Research Hospital, 332 N. Lauderdale, Memphis, TN 38101, USA
                                                                                                                                                                                                                                                                                                                smegmatis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1068 TCAAGGAGAAGGGCTACGACCTGGCCCGTGTGGCCGTTACAAGGTCAACAAGAAGATGTGG 1127
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                                                                                                                                                                                            1 (bases 1 to 3752)
Hetherington, S.V., Watson, A.S. and Patrick, C.C.
Sequence and analysis of the rpoB gene of Mycobacterium
Antimicrob. Agents Chemother. 39 (9), 2164-2166 (1995)
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                                                                                Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 156.8; DB 1;
Pred. No. 5.4e-20;
0; Mismatches 32;
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Mycobacterium smegmatis. Mycobacterium smegmatis
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/gene="rpoB"
194. .3703
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Best Local Similarity 84.6%;
Matches 176; Conservative
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Db 1248 TCGAGTTCGCCGTCGAGTCGCACGACAT 1275

Search completed: November 13, 2002, 01:25:56 Job time : 662.723 secs AY103647 Zea mays AY103418 Zea mays BF484291 WHE2321_E BQ842534 WHE2391_E BG105122 60228994_B BI578713 RF7617.5 BH58452 100809780

BJ125380 BE301556 DG1_72_E0 R86528 RABEST084T BG321153 2m04_05f0 AY103647 Zea mays

C73000 C73000 Rice R8658B RABEST163T R86556 RABEST140T R86510 RABEST202T BF264852 WY CEA001 BJ270031 BJ270031 BJ26380 BJ226380

BL708491 BL70804 BL70804 BL70804 BL70804 BL744734 BL704734 BL704734 BL7060431 BL7060431 BL7060431 BL7060431 BL706159 BL706159 BL706159 BL70609 BL70609

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Scoring table:

Searched:

Perfect score:

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Run

BE406021 AV929492 BJ208458 BB754521

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42 Mycobacterium anaerobic stationary phase library Mycobacterium smequence.
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Murugasu-Oei,B., Tay.A. and Dick,T.
Upregulation of stress response genes and ABC transporters in anaerobic stationary phase Mycobacterium smegmatis
Mol. Genet. 262 (4-5), 677-682 (1999)
                                                                                                                                                                                                                                                                                                                                                                            Mycobacterium smegmatis.
Mycobacterium smegmatis
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mycobacterium Laboratory
Institute of Molecular and Cell Biology
30 Medical Drive, Singapore 117609, Republic of Singapore
18=1 65 974 3011
Fax: 65 779 117
Email: mcbbom@imcb.nus.edu.sq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: mcbbom@imcb.nus.edu.sg
Insert Length: 1282 Std Error: 0.00
Seq primer: T3 Forward; T7 Backward.
Location/Qualifiers
1..1282
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                                                                            AY103647
AY1036418
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BG42534
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BG709105
BE70813
BH604652
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BJ317529
AW056150
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BQ820533
BF627944
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BJ260431
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AI770311/c
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AUTHORS
TITLE
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MEDLINE
COMMENT
                                                                                                                                                                                                                                                                                                                                                       ACCESSION
                                                                                                                                                                                                                                                                                                                                                              VERSION
KEYWORDS
SOURCE
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AY107051 Zea mays
BH897054 3526 1 6
BM601475 170006590
BM590640 170006873
R86542 RABEST103T
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                                             November 12, 2002, 16:59:42 ; Search time 1141.13 Seconds (without alignments) 3037.202 Million cell updates/sec
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                                                                                         1 tcaaggagaagcgctacgac.......ccggtcgaggtcgacgacat 214
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      5.1.3
Compugen Ltd.
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     version -
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Maximum Match 100%
Listing first 45 summaries
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      GenCore
Copyright (c) 1993
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em_gss_pro:*
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                                 nucleic search, using
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em_etr: *
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                                                                                                      // Anotes Westor: Landon All: Bacilli were disrupted using a Mini bead beater (Biospec). RNA was isolated using the RNeasy protocol (Qiagen). Purified RNA was subjected to 2 rounds of digestion with RNase-free DNase I (Promega). DNase I was heat-inactivated at 750C for 5 min. and removed by using RNeasy columns followed by phenol extraction and ethanol precipitation. The RNA preparations were confirmed to be free of genomic DNA contamination by carrying out PCR and RT-PCR using the Access kit (Promega) and primers specific for the histone-like protein gene hip (Lee et al., 1998). cDNA was synthesized using random hexamer primers (Promega) and Stratagene's cDNA synthesis kit. CDNA fragments were ligated into lambda ZAP II vector and packaged in vitro using Stratagene reagents.
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                                  /db_xref="taxon:1772"
/clone_lib="Mycobacterium anaerobic stationary phase
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Submitted (25-APR-2002) Maize Mapping Project, University of
Missouri, Columbia, MO 65211, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 1850)
Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitsitt,M.S.,
Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V.
Maize Mapping Project/DuPont Consensus Sequences for Design
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    65.0%; Score 139.2; DB 9; Length 1282; ilarity 81.8%; Pred. No. 7.4e-21; Conservative 0; Mismatches 33; Indels 6;
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                                                                                            /lab_host="E. coli XL1-Blue MRF'"
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/db_xref="MaizeDB:637903"
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Zea mays PC0135033 mRNA sequence.
AY107051
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2 (bases 1 to 1850)
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3526_1_6_1_E11.1EL_y_1 3526 - Rescuemu Grid K Zea mays genomic, DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Maize genomic sequences found using engineered RescueMu transposon Unpublished (2001)
Contact: Malbot V
Department of Biological Sciences
/clone="PCO135033"
/clone_lib="Maize Mapping Project/DuPont Cornsensus Library"
/note="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed DuPont contigs, this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project"
a 625 c 583 g 311 t
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Fax: 650 725 8221
Email: walbot@stanford.edu
Emy probable ligation site of ends cut by single endonuclease.  
Reverse complemented post-ligation sequence from source sequence.  
Plate: 356_1_6_1 row: 6
Class: transposon-tagged.
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                                                                                                                                                                                                                                                                                  Score 47.4; DB 11; Length 1850;
Pred. No. 0.96;
0; Mismatches 96; Indels 0;
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/organism="Zea mays"
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TITLE
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KEYWORDS
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BM601475 665 bp mRNA linear EST 25-FEB-2002 17000659084020 A.Gam.ad.cDNA.bloodl Anopheles gambiae cDNA clone 19600447016323 5', mRNA sequence.
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designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.zmb.iastate.edu' and follow the links for 'RescueMu.' Grid K was grown at Molokai, Hawaii in Winter 2000-2001. DNA was extracted from leaf punches, double digsteed using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."
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1 (bases 1 to 665)
Holt, R.A., Lin, J.-J., Murphy, S.D., Evans, C.A., Kraft, C.L., Charlab, R., Collins, F.H., Venter, J.C. and Hoffman, S.L.
Celera Anopheles gambiae EST project
Unpublished (2002)
Contact: Holt R.A.
Celera Genomics
A. G. Gude Dr., Rockville, MD 20850, USA
Fex: 2404534580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Vector: pSport1; Site_1: Sal1; Site_2: Not1: Whole adult mosquitoes (mixed sex) frozen on liquid nitrogen 24 hours after human blood feeding. cDNA inserts >500 bp cloned directionally into pSport 1. Not 1 site is 3'.
                                                                                                                                                                                                                                                                                                                                                                                                                        74 CAACCCGGCTCTGGTGACTGCCACCACGCTCACCGAGGAAGACGTCGTCGCCACCATCGG 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         134 GTACCTGGTGCGCCTGCACGAGGGCCAGACCACGATGACCGCCCCCGGCGGCCTCGAGGT 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          245 GGCCGCTGCCGCGGGGGGCAGCTGCCCACCGGCTGCATGGCGGACCTCAACGGCGC 186
                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                               14 CTACGACCTGGCCCGCGTGGGCCGGTACAAGTGAACAAGAAGCTGGGTCTTGGCGGTGC 73
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
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/strain="RSP-ST (Reduced susc. to Permethrin - std.
chromosome)"
                                                                                                                                                                                                                                                                                                21.0%; Score 45; DB 17; Length 569; 53.0%; Pred. No. 2.8; ive 0; Mismatches 85; Indels
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/clone="19600447016323"
/clone_lib="A.Gam.ad.cDNA.blood1"
/dev_stage="Adult"
/lab_host="DH10b"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: HoltRA@celera.com
Plate: NUO1003T45 row: E column: 18
Seg primer: M13 Reverse.
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BM601475.1 GI:18899579
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Best Local 3
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JOURNAL
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1 (bases 1 to 687)

Holt, R.A., Lin,J.-J., Murphy,S.D., Evans,C.A., Kraft,C.L., Charlab, R., Collins,F.H., Venter,J.C. and Hoffman,S.L.
Celera Anopheles gambiae EST project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Vector: pSport; Site_1: Sall; Site_2: Not1: Whole adult mosquitoes (mixed sex) frozen on liquid nitrogen 24 hours after human blood feeding. cDNA inserts >500 bp cloned directionally into pSport 1. Not 1 site is 3'. Clones available through the Malaria Research and Reference Reagent Resource Center (www.malaria.mr4.org)**
Clones available through the Malaria Research and Reference Reagent Resource Center (www.malaria.mr4.org)" 229 c 246 g 105 t
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17000687384060 A.Gam.ad.cDNA.blood1 Anopheles gambiae cDNA clone
19600449721853 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                           68 CGGTGCCAACCCGGCTCTGGTGACTGCCACCACGTCACCGAGGAAGACGTCGTCGCCAC 127
                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                67
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Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Eukaryota; Culicoidea;
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/strain="RSP-ST (Reduced susc. to Permethrin - std.
chromosome)"
                                                                                                                                                           8 GAAGCGCTACGACCTGGCCCGCGTGGCCGGTACAAGGTGAACAAGAAGCTGGGTCTTGG
                                                                                                                                                                                                                                                                                                     128 CATCGGGTACCTGGTGCGCCTGCACGAGGCCAGACCACGATGACCGCCCCGGGCGGCCT
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                                                                                          Length 665;
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                                                                                                                            Indels
                                                                                                                          66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (2002)
Contact: Holt R.A.
Colera Genomics
45 W. Gude Dr., Rockville, MD 20850, USA
Tel: 2404533151
Fax: 2404534580
Email: HoltRa@celera.com
Plate: NU01004A9X row: G column: 23
Seq primer: M13 Reverse.
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-/clone='19600449721853"
-/clone_11b='A.Gam.ad.cDNA.blood1"
-/dev_stage="Adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 13;
                                                                                          DB 13;
                                                                                                         Pred. No. 3.5;
0; Mismatches
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Pred. No. 3.5;
                                                                         Score 44.6;
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                                                                                                                                                                                                                                                                                                                                                                            188 CGAGGTCCCGGTCGAGGTCGACG 210
                                                                                                                                                                                                                                                                                                                                                                                                     GCCGGTCGTCTACGAAGCAGCCG 443
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 African malaria mosquito.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BM590640.1 GI:18886501
                                                                                     Ouery Match 20.8%;
Best Local Similarity 51.2%;
Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20.8%;
51.2%;
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Best Local Similarity
                                  85 a
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KEYWORDS
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                                BASE COUNT
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AUTHORS
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COMMENT
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BM590640
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AV438805 Porphyra yezoensis TU-1 Porphyra yezoensis cDNA clone PS041e12_r 5', mRNA sequence.
AV438805 GI:8594030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact:
Contact:
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Porphyra yezoensis"
/strain="TU-1"
/db_xref="taxon:2788"
/clone="PS041e12_r"
/clone=lbb="Porphyra yezoensis TU-1"
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
                                                                                                                        Nikaldo,I., Asamizu,E., Nakajima,M., Nakamura,Y., Saga,N. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Porphyra yezoensis
Eukaryota: Rhodophyta; Banglophyceae; Banglales; Banglaceae;
                                                                                    65 TGGCGGTGCCAACCCGGCTCTGGTGACTGCCACCGCTCACCGAGGAAGACGTCGTCGC
                                                                                                                                                                                         125 CACCATCGGGTACCTGGTGCGCCTGCACGAGGGCCAGACCACGATGACCGCCCCC 179
                                                                                                                                                                                                                       Generation of 10,154 expressed sequence tags from a l
gametophyte of a marine red alga, Porphyra yezoensis
DNA Res. 7, 223-227 (2000)
20363100
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Best Local Similarity
Matches 82; Conserv
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MEDLINE
COMMENT
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AV438805
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C73000
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/strain="New Zealand White"
/db_xref="texon:9986"
/clone="praBoC103"
/clon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oryctolagus cuniculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R86542 277-AUG-19
RABEST103T Rabbit Osteoclast, Dennis Sakai Oryctolagus cuniculus
cDNA clone pRABOC103 5' similar to cofilin, mRNA sequence.
R86542
                                                                                                                                                68 CGGTGCCAACCCGGCTCTGGTGACTGCCACGACGACGAAGAAGACGTCGTCGCCAC 127
                                                                                                                                                                                                                                                                   187
                                                                                                                                                                                                                                                                                         Gaps
                                              8 GAAGCGCTACGACCTGGCCCGCGTGGGCCGGTACAAGGTGAACAAGAAGCTGGGTCTTGG 67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Other_ESTS: RABEST03BT, RABEST045T, RABEST084T, RABEST140T, RABEST163T, RABEST202T, RABEST229T
Contact: Sakai D
Basic Sciences
University of Southern California
UGC School of Dentistry, 925 West 34th Street, DEN-4220, Los Tel: 2137405563
                                                                                                                                                                                                                                                      128 CATCGGGTACCTGGTGCGCCTGCACGAGGGCCAGACCACGATGACCGCCCCCGGCGGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 275)
Sakai,D., Tong,H.-S. and Minkin,C.
Osteoclast Molecular Phenotyping by Random cDNA Sequencing
Bone 17 (2), 111-119 (1995)
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  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fax: 2137407560
Email: sakai@molbio.usc.edu
Seq primer: T7 promoter.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                           188 CGAGGTCCCGGTCGAGG 210
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  Conservative
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DEFINITION

RESULT 6 R86542

ACCESSION

VERSION KEYWORDS SOURCE

ORGANISM

AUTHORS TITLE JOURNAL MEDLINE COMMENT

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                              67 GCGGTGCCAACCCGGCTCTGGTGACTGCCACGACGCTCGAGGAAGACGTCGTCGCCA 126
                                                                                                         127 CCATCGGGTACCTGGTGCGCCTGCACGAGGGCCAGACCACGATGACCGCCCCCGGCGGCG 186
                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                       C73000 461 bp mRNA linear EST 04-APR C73000 Rice panicle at flowering stage Oryza sativa (japonica cultivar-group) cDNA clone E2649_1A, mRNA sequence. C73000 EST.000 EST.
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                                                                  24 GCGCGCGCCCCCCCCGCTGGTGACCGCCACCCCCCAGCGGCCACGCGCTCACCGCCA
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  Indels
64;
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Length 371;

source

FEATURES

BASE COUNT

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Email: sakai@molbio.usc.edu
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/organism="Oryza sativa (japonica cultivar-group)"
/cultivar="Nipponbare"
/db_tref="taxon:99947"
/clone="E2649_1A"
/clone="lib="Rice panicle at flowering stage"
/dev_stage="flowering stage"
/note="Organ: panicle; Rice cDNA from panicle at flowering stage"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
1 (bases 1 to 214)
Sakai,D., Tong,H.-S. and Minkin,C.
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RABEST163T Rabbit Osteoclast, Dennis Sakai Oryctolagus cuniculus
cDNA clone pRABOC163 5' similar to cofilin, mRNA sequence.
R86588
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                                                                                                                                                                                                                                                                                                                                                                                                                                68 CGGTGCCAACCCGGCTCTGGTGACTGCCACCACGCTCACCGAGGAAGACGTCGTCGCCAC 127
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USC School of Dentistry, 925 West 34th Street, DEN-4220, Los
Angeles, CA 90089-0641
Tel: 2131405563
Fax: 2137407560
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RABEST107T, RabEST202T, RabEST229T
CONTACT: Sakai D
Basic Sciences
                                                                                                                                                                                                                                                                                                                                                                                   Length 461;
                                                                                                                                                                                                                                                                                                                                             1 others
                                                                                                                                                                                                                                                                                                                                                                                                         63; Indels
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56.2%; Pred. No. 6.7;
11ve 0; Mismatches 63;
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96021365
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1 (bases 1 to 235)
Sakal, D., Tong, H.-S. and Minkin, C.
Soteoclast Molecular Phenotyping by Random cDNA Sequencing
Bone 17 (2), 111-119 (1995)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65 TGGCGGTGCCAACCCGGCTCTGGTGACTGCCACCACGTCACCGAGGAAGACGTCGTCGC 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72 GGAGGAGGGCAAGGAGTCCTGGTGGGCGACGTGGGCCAGACCGTGGAGGACCCCTACGC 131
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54.8%; Pred. No. 6.8;
Live 0; Mismatches
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/strain="New Zealand White"
/db_xref="taxon:9986"
Seq primer: T7 promoter.
Location/Qualifiers
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Email: sakai@molbio.usc.edu
Seq primer: T7 promoter.
Location/Qualifiers
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Best Local Similarity
Matches 85; Conserv
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/clone_lib="Rabbit Osteoclast, Dennis Sakai"
//lab_host="E. coli DH12S"
//lab_host="E. coli DH12S"
//note="Vector: pSPORTI; Site_1: Sal1; Site_2: NotI; Poly(A
)+ RNA was purified from a 97% pure population of
osteoclasts prepared from the long bones of 10 day old
rabbits. First strand cDNA was synthesized by priming
with an oligo(dT)-NotI anchor-primer and second strand
cDNA was synthesized by replacement synthesis as described
by Gubler and Hoffman (Gene 25:283, 1983). Following the
addition of Sal1 adapters and NotI digestion, the cDNA was
cloned between the Sal1 (30) and NotI (30) sites of the
pSPORTI (BRL) plasmid vector."

57 a 63 c 81 g 34 t
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/strain="New Zealand White"
/dLxref="taxon:9986"
/clone="pRBADG202"
/clone="pRBADG202"
/lab_host="E. coli DHL2s"
/nab_host="E. coli DHL2s"
/note="vector: pSPORTI; Site_1: SalI; Site_2: NotI; Poly(A) + RNA was purified from a 97% pure population of osteoclasts prepared from the long bones of 10 day old rabbits. First strand cDNA was synthesized by priming
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Sakai,D., Tong,H.-S. and Minkin,C. Osteoclast Molecular Phenotyping by Random cDNA Sequencing
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SCS School of Dentistry, 925 West 34th Street, DEN-4220, Los
Angeles, CA 90089-0641
Tel: 2137405563
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Contact: Sakal D
Basic Sciences
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Pred. No. 6.8;
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54.8%; Pred. No. o...
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/clone-"pRABOC140"
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Email: sakai@molbio.usc.edu
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Hordeum vulgare.

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Hordeum.

I (bases I to 878)

Ming, R., Close, T. J., Kleinhofs, A., Wise, R., Wei, F., Begum, D., Frisch, D., Yu, Y., Henry, D., Palmer, M., Rambo, T., Simmons, J., Choi D.W., Fenton, R.D., Oates, R. and Main, D. Bevelopment of a genetically and physically anchored EST resource for barley genomics: Blumeria infected incompatible (Mial3)

AL Unpublished (2001)

AL On Nov 17, 2000 this sequence version replaced gi:11195846.
with an oligo(dT)-NotI anchor-primer and second strand cholms was synthesized by replacement synthesis as described by Gubler and Hoffman (Gene 25:283, 1983). Following the addition of SalI adapters and NotI digestion, the cDNA was cloned between the SalI (50) and NotI (30) sites of the pspoRTI (8RL) plasmid vector."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HV_CEa010124f Hordeum vulgare seedling green leaf EST 23-OCT-2001 HVCDNA0004 (Blumeria challenged) Hordeum vulgare cDNA clone BF264852 GI:13261763
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C.I. 16155 (Mla13) plants were greenhouse grown in the R
Wise lab at lowa State University, Ames, 1A; 7 day old
green seedlings were challenged with isolate A27 (AvrMla13
                                                                                                                                                                                                                                                                                                                                                                         65 TGCCGGTGCCAACCCGGCTCTGGTGACTGCCACCACGTCACCGAGGAAGACGTCGTCGC 124
                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                             64
                                                                                                                                                                                                                                                                                                                  /organism="Hordeum vulgare"
/cultivar="C116155 (Mla13)"
/db_xref="taxon:45134"
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/clone_Llb="Hv.CE00101214"
/clone_Llb="Hv.Ceum vulgare seedling green leaf EST
/tissue_type="seedling green leaf"
/lab_host="goodling green leaf"
                                                                                                                                                                                                                                                                                    5 GGAGAAGCGCTACGACCTGGCCCGCGTGGGCCGGTACAAGGTGAAGAAGCTGGGTCT
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                                                                                                                                                                                                  Score 43; DB 14; Length 331;
Pred. No. 7.1;
0; Mismatches 70; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100 Jordan Hall, Člemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                               125 CACCATCGGGTACCTGGTGCGCCTGCACGAGGGCC 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CACCTTCGTGCAGATGCTGCCCGACAAGGACTGCC 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clemson University Genomics Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seq primer: AATTAACCCTCACTAAAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           High quality sequence stop: 348.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: rwing@clemson.edu
Total hq bases = 224
                                                                                                                                                                                                  20.1%;
54.8%;
                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clemson University
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                                                                                                                                                                                                                       Similarity
                                                                                                                                 88
                                                                                                                                                                                                                                            85;
                                                                                                                                                                                                Query Match
Best Local S
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KEYWORDS
SOURCE
ORGANISM
                                                                                                                               BASE COUNT
ORIGIN
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COMMENT
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AUTHORS
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TITLE
JOURNAL
COMMENT
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KEYWORDS
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Noubblished (2002)

Contact: Tadasu Shin-1

Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan

Tel: 81-559-81-6855

Fax: 81-559-81-6855
) of Blumeria graminis f. sp. hordei, and leaves were harvested 20 and 24 hr post-inoculation and snap frozen; uninoculated leaves were harvested 20 hr post-inoculation (Wei, Mise). In the TJ Close lab at the University of California, Riverside, total RNA was prepared from each sample pool, equal quantities of all three RNA pools were combined, poly(A) RNA was purified from the mixture, one CDNA ilbrary was made, and I million pfu were in vivo excised to give pBluescript SK(-) cDNA phagemids (Choi, Close). Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Maln). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BJ270031 EST 09-APR-2002 BJ270031 Y. Ogihara unpublished cDNA library, Wh_oh Triticum aestivum cDNA clone whoh5m04 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                       this clone see http://www.genome.clemson.edu/orders Also see Close TJ, Wing R, Kleinhofs A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (http://wheat.pw.usda.gov/ggpages/Dgn/31/cover.html)" 152 c 288 g 232 t l others
                                                                                                                                                                                                                                                                                                                                                                                                                         order
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          125 CACCATCGGGTACCTGGTGCGCCTGCACGAGGCCCAGACCACGATGACCGCCCCCGGCGG 184
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                                                                                                                                                                                                                                                                                                                                                                          above. For more details on library preparation and
                                                                                                                                                                                                                                                                                                                                                                                               sequence analysis see
http://www.genome.clemson.edu/projects/barley. To
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 878;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 43; DB 12; Length 87
Pred. No. 8;
0; Mismatches 100; Indels
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  273 CGCCGGCGACTACGCGGCTGTCG 295
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50.7%;
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Best Local Similarity
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JOURNAL
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KEYWORDS
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1. .618
/organism="Triticum aestivum"
/cultivar="Chinese Spring"
/db_xref="taxon:6565"
/clone="whoh5m04"
/clone="whoh5m0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Lillopsida; Poales; Poaceae; Pooldeae; Triticeae; Triticum.

Triticeae; Triticum.

(bases 1 to 623)
Ogihara, Y. and Murai, K.
Expressed genes in Triticum aestivum
(mpublished (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62 TCTTGGCGGTGCCAACCCGGCTCTGGTGACTGCCACCACGTCACCGAGGAAGACGTCGT 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          269 CCTGGGCTGGCGCCGGCGGTCGTCATCTCCACCAAGCTCTTCTGGGGCGGCCAGGG 328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 42.6; DB 13; Length 6
Pred. No. 9.4;
0; Mismatches 104; Indels
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National Institute of Genetics
Ill Yata, Mishima, Shizuoka 411-8540, J
Tel: 81-559-81-6855
Fax: 81-559-81-6855
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 189 GGGCTCAACATGGAGTACGTCGACGTCG 417
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Location/Qualifiers
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50.2%;
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Best Local Similarity
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/clone="wholisedize"
/clone="wholisedize"
/clone="wholisedize"
/clone="lip="x" Ogihara unpublished cDNA library, Wh_dL"
/tissue_type="crown of seedling"
/dev_stage="reekes" scale 1"
//note="Wector: Lambda Uni-ZAP XR, excised phagemid;
Site_1: EcoRI: Site_2: XhOi; Plants were grown under
Site_1: EcoRI: Site_2: XhOi; Plants were grown under
hydroponic conditions at UC Davis, salt stressed for 12
hours, and for 7 days, then dissected and frozen (Akhunov
in J Dorak Lab). Total RNA was prepared from sheath
tissue, equal quantities of RNA were pooled from the two
samples, polyA was purified from the pooled from the two
samples, polyA was purified from the pooled from the two
samples, polyA was purified from the pooled RNA, a cDNA
library was made, and the CDNA clones were in vivo
exclsed to give pbluescript phagemids in the TJ Close lab
at the University of California, Riverside (Akhunov, Chin
'Chol. Close, Fenton, Kianian, Otto, Simons, Zhang).
Plasmid DNA preparations and DNA sequencing were
performed in the Ob Anderson and all others
14 a 216 c 208 g 84 t lothers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              An EST database from Sorghum: dark-grown seedlings
Unpublished (2000)
Contact: Cordonnier-Pratt MM
Contacts Cordonnier-Pratt MM
Laboratory for Genomics and Bloinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 543 1860
Fax: 706 583 0210
Email: mnpratt@uga.edu
Sequences have been trimmed to exclude PolyA, vector and regions
below Phred quality 16. The threshold for highest quality sequence
is 20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta: Magnoliophyta; Liliopsida: Poales; Poaceae; PACC
clade; Panicoldeae: Andropogoneae; Sorghum.
1 (bases 1 to 479)
Cordonnier-Pratt,M.-M., Gingle,A., Marsala,C., Sudman,M. and Pratt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BE361556 479 bp mRNA linear EST 20-JUL-20
DG1_72_E07.b1_A002 Dark Grown 1 (DG1) Sorghum bicolor cDNA, mRNA
sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      114 CAACGCCGAGGTCTACGCCAACGCCGCGGAGGAGATCATGGGGCAGGCGATCCGGGA 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62 TCTTGGCGGTGCCAACCCGGCTCTGGTGACTGCCACCACGCTCACCGAGGAAGACGTCGT 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     274 cciedecrecececececereficarerecaecaecaecaecaeces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     122 CGCCACCATCGGGTACCTGGTGCGCCTGCACGAGGCCCAGGACCACGATGACCGCCCCGG 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19.9%; Score 42.6; DB 13; 50.2%; Pred. No. 9.4; ive 0; Mismatches 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    394 GCGGCTCAACATGGAGTACGTCGACGTCG 422
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/db_xref~"taxon:4565"
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BE361556.1 GI:9303015
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Best Local Similarity 50.28
Matches 105; Conservative
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                                                                               /organism="Sorghum bicolor"

/db_xref="taxon:4558"

/clone_lib="Dax Grown 1 (DG1)"

/note="Organ: 5-day-old dark-grown seedlings; Vector:

/note="Organ: 7-day-old dark-grown seedlings; Vector:

/note="Organ: 7-day-old dark-grown seedlings; Vector:

/note="Organ: 7-day-old dark-grown seedlings; Vector:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               334 CCCCAACAACATGCTCGCCGACCTCGCCGACGACGCGGGAAGGCTAAGGACTGGGTCAA 393
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Pred. No. 10;
0; Mismatches 101;
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    Location/Qualifiers
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50.5%;
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1: /cgn2_6/ptodata/2/pubpna/USO7_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/DEC_NEW_PUB.seq:*
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5: /cgn2_6/ptodata/2/pubpna/USO7_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/USO7_NEW_PUB.seq:*
7: /cgn2_6/ptodata/2/pubpna/USO8_NEW_PUB.seq:*
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Copyright (c) 1993 - 2002 Compugen Ltd.
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US-09-887-052-3
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APPLICANT: HANS, STEERAN
APPLICANT: HERANN, THOMAS
APPLICANT: HERANN, THOMAS
APPLICANT: HERANN, THOMAS
APPLICANT: HERANN, THOMAS
TITLE OF INVENTION: WUCLEOTIDE SEQUENCES WHICH CODE FOR THE rpsL GENE
FILE REFERENCE: 218472USOX
CURRENT FILING DATE: 2002-02-15
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-12-19
PRIOR FILING DATE: 2001-12-19
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin version 3.1
                 129 ATCGGGTACCTGGTGCGCCTGCACGAGGGCCAGACCACGATGACCGCCCCCGGCGGCGTC 188
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APPLICANT: MOECKEL, Bettina
APPLICANT: BATHE, Brigitte
APPLICANT: HERNANN, Thomas
APPLICANT: PFEFFERLE, Walter
APPLICANT: BINDER, Michael
TITLE OF INVENTION: NUCLEOTIDE SERQUENCES WHICH CODE FOR THE rpob GENE
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                                                                                    1749 GAGATCCCAGTCGAGACCGATGACAT 1774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Corynebacterium glutamicum
                                                                 189 GAGGTCCCGGTCGAGGTCGACGAT 214
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                                                                                                                                                                                 Sequence 5, Application US/10075460 Patent No. US20020155557A1
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                                                                                                                                                                                                                                    APPLICANT: MOCKEL, BETTINA APPLICANT: BATHE, BRIGITTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : NAME/KEY: CDS
: LOCATION: (702)..(4196)
: OTHER INFORMATION:
US-10-075-460-5
                                                                                                                                                                                                                 GENERAL INFORMATION:
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US-09-887-052-1
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APPLICANT: MOECKEL, Bettina
APPLICANT: BATHE, Brightte
APPLICANT: BATHE, Brightte
APPLICANT: BATHE, Brightte
APPLICANT: BEFFERLE, Walter
APPLICANT: BEFFERLE, Walter
APPLICANT: BEFFERLE, Walter
APPLICANT: BATHER, BRIGHA, Michael
TITLE OF INVENTION: NUCLEOTIDE SEEQUENCES WHICH CODE FOR THE rpoB GENE
FILE REFERENCE: 204212USOX
CURRENT FAPLICATION WUMBER: US/09/887,052
PRIOR APPLICATION WUMBER: 2001-06-25
PRIOR FILING DATE: 2001-06-216
PRIOR FILING DATE: 2001-02-16
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68.4%; Pred. No. 2.7e-13;
ative 0; Mismatches 56;
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Pred. No. 2.7e-13;
0; Mismatches 56;
FILE REFERENCE: 204212USOX
CURRENT APPLICATION NUMBER: US/09/887,052
CURRENT FILING DATE: 2001-06-25
FRIOR APPLICATION NUMBER: DE10107229.5
FRIOR PILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 8
SCHTWARE: Patentin version 3.0
SEQ ID NO 1
LENGTH: 5099
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                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Corynebacterium glutamicum
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; Patent No. US20020119537A1
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Best Local Similarity 68.49
Matches 141; Conservative
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Best Local Similarity 68.4
Matches 141; Conservative
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; LOCATION: (702)...(4196)
US-09-887-052-1
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US-09-887-052-3
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APPLICANT: Xue, Y.
APPLICANT: Xue, Y.
APPLICANT: A.
TITLE OF INVENTION: DNA encoding methymycin and pikromycin
FILE REFERENCE: 600.438051
CURRENT FILING DATE: 2001.05-18
FRIOR PILICATION NUMBER: 09/105,537
FRIOR PILING DATE: 1998-06-26
NUMBER OF SEQ ID NOS: 43
SOFTWARE: FASTSEQ for Windows Version 3.0
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18.7%; Score 40; DB 10;
Best Local Similarity 53.1%; Pred. No. 0.15;
Matches 85; Conservative 0; Mismatches 75
  PRIOR APPLICATION NUMBER: JP2000-278571
PRIOR FILING DATE: 2000-09-13
PRIOR APPLICATION NUMBER: JP2001-65815
PRIOR FILING DATE: 2001-03-08
NUMBER OF SEQ ID NOS: 12
SEQ ID NO 7
LENGTH: 3343
                                                                                                                                                                                      ; ORGANISM: Microbacterium liquefaciens US-09-950-772-7
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Patent No. US20020110897A1
GENERAL INFORMATION:
APPLICANT: Sherman, D.H.
APPLICANT: Liu, H.
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Patent No. US20020102713A1

GENERAL INFORMATION:
APPLICANT: SUZUKI, Shunichi
APPLICANT: VOKOZEKI, Kence
TITLE OF INVENTION: 5-SUBSTITUTED HYDANTOIN RACEMASE, DNA CODING FOR THE RACEMASE,
TITLE OF INVENTION: 5-SUBSTITUTED HYDANTOIN OPTICALLY ACTIVE AMINO ACIDS
FILLE REFERENCE: 212131805
CURRENT APPLICATION NUMBER: US/09/950,772

CURRENT FILING DATE: 2001-09-13
                                                                                                                                                                                                                                                                      Sequence 5, Application US/09887052

Sequence 5, Application US/09887052

Patent No. US2020119537A1

GENERAL INFORMATION:
APPLICANT: WOECKEL, Bettina
APPLICANT: BATHE, Brigitte
APPLICANT: PFEFFRLE, Walter
APPLICANT: BINDER, Michael
TILE REFERENCE: 204212US0X
CURRENT APPLICATION NUMBER: US/09/887,052

CURRENT APPLICATION NUMBER: DEIO107229.5

PRIOR FILING DATE: 2001-06-25

PRIOR FILING DATE: 2001-02-16

NUMBER OF SEQ ID NOS: 8

SOFTWARE: Patentin version 3.0

SEQ ID NO 5

LENTH: SO99
1578 AAGGCTACGACCTGGCTCGCTTGGTCGTTACAAGATCAACCGCAAGCTCGGCCTTGGT 1637
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Pred. No. 2.7e-13;
0; Mismatches 56;
                                                                                                                                                                           TYPE: DNA ORGANISM: Corynebacterium glutamicum
                                                                                                                                                  189 GAGGTCCCGGTCGAGGTCGACGT 214
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Best Local Similarity 68.4%;
Matches 141; Conservative
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; LOCATION: (702)..(4196)
US-09-887-052-5
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US-09-887-052-5
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US-09-950-772-7
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GENERAL INFORMATION:
APPLICANT: Leach, Martin D.
APPLICANT: Methaban, Fuad,
APPLICANT: Methaban, Fuad,
APPLICANT: Methaban, Fuad,
APPLICANT: Methaban, Fuad,
APPLICANT: Law, Debbie
APPLICANT: Law, Debbie
APPLICANT: Topper, Jamela
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APPLICANT: Topper, Jamela
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APPLICANT: Law, Debbie
APPLICANT: Law, Debbie
APPLICANT: Law, Debbie
APPLICANT: Applicant Jamela
TITLE OF INVENTION: Thereby
FILE REPERENCE: 2402-013 (CURRENT APPLICATION NUMBER: US-209-05-30
RIOR APPLICATION NUMBER: US-200-05-30
NUMBER OF SEQ ID NOS: 2125
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  228 CCTGGCGACCTGAACGCGATCCACCGATCTGGATGCCCGACGGGGGGGTGC 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68 CGGTGCCAACCCGGCTCTGGTGACTGCCACGTCACCGAGGAAGACGTCGTCGCCAC 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  168 CAGCGCGCTCGTCGTCACGATCGCCGTGATCGTCGCCGCGGTCGGCATCGTGATGAC 227
                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                    2 CAAGGAGAAGCGCTACGACCTGGCCCGCTGGGCCGGTACAAGGTGAACAAGAAGCTGGG 61
                                                                                                                                                                                                                                                                                                                                  Length 2898;
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; LOCATION: (31)..(584)
; OTHER INFORMATION: wherein any n is one of a or t or g or c
US-09-867-550-669
                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                            Score 37.6; DB 10;
Pred. No. 0.51;
0; Mismatches 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match 17.1%; Score 36.6; DB 10; Best Local Similarity 53.1%; Pred. No. 0.78; Matches 78; Conservative 0; Mismatches 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2013 GGACTACGAGGTCTCCATCGACGCCGACTGCA 2044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              182 CGGCCTCGAGGTCCCGGTCGAGGTCGACGACA 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 669, Application US/09867550 Patent No. US20020082206A1
                                                                                                                                                                                                                                                                                                                               17.6%;
48.6%;
        PRIOR FILING DATE: 2000-08-09
                              NUMBER OF SEQ ID NOS: 49
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 48.6
Matches 103; Conservative
                                                                                                       LENGTH: 2898
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
                                                                                                                                                                                                                  ; NAME/KEY: CDS
; LOCATION: (1)..(2898)
US-09-737-149-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           us-09-867-550-669
                                                                                    SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
                                                                                                                                                                                              FEATURE
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                                                                                               GENERAL INFORMATION:

APPLICANT: SUZUKI, Shunichi
APPLICANT: SUZUKI, Shunichi
APPLICANT: ONISHI, No. US20020102713Alimasa
APPLICANT: VOKOZEKI, Kenzo
TITLE OF INVENTION: 5-SUBSTITUTED HYDANTOIN RACEMASE, DNA CODING FOR THE RACEMASE, AN
TITLE OF INVENTION: PROCESSES FOR PRODUCING OPTICALLY ACTIVE AMINO ACIDS
CURRENT APPLICATION NUMBER: US/09/950,772
CURRENT FILING DATE: 2001-09-13
PRIOR PRILING DATE: 2000-09-13
PRIOR FILING DATE: 2000-09-13
PRIOR FILING DATE: 2001-09-3
PRIOR FILING DATE: 2001-09-3
SOFTWARE: Patentin version 3.1
SSO ID NOS: 12
SSOFTWARE: Patentin version 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 GTTCGACGTCATTGTGAAGAACTGTCGGGGGTTTCCAGTCAGGGCATCATCGAAGCCGA 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Spaderna, Steven K
APPLICANT: Ouinn, Kerry E.
APPLICANT: Ouinn, Kerry E.
APPLICANT: Shimkers, Richard A.
APPLICANT: Shimkers, Richard A.
APPLICANT: Shimkers, Richard A.
APPLICANT: Spytek, Kimberly A.
TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same FILE REFERENCE: 15966-620 CIP
CURRENT FILING DATE: 1090-12-14
PRIOR APPLICATION NUMBER: 60/170,564
PRIOR APPLICATION NUMBER: 60/170,564
PRIOR APPLICATION NUMBER: 60/173,165
PRIOR FILING DATE: 1999-12-27
PRIOR FILING DATE: 1999-12-27
PRIOR FILING DATE: 1999-12-29
PRIOR FILING DATE: 1999-12-29
PRIOR APPLICATION NUMBER: 60/173,544
PRIOR FILING DATE: 1999-12-29
PRIOR PRILING DATE: 1999-12-29
PRIOR APPLICATION NUMBER: 60/174,404
PRIOR PLING DATE: 2000-01-04
PRIOR APPLICATION NUMBER: 60/174,962
PRIOR APPLICATION NUMBER: 60/174,962
PRIOR APPLICATION NUMBER: 60/174,962
PRIOR APPLICATION NUMBER: 60/223,929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     123 CGCCCGGACCATCGATGCCGCAGGCAGGTTCGTGATGCCCGGTGTGGTCGATGA 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         158 CCAGACCACGATGACCGCCCCGGCGGCCTCGAGGTCCCGGTCGAGGTCGACGA 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1380;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       85; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17.8%; Score 38; DB 10
51.1%; Pred. No. 0.38;
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Microbacterium liquefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3, Application US/09737149 Patent No. US20020077466A1
                                                     Sequence 3, Application US/0995077
Patent No. US20020102713A1
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Matches 89; Conservative
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: LOCATION: (1)..(1377)
: OTHER INFORMATION:
US-09-950-772-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 1380
RESULT 8
US-09-950-772-3
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Ohlsen, Kari L.
Zyskind, Judith W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   122 TGCTCGCCGAGGTCGAC 138
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                            89; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 54.0 Matches 74; Conservative
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-878-574-3598
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                                                                                                                                                                                             Sequence 76660, Application US/03864761
SEQUENCE SEQUENCE SEQUENCE OF SEQUENCE
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INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.9
INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1
INFORMATION: NT HIT: AB030176.1, EVALUE 4.00e-97
INFORMATION: EST_HUMAN HIT: BE089551.1, EVALUE 1.00e-94
INFORMATION: SWISSPROT HIT: 09Y2J8, EVALUE 1.00e-29
                                           288 GCAGAACACCGGCGAGGTCAACATCCT 314
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OTHER INFORMATION: EXPRESSED IN BT474,
OTHER INFORMATION: EXPRESSED IN BONE M
OTHER INFORMATION: EXPRESSED IN BRAIR.
         188 CGAGGTCCGGTCGAGGTCGACGACAT 214
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DB 10; Length 221;

Score 36.2;

16.98;

Query Match

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Sequence 3598, Application US/09878574

Patent No. US20020110548A1

GENERAL INFORMATION:

APPLICANT: Byrum, Joseph R.

APPLICANT: La Rosa, Thomas J.

APPLICANT: Thompson, Michael D.

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: UNDER: US 109/09/0878,574

CURRENT FILING DATE: 2001-12-21

PRIOR APPLICATION NUMBER: 09/333,535

PRIOR APPLICATION NUMBER: 09/333,535

PRIOR APPLICATION NUMBER: 1999-06-14

NUMBER OF SEQ ID NOS: 15775
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                                                                                                             62 ACCTGGAGGCCTCCTCACGTGGCGCGTCGCCGGACGAGGCGGTGA 121
                                        Gaps
                                                                               14 CTACGACCTGGCCCGCTGGCCCGGTACAAGGTGAACAAGAAGCTGGGGTCTTGGCGGTGC 73
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Live 0; Mismatches 63; Indels
                                   88; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: DNA
; OGGANISM: Glycine max
: OTHER INFORMATION: Clone ID: LIB3028-008-Q1-B1-C6
US-09-878-574-3598
  Pred. No. 0.91;
50.38; Pred. no.
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Patent No. US20020061569A1
GENERAL INFORMATION:
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PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SCOTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4131
LENGTH: 3057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Search completed: November 12, 2002, 16:57:53 Job time: 38.7711 secs
                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 55.0%
Matches 71; Conservative
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ORGANISM: Zea mays
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US-09-923-876-2475
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LENGTH: 242
                                                                                                                                                                          TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    129 ATCGGTACCTGGTGCGCCTGCACGAGGGCCAGACCACGATGACCGCCCCCGGCGGCGCCTC 188
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APPLICANT: Object, Kari L.
APPLICANT: Object, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Travick, John D.
APPLICANT: Travick, John D.
APPLICANT: Transdroto, Robert T.
APPLICANT: Yamanoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: 1000-114
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT APPLICATION NUMBER: 00/191,078
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-25
PRIOR FILING DATE: 2000-05-25
PRIOR FILING DATE: 2000-05-25
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 60/224,578
PRIOR APPLICATION NUMBER: 60/225,578
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR PELING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match 16.9%; Score 36.2; DB 10; Best Local Similarity 53.1%; Pred. No. 1.1; Matches 77; Conservative 0; Mismatches 68;
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-12-26
PRIOR FILING DATE: 2001-12-26
PRIOR FILING DATE: 2001-12-26
PRIOR FILING DATE: 2001-12-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FASKED FOR WINDOWS VERSION 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4131, Application US/09815242
Patent No. US20020061569A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : NAME/KEY: CDS
: LOCATION: (1)...(1914)
US-09-815-242-7960
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US-09-815-242-4131
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Sequence 2475, Application US/09923876

Patent No. US2002001395841

GENERAL INFORMATION:

APPLICANT: Lalgudi, Raghunath V.

APPLICANT: Lalgudi, Laura Y. (Ito)

APPLICANT: Sherman, Bradley K.

TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING
FILE REFERENCE: DL-0012-1 CON

CURRENT APPLICATION NUMBER: US/09/923,876

CURRENT APPLICATION NUMBER: 09/298,329

PRIOR FILING DATE: 1999-04-21

PRIOR APPLICATION NUMBER: 60/085,331

PRIOR PILING DATE: 1999-06-05

NUMBER OF SEQ ID NOS: 6332

SOFTWARE: PERL PROFram
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                                                                                                                Gaps
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                                                                      Length 3057;
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; OTHER INFORMATION: Incyte ID No. US20020013958A1 700160665H1
US-09-923-876-2475
                                                                                                            Indels
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Best Local Similarity 57.0%; Pred. No. 1.3;
Matches 65; Conservative 0; Mismatches 49;
                                                                  16.9%; Score 36.2; DB 10;
55.0%; Pred. No. 1.1;
tive 0; Mismatches 58;
ORGANISM: Pseudomonas aeruginosa US-09-815-242-4131
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NAME: Mueting, Ann M.
REGISTRATION NUMBER: 33,977
REFERENCE/DOCKET NUMBER: 150.105US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-339-0331
TELEFAX: 612-339-3061
                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                   ; Sequence 1, Application US/08250030
; Patent No. 5643723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 612-339-3061
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 58.3%;
Best Local Similarity 77.6%;
Matches 166; Conservative
                                                                                                                                                                                                                                                                                                              STREET: 3500 IDS Center CITY: Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                       Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 970 base pairs
TYPE: nucleic acid
68750
68750
68750
2089
2634
                                                       2634
44377
44377
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23673
4104
4104
4104
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TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
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Sequence 10, Appli
Sequence 10, Appli
Sequence 11, Appli
Sequence 11, Appli
Sequence 10, Appli
Sequence 1, Appli
Sequence 8, Appli
Sequence 3, Appli
Sequence 67, Appli
Sequence 11, Appli
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2286.857 Million cell updates/sec
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                                                                                                               1 tcaaggagaaagcgctacgac..........ccggtcgaggtcgacgacat 214
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Sequence 57,
Sequence 57,
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Sequence 2
Sequence 2
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PcTUS_COMB.seq:*
  GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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2 US-08-107-510
2 US-08-461-775-10
2 US-08-461-775-11
3 US-09-031-606-11
4 US-09-192-104-1
4 US-09-192-104-1
4 US-09-292-768-3
4 US-09-292-768-3
4 US-09-292-768-5
4 US-09-292-768-6
5 US-09-105-537-1
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US-09-479-409-14
US-09-479-453-14
US-09-479-453-29
US-09-479-453-29
US-09-568-102-1
US-09-568-102-1
US-09-568-102-1
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US-09-082-614A-57
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                                                                                                                                                               441362 seqs, 153338381 residues
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                                      OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                        Maximum Match 100%
Listing first 45 summaries
                                                                                                                                  IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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length: 2000000000
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DB seq
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GENERAL INFORMATION:
APPLICANT: Persing, David H.
APPLICANT: Persing, David H.
TITLE OF INVENTION: Detection of a Genetic Locus Encoding
TITLE OF INVENTION: Resistance to Rifampin in Mycobacterial Cultures and in
TITLE OF INVENTION: Clinical Specimens
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schwegman, Lundberg & Woessner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ä
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Sequence 2
Sequence 5
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Pred. No. 1.8e-21;
0; Mismatches 42; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/250,030
FILING DATE: 25-MAY-1994
CLASSIFCATION: 435
ATTORNEY/AGENT INFORMATION:
US-09-568-486-1

US-09-568-472-1

US-09-568-472-1

US-09-291-922-25

US-08-196-218-31

US-08-196-218-31

US-08-804-227C-7

US-08-804-198-1

US-09-029-603-4

US-09-029-603-4

US-09-928-213B-7

US-09-928-213B-7

US-09-928-213B-7

US-09-928-213B-7

US-09-93-93-94

US-08-453-595A-94

US-08-266-161A-94

US-08-266-161A-94
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RESULT 4
US-09-082-614A-57
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121 TCGCCACCATCGGGTACCTGGTGCGCCTGCACGAGGGCCAGACCACGATGACCGCCCCGG 180
                                                                                  61 GTCTTGGCGGTGCCAACCCGGCTCTGGTGACTGCCACGACGCTCACCGAGGAAGACGTCG 120
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                                                                                                                                                                                                                                             Sequence 1, Application PC/TUS9506790
GENERAL INFORMATION:
APPLICANT: And POFTMATION for Medical Education and Research
APPLICANT: and HOFFMANN-LA Roche Inc.
TTTLE OF INVENTION: Detection of a Genetic Locus Encoding
TITLE OF INVENTION: Resistance to Rifampin
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: FLORM:
COMPUTER: TEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06790
FILING DATE: 26-MAY-1995
ATTORNEY APPLICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              42;
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                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Schwegman, Lundberg & Woessner
STREET: 3500 IDS Center
CITY: Minneapolis
                                                                                                                                                   200 GCGGCGTCGAGGTGCCGGTGGAACCGACGACAT 233
                                                                                                                                 181 GCGCCTCGAGGTCCCGGTCGAGGTCGACGACAT 214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TAME: Reasch, Kevin W.
REGISTRATION NUMBER: 35,651
REFERENCE/DOCKET NUMBER: 15
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-339-0331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 612-339-0331
TELEFAX: 612-339-3061
INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 970 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
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61 GTCTTGGCGGTGCCAACCCGGCTCTGGTGACTGCCACCACGCTCACCGAGGAAGACGTCG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 TCAAGGAGAAGCGCTACGACCTGGCCCGCTGGGCCGGTACAAGGTGAACAAGAAGCTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                             APPLICANT: Bodmer, Thomas
TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
TITLE OF INVENTION: in Mycobacterium Tuberculosis
NUMBER OF SEQUENCES: 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 3447;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                55; Indels
                                                                                                                                                                                                                                                                                ADDRESSEE: Finnegan, Henderson, Farabow, Garrett
ADDRESSEE: Dunner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Parentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/313,185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 104; DB 2;
Pred. No. 1.8e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 02356.0068-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 GCGCCTCGAGGTCCCGGTCGAGGTCGACGT 214
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                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READBBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
Sequence 57, Application US/08313185
Patent No. 5851763
GENERAL INFORMATION:
                                                                                                       APPLICANT: Zhang, Ling
APPLICANT: Honore, Nadine
APPLICANT: Telenti, Amalio
Amplicant: Telenti, Amalio
                                                                                                                                                                                                                                                                                                                    STREET: 1300 I Street, N.W. CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
INFURMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 3447 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 71.5%;
Matches 153; Conservative
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N: 435
                                                                                Cole, Stewart
Young, Douglas
Zhang, Ying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
                                                         APPLICANT: Heym, Beate
                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                    20005-3315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 12 CLASSIFICATION:
                                                                            APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-313-185-57
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|Db 2843522 GTCG 2843519
                                    GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                     TYPE: DNA
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                               GENERAL INFORMATION:
APPLICANT: Heym, Beate
APPLICANT: Cole, Stewart
APPLICANT: Young, Douglas
APPLICANT: Zhang, Ying
APPLICANT: Telenti, Amalio
APPLICANT: Bodomer, Thomas
TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
TITLE OF INVENTION: in Mycobacterium Tuberculosis
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 3447;
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                                                                                                                                                                                                                                                                                     ADDRESSEE: Finnegan, Henderson, Farabow, Garrett
ADDRESSEE: Dunner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
APPLICATION NUMBER:
FLING DATE: 12-0CT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 02356.0068-00000
TELECOMMUNICATION INFORMATION:
TELEFRAX: (202) 408-4000
TELEFRAX: (202) 408-4000
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 GCGCCTCGAGGTCCCGGTCGAGGTCGACGT 214
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/082,614A
Sequence 57, Application US/09082614A Patent No. 6124098
                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 3447 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                        Dunner
                                                                                                                                                                                                                                                                                                                                                                                         USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84 CTGGTGACTGCCACCACGCTCACCGAGGAAGACGTCGTCGCCACCATCGGGTACCTGGTG 143
                  APPLICANT: WHITE, Owen R.
APPLICANT: WHITE, Owen R.
APPLICANT: PRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-22007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           144 CGCCTGCACGAGGCCAGACCACGATGACCGCCCCCGGCGGCCTCGAGGTCCCGGTCGAG 203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 43.2; DB 4; Length 4411529;
Pred. No. 0.089;
0; Mismatches 88; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: MAZOIER, Philippe
APPLICANT: MAZOIER, Philippe
APPLICANT: GUGLIEMI, Gerard
TITLE OF INVENTION: REGULATORY NUCLEOTIDE SEQUENCE OF THE
TITLE OF INVENTION: INITIATION OF TRANSCRIPTION
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSE: Burns, Doane, Swecker & Mathis
STREET: George Mason Bidg., Washington & Prince Sts.
CITY: Alexandria
STREET: United States
ZIP: 222313-1404
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/050,313
FILING DATE: 10-M2-1993
APPLICATION NUMBER: FR 901186
FILING DATE: 10-SEP-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 5858773
GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20.2%;
52.2%;
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MEDIUM TYPE: Floppy disk
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Best Local Similarity 52.2%
Matches 96; Conservative
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Sequence 10, Application US/09031606
Patent No. 6133404
GENERAL THORNMATION:
APPLICANT: MAZODIER, Philippe
APPLICANT: GUGLIEMI, Gerard
TITLE OF INVENTION: REGULATORY NUCLECTIDE SEQUENCE OF THE TITLE OF INVENTION: INITIATION OF TRANSCRIPTION
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: George Mason Bldg., Washington & Prince Sts.
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
IP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                              Ouery Match
19.3%; Score 41.2; DB 2;
Best Local Similarity 49.5%; Pred. No. 0.12;
Matches 106; Conservative 0; Mismatches 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/031,606
FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 GCGCCTCGAGGTCCCGGTCGAGGTCGACGACAT 214
NAME: Crane-Feury, Sharon E
REGISTRATION NUMBER: 36,113
REFERENCE/DOCKET NUMBER: 010830-035
TELECHMUNICATION INFORMATION:
TELEPANE: (703) 836-620
TELEPANE: (703) 836-2021
INFORMATION FOR SEO ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 1620 base pairs
TYPE: nuclet caid
TYPE: nuclet caid
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APPLICATION NUMBER: US 08/050,313
FILING DATE: 10-MAy-1993
APPLICATION NUMBER: FR 901186
FILING DATE: 10-SEP-1990
ATTORNEY/AGENT INFORMATION:
NAME: Crane-Feury, Sharon E
REGISTRATION NUMBER: 36,113
                                                                                                                                                                                                                                    MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                      NAME/KEY: CDS
LOCATION: 1..1620
                                                                                                                                                                                                                   linear
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US-08-461-775-10
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61 GTCTTGGCGGTGCCAACCCGGCTCTGGTGACTGCCACCACGCTCACCGAGGAAGACGTCG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 41.2; DB 3; Length 1620;
Pred. No. 0.12;
0; Mismatches 108; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSE: Burns, Doane, Swecker & Mathis
STREET: George Mason Bldg., Washington & Prince Sts.
CITY: Alexandria
CITY: Alexandria
COUNTR: Virginia
COUNTR: Virginia
COUNTR: READABLE FORM:
MEDIUM TYPE: FORM:
MEDIUM TYPE: FORM:
COMPUTER: PROPPY disk
COMPUTER: PROPPY disk
COMPUTER: PROPPY COMPATIBLE
COMPUTER: PROPPY CO
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 GCGGCCTCGAGGTCCCGGTCGAGGACGACAT 214
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CLASSIFTCATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/050,313
FILING DATE: 10-MAY-1993
APPLICATION NUMBER: FR 901186
FILING DATE: 10-SEP-199
ATTORNEY/AGENT INFORMATION:
NAME: Crane-Feury, Sharon E
REGISTRATION NUMBER: 36,113
REFERENCE/DOCKET NUMBER: 36,113
REFERENCE/DOCKET NUMBER: 010830-035
TELECOMMUNICATION INFORMATION:
REFERENCE/DOCKET NUMBER: 010830-035 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 11, Application US/08461775
Patent No. 5858773
GENERAL INFORMATION:
APPLICANT: MAZODIER, Philippe
APPLICANT: GUGLIEMI, Gerard
                                                                                  TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 1620 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
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Best Local Similarity 49.5%;
Matches 106; Conservative
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US-08-461-775-11
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nucleic acid
                                                                                                                                     Local Similarity
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                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                          61 GTCTTGGCGGTGCCAACCCGGCTCTGGTGACTGCCACCACGCTCACCGAGGAAGACGTCG 120
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                                                                                                                                                                                                                                                                     1 TCAAGGAGAAGCGCTACGACCTGGCCCGCTGGGCCGGTACAAGGTGAACAAGAAGCTGG 60
                                                                                                                                                                                                      Length 2668;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: MAZODIER, Philippe
APPLICANT: GUGLIEMI, Gerard
TITLE OF INVENTION: REGULATORY NUCLEOTIDE SEQUENCE OF THE
TITLE OF INVENTION: INITIATION OF TRANSCRIPTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: George Mason Bldg., Washington & Prince Sts.
CITY: Alexandria
                                                                                                                                                                                                   Score 41.2; DB 2;
Pred. No. 0.13;
0; Mismatches 108;
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/031,606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 GCGCCTCGAGGTCCCGGTCGAGGTCGACGACAT 214
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PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/050,313
FILING DATE: 10-MAY-1993
APPLICATION NUMBER: FR 9011186
FILING DATE: 10-SEP-1990
ATTORNEY, AGENT INFORMATION:
NAME: Crane-Feury, Sharon E
REGISTRATION NUMBER: 36,113
REFERENCE/DOCKET NUMBER: 30,113
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 11, Application US/09031606; Patent No. 6153404; GENERAL INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 268 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                          : TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-461-775-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                                 Query Match
19.3%;
Best Local Similarity 49.5%;
Matches 106; Conservative
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LENGTH: 2668 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                      61 GTCTTGGCGGTGCCAACCCGGCTCTGGTGACTGCCACGCTCACCGAGGAAGACGTCG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                             121 TCGCCACCATCGGGTACCTGGTGCGCCTGCACGAGGCCAGACCACGATGACCGCCCCGG 180
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                                                                                                                                          Length 2668;
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19.2%; Score 41; DB 4; Length 1926;
Best Local Similarity 51.4%; Pred. No. 0.14;
Matches 95; Conservative 0; Mismatches 90; Indels
                                                                                                                                  19.3%; Score 41.2; DB 3; Length 20
49.5%; Pred. No. 0.13;
Live 0; Mismatches 108; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INC. 202003
GENERAL INC. 202003
GENERAL INC. MUSCARATION:
APPLICANT: Alexander Blinkovsky
APPLICANT: Elizabeth Golightly
APPLICANT: Elizabeth Golightly
APPLICANT: Thomas Mathiasen
APPLICANT: Thomas Mathiasen
APPLICANT: Lene V. Kofod
APPLICANT: Chigusa Shizuoka
TITLE OF INVENTION: Houli
TITLE OF INVENTION: Houly sates
FILE REFERENCE: 5253.500-US
CURRENT APPLICATION HUMBER: US/09/079,955A
CURRENT APPLICATION NUMBER: US/09/079,955A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2296 GCGAGTACGGCGACCTGGTCAAGGCCGGCGTCAT 2329
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US-03-079-955-10
Sequence 10, Application US/09079955A
Fatent No. 646509
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STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                             Best Local Similarity
Matches 106; Conservative
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1861 AAGCCCTATTCCTCGCTTACCGTAACGAGACTATTACACCGAAGGCGCGCTGGTGTG 1920
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 8, Application US/08881784
Patent No. 6083331
GENERAL INFORMATION:
APPLICANT: Croteau, Rodney B.
APPLICANT: Lupien, Shari L.
APPLICANT: Karp, Frank
TITLE OF INVENTION: THE PRODUCTION OF LIMONENE HYDROXYLASES
NUMBER OF SEQUENCES; S8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chilstensen, O'Connor, Johnson and Kindness
                                                                                                                                                                                                                                                                                                                                                                       Query Match
19.2%; Score 41; DB 4; Length 3000;
Best Local Similarity 51.4%; Pred. No. 0.14;
Matches 95; Conservative 0; Mismatches 90; Indels
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APPLICATION NUMBER: US/08/881,784
               EARLIER APPLICATION NUMEER: 1465/97
EARLIER FILING DATE: 1997-12-16
EARLIER APPLICATION NUMBER: 198 00670
EARLIER FILING DATE: 1998-05-15
EARLIER FILING DATE: 1998-05-15
NUMBER: O9/192,104
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 3000
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STREET: 1420 Fifth Avenue, Suite 2800
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NAME: Shelton, Dennis K.
REGISTATION NUMBER: 26,997
REFERENCE/DOCKET NUMBER: WSUR19777
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 224-0718
TELEFAX: (206) 224-0718
TELEFAX: (206) 224-079
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLIUM TYPE: Floppy disk COMPUTER: IBM PC COMpatible OPERATING SYSTEM: PC-DOS/MS-
EARLIER FILING DATE: 1997-12-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                        ; TYPE: DNA
; ORGANISM: Sphingomonas
US-09-543-446-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27 CGCGTGGGCCGGTACAAGGTGAACAAGAAGCTGGGTCTTGGCGGTGCCAACCCGGCTCTG 86
                                                                                      GENERAL INFORMATION:

APPLICANT: Alexander Blinkovsky
APPLICANT: Tony Byun
APPLICANT: Tony Byun
APPLICANT: Tony Byun
APPLICANT: Alan V. Klotz
APPLICANT: Alan Sloma
APPLICANT: Maria Tang
APPLICANT: Lene Venke Kofod
TITLE OF INVENTION: Polypeptides Having Aminopeptidase
TITLE OF INVENTION: ACTIVITY And Nucleic Acids Encoding Same
TITLE OF INVENTION: ACTIVITY And Nucleic Acids Encoding
TITLE OF INVENTION: ACTIVITY And Nucleic Acids Encoding
CURRENT FILIE OF INVENTION: ACTIVITY And Nucleic Acids Encoding
CURRENT FILIE DATE: 1999-11-16
EARLIER FILING DATE: 1999-11-16
EARLIER FILING DATE: 1999-12-16
EARLIER FILING DATE: 1998-05-15
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FASSESQ for Windows Version 4.0
FEACULE.
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Petent No. 6303360

GENERAL INFORMATION:
APPLICANT: Tony Byun
APPLICANT: Alan V. Klotz
APPLICANT: Alan V. Klotz
APPLICANT: Alan V. Klotz
APPLICANT: Maria Tang
APPLICANT: Mikio Fujii
APPLICANT: Alan V. Klotz
APPLICANT: Cliqua Marumoto
APPLICANT: Alan V. Waria Marinopeptidase
TITLE OF INVENTION: Polypeptides Having Aminopeptidase
TITLE OF INVENTION: Activity And Nucleic Acids Encoding Same
TITLE OF INVENTION: Activity And Nucleic Acids Encoding
CURRENT APPLICATION NUMBER: US/09/543,446

CURRENT FILING DATE: 2000-04-05

EARLIER APPLICATION NUMBER: 60/069719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 51.4%; Pred. No. 0.14;
Matches 95; Conservative 0; Mismatches 90; Indels
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                                                    Sequence 1, Application US/09192104B
Patent No. 6184020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: DNA
; ORGANISM: Sphingomonas
US-09-192-104-1
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                            US-09-192-104-1
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TYPE: DNA
ORGANISM: Artificial Sequence
                               203 GGTCGACGACAT 214
                                                                450 CGTCCGCTCCTT 461
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; LOCATION: (19)..(1518)
US-09-292-768-67
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US-09-292-768-67
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Best Local (
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Fetent No. 6194185
GENERAL INFORMATION:
APPLICANT: Croteau, Rodney B
APPLICANT: Croteau, Rari L
APPLICANT: Exp. Frank
TITLE OF INVENTION: ECOMBINANT MATERIALS AND METHODS FOR THE PRODUCTION OF
TITLE OF INVENTION: LIMOMENE HYDROXYLASES
FILE REFERENCE: wsur13463
CURRENT APPLICATION NUMBER: 02/09/292,768
CURRENT FILING DATE: 1999-04-14
EARLIER FILING DATE: 1999-06-24
NUMBER OF SEQ ID NOS: 70
SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                       143 GCGCCTGCACGAGGCCAAGACCACGATGACCGCCCCCGGCGGCGTTCGAGGTCCCGGTCGA 202
                                                                                                                                                                                                                                                                                                                                                                                                                            190 CAGCGTGCACTGGCCCAGATGCGGAAGATCTGCGTCTCCGAGCGTCGTCAGCGCCCCGCAA 449
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                                                                                                                                                                                          Query Match
18.7%; Score 40; DB 3; Length 1665;
Best Local Similarity 50.5%; Pred. No. 0.23;
Matches 97; Conservative 0; Mismatches 95; Indels
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Pred. No. 0.23;
0; Mismatches
                TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
ORIGINAL SOURCE:
ORGANISM: Mentha x piperita
IMMEDIATE SOURCE:
CLONE: pPM17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18.7%;
50.5%;
LENGTH: 1665 base pairs
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ORGANISM: Mentha piperita
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           203 GGTCGACGACAT 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         450 CGTCCGCTCCTT 461
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; LOCATION: (19)..(1518)
US-09-292-768-3
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Best Local Similarity
Matches 97; Conserva
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REBUILT IN RESULT 18 (1971)

10 S-09-232-768-67

Sequence 57, Application US/09292768

Patent No. 61918

APPLICANT: Cupter, Shari L

APPLICANT: Check L

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Mycobacterium chel Mycobacterium absc Mycobacterium fort Mycobacterium mailm Mycobacterium gviu Mycobacterium gord Mycobacterium gord Mycobacterium ilav Mycobacterium ilav
SUMMARIES	AASO5207 AASO5219 AASO5214 AASO5214 AASO5218 AASO5201 AASO5201 AASO5211
DB	222222222
% Query re Match Length DB I	211 208 208 208 208 208 208 208
% Query Match	100.0 87.3 71.8 68.6 66.5 65.0 65.0 64.3
Score	214 186.8 153.6 146.8 140.4 140.4 139.2
Result No.	10m400C00

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	13	124.8		27.0		AATU96/6	
	202	124.8				AAHDI9/6	
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E S	Мусо	Mycobacterium chelonae	um che	elonae r	rpoB g	gene fragment.	
× 3	NON-	Non-tuberoulous		400000	1	£	
K	PCR-	PCR-restriction		mycobacteria; rpoB fragment length pol	егта; lend	gene tragment; NTM; vmorphism analysis.	HIV; PRA; RFLP;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         various Mycobacterial species. These rpoB gene fragments can be used in the diagnosis and identification of Mycobacterium species using a novel PCR-restriction fragment length Polymorphism analysis (PRA) method. The method comprises obtaining a restriction fragment length polymorphism analysis (PRA) amplifying and digesting the DNA fragment from the microorganism to be identified and comparing the RELP patterns from the Microorganism to be identified and comparing the RELP patterns from the known rpoB gene fragments with the unidentified fragment. The rpoB gene fragments are useful to identify a wide range of Mycobacterium species, e.g. for diagnosis or to obtain epidemiological and pathogenesis information for selection of appropriate therapies, including M. tuberculosis, M. leprae and on tuberculosis mycobacteria (NTM) encountered in subjects infected with human immunodeficiency virus (HIV). Analysis of the rpoB gene fragments is rapid, precise, simple and cost effective (only 1 PCR required), and can differentiate between many species in a single experiment, including those difficult to distinguish by usual biochemical ests. Also described are oligonicleotide probes (AASO5227-AASO5242) for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Non-tuberculous mycobacteria; rpoB gene fragment; NTM; HIV; PRA; RFLP; PCR-restriction fragment length polymorphism analysis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                   GTCTTGGCGGTGCCAACCCGGCTCTGGTGACTGCCACCACGCTCACCGAGGAAGACGTCG 120
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                                                                                                                                                                                                                                                                                                                                  DB 22; Length 214;
                                     The present sequence for Mycobacterium chelonae rpoB gene fragment is 1 of 24 rpoB gene fragments (AASO5201-AASO5224)
                                                                                                                                                                                                                                                                                                                               100.0%; Score 214; DB 22; Length 100.0%; Pred. No. 9e-39; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Park HJ;
                                                                                                                                                                                                                                                                                                    Sequence 214 BP; 41 A; 72 C; 72 G; 29 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kim Y,
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            Claim 1; Page 42; 50pp; English
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Matches 214; Conservative
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The present sequence for Mycobacterium abscessus rpoB gene fragment is 1 of 24 rpoB gene fragments (AAS05201-AAS05224) from various Mycobacterial species. These rpoB gene fragments can be used in the diagnosis and identification of Mycobacterium species using a novel PCR-restriction fragment length polymorphism analysis (RRA) method comprises obtaining a restriction fragment length polymorphism (RFLP) pattern of the 24 rpoB gene fragments; isolating, amplifying and digesting the DNA fragmen from the Microorganism to be identified and comparing the RFLP patterns from the Microorganism to be identified and comparing the RFLP patterns from the known rpoB gene fragments with the unidentified fragment. The rpoB gene fragments with the unidentified and pathogenesis information for are useful to identify a wide range of Mycobacterium species, e.g. for diagnosis or to obtain epidemiological and pathogenesis information for selection of appropriate therapies, including M. tuberculosis, M. laprae and non-tuberculous mycobacteria (NTM) encountered in subjects infected with human immunodeficiency virus (HIV). Analysis of the rpoB gene fragments is rapid, precises, simple and cost effective (only 1 pCR required), and can differentiate between many species in a single experiment, including those difficult to distinguish by usual blochemical defertion sensition workharerial sensited.
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ds.
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                                                       New DNA fragments from the rpoB gene of mycobacteria, useful f
diagnosis and identification of many mycobacterial species by
restriction fragment length polymorphism
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"red, No. 9.6e-33;
"hes 17; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 214 BP; 45 A; 69 C; 72 G; 28 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     87.3%; Score ... 9.6e-.92.1%; Pred. No. 9.6e-.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       detecting specific Mycobacterial species.
                                                                                                                                                                                      Claim 1; Page 46; 50pp; English.
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Matches 197; Conservative
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WPI; 2001-300520/31.
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us-09-697-123b-7.rng

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The present sequence for Mycobacterium fortuitum rpoB gene fragment is 1 of 24 rpoB gene fragments (AAS05201-AAS05224) from various Mycobacterial species. These rpoB gene fragments can be used in the diagnosis and identification of Mycobacterium species using a novel PCR-restriction fragment length polymorphism analysis (PRA) comprises obtaining a restriction fragment length polymorphism (RFLP) pattern of the 24 rpoB gene fragments (PRA) capping and digesting the DNA fragment from the microorganism to be identified and comparing the RFLP patterns from the known rpoB gene fragments with the unidentified fragment. The rpoB gene fragments from the comparing the RFLP patterns from the known rpoB gene are useful to identify a wide range of Mycobacterium species. e.g. for diagnosis or to obtain epidemiological and pathogenesis information for selection of appropriate theraphes, including M. tuberculosis, M. leprae and non-tuberculous mycobacteria (HTW) encountered in subjects infected with human immunodeficiency virus (HTW) analysis of the rpoB gene fragments is rapid, precise, simple and cost effective (only 1 pcR required), and can differentiate between many species in a single experiment, including those difficult to distinguish by usual blochemical according a process. Also described are oligonucleotide probes (AAS05227-AAS05242) for a fragment in a process in a single accounter of a process in a single and can be also a process in a single and can be also an additional and can be processed and a processed and 
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ds.
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                                                                                                                                                                                                                                                                                 New DNA fragments from the rpoB gene of mycobacteria, useful for diagnosis and identification of many mycobacterial species by restriction fragment length polymorphism
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                                                                                                                                                     Kim Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 208 BP; 43 A; 69 C; 69 G; 27 T; 0 other;
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                                                                                                                                                  Cho S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               detecting specific Mycobacterial species.
                                                                                                                                          Park YK, Bai G, Kim S,
                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 46; 50pp; English.
                                                                       (ERUM-) ERUME BIOTECH CO LTD.
       99KR-0046795
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                                                                                                                                                                                                                 WPI; 2001-300520/31.
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27-OCT-1999;
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                                                                                                                                              Lee H,
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fragment is 1 of 24 rpoB gene fragments (AASO5201-AASO5224) from
fragment is 1 of 24 rpoB gene fragments can be used
various Mycobacterial species. These rpoB gene fragments can be used
in the diagnosis and identification of Mycobacterium species using a
novel PCR-restriction fragment length polymorphism analysis (PRA)
method. The method comprises obtaining a restriction fragment length
cc polymorphism (RFLP) pattern of the 24 rpoB gene fragments: isolating,
amplifying and digesting the DNA fragment fragments: isolating,
cc polymorphism (RFLP) pattern of the 24 rpoB gene fragments isolating,
cc pelmittied and comparing the RFLP patterns from the microorganism to
be identified and comparing the RFLP patterns from the shown rpoB gene
cc ragments with the unidentified fragment. The rpoB gene fragments
cc are useful to identify a wide range of Mycobacterium species, e.g. for
diagnosis or to obtain epidemiological and pathogenesis information for
cc selection of appropriate theraples, including M. tuberculosis, M. leprae
and non-tuberculous mycobacteria (NTW) encountered in subjects infected
with human immunodeficiency virus (HTW). Analysis of the rpoB gene
cc fragments is rapid precise, simple and cost effective (only 1 PCR
required), and can differentiate between many species in a single
cxperiment, including those difficiult to distinguish by usual blochemical
cests. Also described are oligonucleotide probes (AASO5227-AASO5242) for
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                                                                                                                                                                                                                                      Park HJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence for Mycobacterium malmoense rpoB
                                                                                                                                                                                                                                    Kim Y,
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                                                                                                                                                                                                                                  Cho
                                                                                                                                                                                                                                  Kim S,
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                                                                                                                                                                                                                             Park YK, Bai G,
                                                                                                                                                                                                                                                                  WPI; 2001-300520/31.
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us-09-697-123b-7.rng

AAS05218 standard; DNA; 211 BP

(first entry)

07-SEP-2001

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The present sequence for Mycobacterium avium rpoB gene fragment is 1 of 24 rpoB gene fragments (AAS05201-AAS05224) from various Mycobacterial species. These rpoB gene fragments can be used in the diagnosis and identification of Mycobacterium species using a novel PCR-restriction fragment length polymorphism analysis (PRA) comprises obtaining a restriction fragment length polymorphism (RFLP) pattern of the 24 rpoB gene fragments (RFLP) pattern of the 24 rpoB gene fragments; isolating, amplifying and digesting the DNA fragment from the microorganism to be identified and comparing the RFLP patterns from the known rpoB gene fragments with the unidentified fragment. The rpoB gene fragments of angential to identified fragment. The rpoB gene fragments are useful to identify a wide range of Mycobacterium species, e.g. for diagnosis or to obtain epidemiological and pathogenesis information for selection of appropriate therapies, including M. tuberculosis, M. leprae and non-tuberculous mycobacteria (MrW) encountered in subjects infected with human immunodeficiency virus (HIV). Analysis of the rpoB gene fragments is rapid, precise, simple and cost effective (only 1 pcR required), and can differentiate between many species in a single experiment, including those difficult to distinguish by usual blochemical defenction of described are oligonucleotide probes (AAS05227-AAS05242) for
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                                       Non-tuberculous mycobacteria; rpoB gene fragment; NTM; HIV; PRA; RFLP; PCR-restriction fragment length polymorphism analysis; ds.
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nes 31;
                                                                                                                                                                                                                                                                                                                                         Kim Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 208 BP; 44 A; 69 C; 69 G; 26 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                           Cho S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              detecting specific Mycobacteríal species.
  Mycobacterium avium rpoB gene fragment.
                                                                                                                                                                                                                                                                                                                                       Park YK, Bai G, Kim S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 44; 50pp; English.
                                                                                                                                                                                                                                                                                                  (ERUM-) ERUME BIOTECH CO LTD.
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                                                                                                   Mycobacterium avium.
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Best Local S
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RESULT 6 AAS05218

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The present sequence for Mycobacterium flavescens rpoB gene fragment is 1 of 24 rpoB gene fragments (AAS05201-AAS05224) from various Mycobacterial species. These rpoB gene fragments can be used in the diagnosis and identification of Mycobacterium species using a novel pCR-restriction fragment length polymorphism analysis (PRA) polymorphism (RFLE) pattern of the 24 rpoB gene fragment isolating, polymorphism (RFLE) pattern of the 24 rpoB gene fragment isolating, amplifying and digesting the DNA fragment from the microorganism to be identified and comparing the RFLP patterns from the known rpoB gene fragments with the unidentified fragment. The rpoB gene fragments are useful to identify a wide range of Mycobacterium species, e.g. for fragments with the unidentified and pathogenesis information for selection of appropriate therapies, including M. tuberculosis, M. leprae and non-tuberculous mycobacteria (NTM) encountered in subjects infected inth human immunodeficiency virus (HTV). Analysis of the rpoB gene fragments is rapid, precise, simple and cost effective (only 1 PCR required), and can differentiate between many species in a single experiment, including those difficult to distinguish by usual blochemical effecting specific Mycobacterial species.
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                                                                                                                                                                                                                                                                                   HIV; PRA; RFLP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New DNA fragments from the rpoB gene of mycobacteria, useful f
diagnosis and identification of many mycobacterial species by
restriction fragment length polymorphism
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                                                                                                                                                                                                  Mycobacterium flavescens rpoB gene fragment.
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                                                                                                                                                                                                                                                                                                                                                                           Mycobacterium flavescens.
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NO SECOND CONTRACTOR OF SECOND
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178 GTGGAGTCGAGGTCCCGTCGAGGTCGACGACAT 211
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AAS05201 standard; DNA; 208 AAS05201 RESULT

AAS05201;

(first entry) 07-SEP-2001

Mycobacterium gordonae type I rpoB gene fragment.

Non-tuberculous mycobacteria; rpoB gene fragment; NTM; HIV; PRA; RFLP; PCR-restriction fragment length polymorphism analysis; ds.

Mycobacterium gordonae type I.

WO200131061-A1.

03-MAY-2001

27-OCT-2000; 2000WO-KR01223.

27-OCT-1999;

99KR-0046795.

(ERUM-) ERUME BIOTECH CO LID.

Park HJ; Kim Y, ŝ Cho Park YK, Bai G, Kim S, Lee H,

WPI; 2001-300520/31.

New DNA fragments from the rpoB gene of mycobacteria, useful for diagnosis and identification of many mycobacterial species by restriction fragment length polymorphism

Claim 1; Page 40; 50pp; English.

The present sequence for Mycobacterium gordonae type I rpoB gene fragment is 1 of 24 rpoB gene fragments (AAS02201-AAS0224) from various Mycobacterial species. These rpoB gene fragments can be used in the diagnosis and identification of Mycobacterium species using a novel PCR-restriction fragment length polymorphism analysis (PRA) comprises obtaining a restriction fragment length polymorphism (RFuP) pattern of the 24 rpoB gene fragments; isolating, amplifying and digesting the DNA fragment from the microorganism to be identified and comparing the RFuP patterns from the known rpoB gene fragments with the unidentified fragment. The rpoB gene fragments of fagnesis or to obtain epidemiological and pathogenesis information for a selection of appropriate therapies, including M. tuberculosis, M. leprae and non-tuberculous mycobacteria (MTM) encountered in subjects infected with human immunodeficiency virus (HTW) analysis of the rpoB gene fragments is rapid, precise, simple and cost effective (only 1 PCR required), and can differentiate between many species in a single experiment, including those difficult to distinguish by usual biochemical certerium sensitive manific moniting manification. detecting specific Mycobacterial species. 

Sequence 208 BP; 46 A; 71 C; 65 G; 26 T; 0 other;

ä Gaps ; 9 DB 22; Length 208; Indels Ouery Match 65.0%; Score 139.2; DB 22; Best Local Similarity 81.8%; Pred. No. 3.4e-22; Matches 175; Conservative 0; Mismatches 33;

9 9 1 TCAAGGAGAAGCGCTACGACCTGGCCCGCTGGGCCGGTACAAGGTGAACAAGAAGCTGG q

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61 GTCTTGGGGGTGCCAACCCGGCTCTGGTGACTGCCACCACGCTCACCGAGGAAGACGTCG 120 ò

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PRA; RFLP;
TCGCCACCATCGGGTACCTGGTGCGCCTGCACGAGGGCCAGGACCACGATGACCGCCCCCG 180
       for
                                                                                                                                                                                                                                                                      New DNA fragments from the rpoB gene of mycobacteria, useful fidagnosis and identification of many mycobacterial species by restriction fragment length polymorphism
                                                                                                                                      HIV;
ds.
                                                                                                                                   Non-tuberculous mycobacteria; rpoB gene fragment; NTM; PCR-restriction fragment length polymorphism analysis;
                                                                                                                                                                                                                                               Park
                                                                                                                                                                                                                                               Kim Y,
                             214
                                   Mycobacterium marinum rpoB gene fragment.
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                            GCGCCTCGAGGTCCCGGTCGAGGTCGACGACAT
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                                                                             BP.
                                                                                                                                                                                                                                              G, Kim
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                                                                                                                                                                                                                99KR-0046795.
                                                                           AAS05211 standard; DNA; 208
                                                                                                      07-SEP-2001 (first entry)
                                                                                                                                                         Mycobacterium marinum.
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                                                                                                                                                                                                                                             Park YK,
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                                                                                          AAS05211;
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121
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Claim 1; Page 43; 50pp; English.

The present sequence for Mycobacterium marinum rpoB gene fragment is 1 of 24 rpoB gene fragments (AAS05201-AAS05224) from values Mycobacterial species. These rpoB gene fragments can be used in the diagnosis and identification of Mycobacterium species using a novel PCR-restriction fragment length polymorphism analysis (PRA) (method. The method comprises obtaining a restriction fragment length polymorphism (RFLP) pattern of the 24 rpoB gene fragments; isolating, amplifying and digesting the DNA fragment from the microorganism to comparing the DNA fragment from the Microorganism to it fragments with the unidentified fragment. The rpoB gene fragments of the 10 dentified and comparing the RFLP patterns from the Known rpoB gene fragments of diagnosis or to obtain epidemiological and pathogenesis information for selection of appropriate therapies, including M. tuberculosis, M. leprae and non-tuberculous mycobacteria (NTM) encountered in subjects infected (mith human immunodeficiency virus (HTW). Analysis of the rpoB gene caquired), and can differentiate between many species in a single experiment, including those difficult to distinguish by usual blochemical casts. Also described are oligonucleotide probes (AAS05227-AAS05242) for equired).

Sequence 208 BP; 45 A; 69 C; 68 G; 26 T; 0 other;

9 Query Match
65.0%; Score 139.2; DB 22; Length 208;
Best Local Similarity 81.8%; Pred. No. 3.4e-22;
Matches 175; Conservative 0; Mismatches 33; Indels 6;

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1 TCAAGGAGAAGGGCTACGACCTGGCCCGCGTGGGCCGGTACAAGGAGGTGAACAAGAAGCTGG 60 ŏ

1;

Gaps

9

Indels

Length 208;

DB 22;

Score 137.6; DB 22; Pred. No. 7.7e-22; 0; Mismatches 34;

64.3%; 81.3%;

Best Local Similarity 81.3 Matches 174; Conservative

Query Match

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The present sequence for Mycobacterium ulcerans rpoB gene fragment is 1 of 24 rpoB gene fragments (AAS05201-AAS05224) from various Mycobacterial species rpoB gene fragments can be used in the diagnosis and identification of Mycobacterium species using a novel PCR-restriction fragment length polymorphism analysis (PRA) method comprises obtaining a restriction fragment length polymorphism (RELP) pattern of the 24 rpoB gene fragments; isolating, amplifying and digesting the DNA fragment from the microorganism to be identified and comparing the RFLP patterns from the known rpoB gene fragments with the unidentified fragment. The rpoB gene fragments is colection of appropriate therapies, including M. tuberculosis, M. leprae and non-tuberculous mycobacteria (MTM) encountered in subjects infected with human immunodeficiency virus (HTV). Analysis of the rpoB gene fragments is rapid, precises, simple and cost effective (only 1 PCR required), and can differentiate between many species in a single experiment, including those difficult to distinguish by usual biochemical referentian analysis of the roors.
                                                                                                                                                                                                                                                                                                                                                                                                                                Non-tuberculous mycobacteria; rpoB gene fragment; NTM; HIV; PRA; RFLP; PCR-restriction fragment length polymorphism analysis; ds.
                                                                                                                61 GTCTTGGCGGTGCCAACCCGGCTCTGGTGACTGCCACCACGCTCACCGAGGAAGACGTCG 120
                                                                      1 TCAAGGAGAAGGCGTACGACCTGGCCCGGGTGGGCCGGTACAAGACGCTCAAGAAGGCTCG 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New DNA fragments from the rpoB gene of mycobacteria, useful f
diagnosis and identification of many mycobacterial species by
restriction fragment length polymorphism
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                                                                                                                                                                                181 GCGGCCTCGAGGTCCCGGTCGAGGTCGACGT 214
                                                                                                                                                                                                     175 GCGGTGTCGAGGTGCCGGTCGAGACCGACGT 208
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                                                                                                                                                                                                                                                                                                AAS05210 standard; DNA; 208 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mycobacterium ulcerans.
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Sequence 208 BP; 45 A; 68 C; 67 G; 28 T; 0 other;

detecting specific Mycobacterial species.

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The present sequence for Mycobacterium gordonae type II rpoB gene fragment is 1 of 24 rpoB gene fragments (AASO5201-AASO5214) from varIvobs Mycobacterial species. These rpoB gene fragments can be used in the diagnosis and identification of Mycobacterium species using a novel PCR-restriction fragment length polymorphism analysis (PRA) method comprises obtaining a restriction fragment length polymorphism (RFLP) pattern of the 24 rpoB gene fragments; isolating, amplifying and digesting the DNA fragment from the microorganism to be identified and comparing the RFLP patterns from the known rpoB gene fragments with the unidentified fragment. The rpoB gene fragments of fragments is considered and patterns from the known rpoB gene fragments of the contain epidemiological and pathogenesis information for selection of appropriate therapies, including M. tubbacculosis, M. leprae and non-tuberculous mycobacteria (NTM) encountered in subjects infected with human immunodeficiency virus (HIV). Analysis of the rpoB gene fragments is rapid, precise, simple and cost effective (only 1 PCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Non-tuberculous mycobacteria: rpoB gene fragment; NTM; HIV; PRA; RFLP; PCR-restriction fragment length polymorphism analysis; ds.
                                                                                              61 GCCTGAACGCCGGCCAGC-----CATCACCAGCTCGACGCTGACCGAGGAAGACGTCG 114
                                                                                                                                          TCGCCACCATCGGGTACCTGGTGCGCCTGCACGAGGGCCAGACCACGATGACCGCCCCCG 180
                                                                                                                                                              GTCTTGGCGGTGCCAACCCGGCTCTGGTGACTGCCACCACGCTCACCGAGGAAGACGTCG 120
1 TCAAGGAGAAGCGCTACGACCTGGCCCGGTGGCCCGGTACAAGGTGAACAAGAAGCTGG 60
                  New DNA fragments from the rpoB gene of mycobacteria, useful for diagnosis and identification of many mycobacterial species by restriction fragment length polymorphism
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required), and can differentiate between many species in a single experiment, including those difficult to distinguish by usual biochemical tests. Also described are oligonucleotide probes (AAS05227-AAS05242) for detecting specific Mycobacterial species.
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                                                                                                                                                          Length 208;
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                                                                                                                                                                                                      Indels
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                                                                                                            Sequence 208 BP; 45 A; 62 C; 73 G; 28 T; 0 other;
                                                                                                                                                   63.6%; Score 136; DB 22;
80.8%; Pred. No. 1.7e-21;
Live 0; Mismatches 35;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                   Query Match 63.6
Best Local Similarity 80.8
Matches 173; Conservative
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are useful to identify a wide range of Mycobacterium species, e.g. for diagnosis or to obtain epidemiological and pathogenesis information for selection of appropriate therapies, including M. tuberculosis, M. leprae and non-tuberculous mycobacteria (NTM) encountered in subjects infected with human immunodeficiency virus (HIV). Analysis of the rpoB gene fragments is raphd, precise, simple and cost effective (only 1 PCR required), and can differentiate between many species in a single experiment, including those difficult to distinguish by usual blochemical facts. Also described are oligonuclectide probes (AASO5227-AASO5242) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Non-tuberculous mycobacteria; rpoB gene fragment; NTM; H1V; PRA; RFLP; PCR-restriction fragment length polymorphism analysis; ds.
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                                                                                                                                                                                                                                                                                                                             Length 208;
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                                                                                                                                                                                                                                                                                                                          DB 22;
                                                                                                                                                                                                                                                                         Sequence 208 BP; 48 A; 71 C; 64 G; 25 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                         Pred. No. 3.9e-21
                                                                                                                                                                                                                                                                                                        62.8%; Scor.
80.4%; Pred. No. 3...
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                                                                                                                                                                                                                        detecting specific Mycobacterial species.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-300520/31.
                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 172; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Park YK,
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novel PCR-restriction fragment length polymorphism analysis (PRA)

method. The method comprises obtaining a restriction fragment length

polymorphism (RFLP) pattern of the 24 rpoB gene fragments; isolating,

amplifying and digesting the DNA fragment from the microorganism to

creaments with the unidentified fragment. The rpoB gene fragment ship are useful to identify a wide range of Mycobacterium species, e.g. for

diagnosis or to obtain epidemiological and pathogenesis information for

selection of appropriate therapies, including M. tuberculosis, M. leprae

and non-tuberculous mycobacteria (MTM) encountered in subjects infected

with human immunodeficiency virus (HTW). Analysis of the rpoB gene

required), and can differentiate between many species in a single

experiment, including those difficult to distinguish by usual biochemical

cestering and described are oligonucleotide probes (AASO5227-AASO5242) for
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                                                                                                                                                                                                                                                                                                                                                                                                                                  61 GTCTTGGCGGTGCCAACCCGGCTCTGGTGACTGCCACGCTCACCGAGGAAGACGTCG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New DNA fragments from the rpoB gene of mycobacteria, useful for diagnosis and identification of many mycobacterial species by restriction fragment length polymorphism -
                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                          DB 22; Length 208;
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                                                                                                                                                                                                                                                                       Sequence 208 BP; 46 A; 69 C; 63 G; 30 T; 0 other;
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                                                                                                                                                                                                                                                                                                        Score 132.8; DB 2;
Pred. No. 8.9e-21;
); Mismatches 37,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 GCGCCTCGAGGTCCCGGTCGAGGTCGACGACAT 214
                                                                                                                                                                                                                                            detecting specific Mycobacterial species.
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                                                                                                                                                                                                                                                                                       62.18; Score
v 79.98; Pred
0; V
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AAS05208
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fragment is 1 of 24 rpoB gene fragments (AAS05201-AAS05224) from
various Mycobacterial species. These rpoB gene fragments can be used
in the diagnosis and identification of Mycobacterium species using a
novel PCR-restriction fragment length polymorphism analysis (PRA)
method. The method comprises obtaining a restriction fragment length
covel PCR-restriction fragment length polymorphism analysis (PRA)
method. The method comprises obtaining a restriction fragment length
covel PCR-restriction of the 24 rpoB gene fragments: isolating,
amplifying and digesting the DNA fragment from the microorganism to
be identified and comparing the RELP patterns from the known rpoB gene
fragments with the unidentified fragment. The rpoB gene fragments
created to identify a wide range of Mycobacterium species, e.g. for
diagnosis or to obtain epidemiological and pathogenesis information for
selection of appropriate therapies, including M. tuberculosis, M. leprae
and non-tuberculous mycobacteria (NTW), analysis of the rpoB gene
crequired), and can differentiate between many species in a single
experiment, including those difficult to distinguish by usual biochemical
tests. Also described are oligonuclectide probes (AAS05227-AAS05242) for
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ds.
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                                                                                                                                                                                                                                                                                                                                                                                                          62.1%; Score 132.8; DB 22; Length 208; 79.9%; Pred. No. 8.9e-21;
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PCR-restriction fragment length polymorphism analysis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          37;
                                  present sequence for Mycobacterium kansasii
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                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
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Claim 1; Page 42; 50pp; English.
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Matches 171; Conservative
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Cho

G, Kim S,

Bai

Park YK,

99KR-0046795

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                                           (ERUM-) ERUME BIOTECH CO LTD.
               27-OCT-1999;
                                                                           Lee H,
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                                                                                                                     The present sequence for Mycobacterium xenopi rpoB gene fragment is 1 of 24 rpoB gene fragments (AASO5201-AASO521) from various Mycobacterial species. These rpoB gene fragments can be used to the diagnosis and identification of Mycobacterium species using a novel PCR-restriction fragment length polymorphism malysis (PRA) comprises obtaining a restriction fragment length colymorphism (RFLP) pattern of the 24 rpoB gene fragments; isolating, amplifying and digesting the DNA fragment from the microorganism to be identified and comparing the RFLP patterns from the known rpoB gene fragments with the unidentified fragment. The rpoB gene fragments of the indentified fragment in the prob gene fragments of contains to indentified fragments from the known rpoB gene fragments with the unidentified fragment. The rpoB gene fragments of of apropriate therapies, including N. tuberculosis, M. leprae and non-tuberculous mycobacteria (NTM) encountered in subjects infected fragments is rapid, precise, simple and cost effective (only 1 PCR cequired), and can differentiate between many species in a single tests. Also described are oligonucleotide probes (AASO5227-AASO5242) for Adaptive and including those difficult to distinguish by usual biochemical contains and including those difficult and probes (AASO5227-AASO5242) for Adaptive and and are oligonucleotide probes (AASO5227-AASO5242) for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'Match 59.8%; Score 128; DB 22; Length 208; Local Similarity 78.5%; Pred. No. 1e-19; les 168; Conservative 0; Mismatches 40; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 1e-19;
0; Mismatches 40; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 208 BP; 51 A; 65 C; 67 G; 25 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mycobacterium tuberculosis rpoB gene fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         175 GTGGCGTCGAGGTGCCGGTGGAGACCGACAT 208
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                                                                                                                                                                                                                                                                                                                                                                                                                                 detecting specific Mycobacterial species.
                                                                                               Claim 1; Page 47; 50pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BP
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The present sequence for Mycobacterium tuberculosis rpoB gene fragment is 1 of 24 rpoB gene fragments (AASO5201-AASO524) from cardinal waycobacterial species. These rpoB gene fragments can be used in the diagnosis and identification of Mycobacterium species using a novel PCR-restriction fragment length polymorphism analysis (PRA) cemethod comprises obtaining a restriction fragment length polymorphism analysis (PRA) pattern of the 24 rpoB gene fragments; isolating, amplifying and digesting the DNA fragment from the microorganism to be identified and comparing the RFLP patterns from the known rpoB gene fragment with the unidentified fragment. The rpoB gene fragments with the unidentified fragment. The rpoB gene fragments of comparing the RFLP patterns from the known rpoB gene cragments with the unidentified fragment. The rpoB gene fragments of agnosis or to obtain epidemiological and pathogenesis information for selection of appropriate therapies, including the unidentified fragment is constituted in subjects infected and non-tuberculous mycobacteria (RTMM) encountered in subjects infected fragments is rapid, precise, simple and cost effective (only 1 pCR required), and can differentiate between many species in a single experiment, including those difficult to distinguish by usual blochemical creater in analysis of the rose of experiment in condition are obtained are oil general problems (RESS-277-AASO52277-AASO52277-AASO52277-AASO52277-AASO52277-AASO52277-AASO52277-AASO52277-AASO52277-AASO52277-AASO52277-AASO52277-AASO52277-AASO52277-AASO52277-AASO52277-AASO52277-AASO52277-AASO52277-AASO52277-AASO52277-AASO52277-AASO52277-AASO52277-AASO52277-AASO52277-AASO52277-AASO52277-AASO52277-AASO52277-AASO52277-AASO52277-AASO52277-AASO52277-AASO52277-AASO52277-AASO52277-AASO52277-AASO52277-AASO52277-AASO52277-AASO52277-AASO52277-AASO52277-AASO52277-AASO52277-AASO52277-AASO52277-AASO52277-AASO52277-AASO52277-AASO52277-AASO52277-AASO52277-AASO52277-AASO52277-AASO52277-AASO52277-AASO52277-AASO52277-AASO52277-AASO52277-AASO522
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 GGCTGCATGTCGGCGAGCC----CATCACGTCGTCGACGCTGACCGAAGAAGACGTCG 114
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     Park HJ;
Kim Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 208 BP; 46 A; 62 C; 67 G; 33 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 41; 50pp; English.
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Matches 166; Conservative
                                                                                    WPI; 2001-300520/31.
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GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.

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November 12, 2002, 16:50:46 ; Search time 654.37 Seconds (without alignments) 9517.553 Million cell updates/sec
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1 tcaaggagaagagctacgac......ccggtcgaggtcgacgacat 214
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Scor 132. 124.	0 0000	- i	BB	ID MSD24494 MT0318818 MT0318819	Description U24494 Mycobacter1 AJ118818 Mycobacte
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RESULT 1 MSU24494 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE	- w	SU24494 YCODACTE 24494.1 YCODACTE YCODACTE YCODACTE ACTINOMYC YCODACTE ACTINOMYC YCODACTE ACTINOMYC YCODACTE ACTINOMYC YCODACTE ACTINOMYC	rium smec GI:79034 GI:79034 rium smec rium smec Firmicut etales; C rium. 375 ton, S.V.,	smegma 10347 smegma smegma: cutes 5; Corr	ALIGNMENTS 3752 bp DNA DNA polymerase Linobacteria; A	DNA linear BCT 02-MAR-2000 ase (rpoB) gene, complete cds. a; Actinobacteridae; Mycobacteriaceae;

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AJ318818.1
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RKRROPYTULIKALGWTHEREFEEDELMGTLEEGTTSGTDEALLDIYRKINGE
PPTKESAQTLLENLFKEKRYDLARVGRYKVNKKLGLNAGKPITSSTLTEEDVVATIE
YLVRIHEGGYSFYTYDEGVERAVESHDIDHFGNRRLRYVGELIGORIRRRERVR
ERWTTODVEA ITPOTLJINEVVAA KEFFCTSGLSGFMDGNNPLSGLTHKRLSALG
PGGLSRERAGLEVRDVHPSHYGRMCPIETPEGPNIGLIGSLSGYYARVNFFGFIETPYR
KVVEGVYTDOIDYLTADEEDRHVVAQANSPTDENGRFTEDRYWRKKGEVEFSADG
VDYMDVSPRQMVSVATAMIPFLEHDDANRALMGANMORQAVPLVRSEAPLVGTGMELR
AAIDAVTWSSHKTGYIEEVSADYITVWAADOGTROSYRLRKFARSHGTCANQRRIVDA
GQRYEAGGVIADGFCTQNGEMALGKNLLVAIMPWEGHNYEDAIILSNRLVEEDVLTSI
HIEBEIDARGYKICAREITRYIPKLSDEVLADLDEPRIVRIGHSONDELPVGVV
KGFTELTPERELLARIFGRARRVBGTSLKVPHGESGKVIGIRVFSREDDELPVGVV
ELVRVYVAQKRKISDGKLARRHGNKGVIGKILPVEDMPFLDOGTPVOILLNTHRGCRV
VLNIGGOLIEFTHGROARAGNNIDVLAGVPDARAKLEELTSARPGSTVATT
                                                                                                                                                                                                                                                                                                                                                                                                           /translation="MLEGCILAVSSOSKSNAJTNNSVRGAPNGVSFAKLREPLEVRGL
LDVQTDSFEWLVGSRRVRQAAIDRGEENPVGGLEEVLAELSPIEDFSGSWSLSFSDPR
FDEVKASVDECKDKDMTYAAPLFVTAEFINNNTGEIKSQTVFWGDFPWTEKGTFIIN
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GRVKVYEAIVKGENIPEPGIPESFKVLLKELQSLCLNVEVLSSDGRAIEMRDGDDEDL
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                                                                                                              Infectious Diseases,
Lauderdale, Memphis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #MIU318818 610 bp DNA circular BCT 09-AUG-2
Mycobacterium tuberculosis partial rpoB gene for RNA polymerase
beta subunit, isolate 1415-97.
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Antimicrob. Agents Chemother. 39 (9), 2164-2166 (1995) 96050766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                        Submitted (11-APR-1995) Seth V. Hetherington,
St. Jude Children's Research Hospital, 332 N.
TN 38101, USA
                                                                                                                                                                                              /organism="Mycobacterium smegmatis"
/db_xref="taxon:1772"
194. .3703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37;
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Pred. No. 1.7e-13;
0; Mismatches 37
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                                                                                                                                                                                                                                                                                                                                                           /product="DNA polymerase"
/protein_id="AAA91426.2"
/db_xref="G1:7144498"
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194. .3703
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ilarity 79.9%;
Conservative
                                                    2 (bases 1 to 3752)
Hetherington, S.V.
Direct Submission
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                                     8540740
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DEFINITION
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ORIGIN
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                                                                                                                                                                                                                                   gene
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                                                                     AUTHORS
                                                                                                          JOURNAL
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                  MEDLINE
                                       PUBMED
                                                        REFERENCE
 JOURNAL
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Herrera,L., Jimenez,M.S. and Saez,J.A. Molecular analysis of rifampin-resistant Mycobacterium tuberculosis isolated in Spain (1996-2001). Description of new alleles into rpos gene and review
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KLGHYGEPTTSSTLTBEDVATIELTVRLHEGGTTMTVPGGVEVPVETDDIDHFGNR
KLRTVGELIQONGIRGSRMERVYREMTTQDVEAITPGTLINIRPVVAAIKEFFGTS
QPSQFMGQNNPLSGLTHKRRLSALGPGGLSRERAGLEVRDVHP"
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                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (07-AUG-2001) Herrera L., Servicio Bacteriologia, Centro
Nacional Microbiologia., Ctra. Majadahonda-Pozuelo, Km 2.5,
Majadahonda. Madrid. 28220, SPAIN
Location/Qualifiers
               RNA polymerase beta subunit; rpoB gene.
Mycobacterium tuberculosis.
Mycobacterium tuberculosis
Bacteria; Actinobacteria; Actinobacteria; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene for RNA polymerase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80 TCAAGGAGAAGCGCTACGACCTGGCCCGCGTCGGTCGTATAAGGTCAACAAGAAGCTCG 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCGCCACCATCGGGTACCTGGTGCGCCTGCACGAGGGCCAGACCACGATGACCGCCCCCG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    253
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Mycobacterium tuberculosis partial rpoB gene for RNA polymera beta subunit, isolate 1417-97.
AJ318819
AJ318819.1 GI:22208414
RNA POLYMerase beta subunit; rpoB gene.
Mycobacterium tuberculosis.
Mycobacterium tuberculosis.
Mycobacterium tuberculosis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
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//organism="Mycobacterium tuberculosis"
//solate="1415-97"
//db_xref="taxon:1773"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="RNA polymerase beta subunit"
/protein_id="CAC87035.1"
/db_xref="G1:22208413"
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Pred. No. 4.9e-
0; Mismatches
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GI:22208412
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ilarity 77.6%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="rpoB"
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                                                                                                                                             tuberculosis complex
                                                                                                                                                                                                                                                                                                               2 (bases 1 to 610)
Herrera, L.
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Direct Submission
Submitted (07-AŭG-2001) Herrera L., Servicio Bacteriologia, Centro
Nacional Microbiologia., Ctra. Majadahonda-Pozuelo, Km 2.5,
Majadahonda. Madrid. 28220, SPAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Herrera, L., Jimenez, M.S. and Saez, J.A.
Molecular analysis of rifampin-resistant Mycobacterium tuberculosis
isolated in Spain (1996-2001). Description of new alleles into rpos
gene and review
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             circular BCT 09-AUG-2002
gene for RNA polymerase
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Submitted (07-AUG-2001) Herrera L., Servicio Bacteriologia, Centro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RNA polymerase beta subunit; rpoB gene.
Mycobacterium tuberculosis.
Mycobacterium tuberculosis
Bycobacterium tuberculosis
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 616;
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                                                                                                                                                                          tuberculosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 124.8; DB 1
Pred. No. 4.9e-12;
0; Mismatches 42
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beta subunit, isolate 2540-97.
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                                                                                                                                                                   /organism="Mycobacterium //organism="1763-97" //db_xref="taxon:1773" 1. .615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 GCGCCTCGAGGTCCCGGTCGAGGTCGACGACAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AJ318815.1 GI:22208406
                                                                                                                                                                                                                                     /gene="rpoB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 58.3%;
Best Local Similarity 77.6%;
Matches 166; Conservative
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                                            (bases 1 to 616)
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              gene and rev
Unpublished
                                                         Herrera, L.
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                                                                                                                                                                                                                                                                                                                                                                                                                             125
                                                                                                                                                        source
                                         REFERENCE
AUTHORS
TITLE
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MTU318815
                                                                                       JOURNAL
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TITLE
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AUTHORS
TITLE
JOURNAL
                            JOURNAL
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KEYWORDS
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/codon_start=1
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/product="RNA polymerase beta subunit"
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QPSQFNGQNNPLGSCHHKRRLSALGPGGLSRERAGLEVRDVHP"
                                              Herrera,L., Jimenez,M.S. and Saez,J.A.
Molecular analysis of rifampin-resistant Mycobacterium tuberculosis isolated in Spain (1996-2001). Description of new alleles into rpob gene and review
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Molecular analysis of rifampin-resistant Mycobacterium tuberculosis
isolated in Spain (1996-2001). Description of new alleles into rpoB
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   Mycobacteriaceae; Mycobacterium; Mycobacterium
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Mycobacterium tuberculosis.
Mycobacterium tuberculosis.
Bacteria; Actinobacteria; Actinobacteria; Actinobacteria; Actinobacteria; Actinobacteria; Actinobacteriace; Mycobacteriace; Mycobacterium; Mycobacterium tuberculosis complex.
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gene for RNA polymerase
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                                                                                                                                                        Direct Submission
Submitted (07-AUG-2001) Herrera L., Servicio Bacteriologia,
Nacional Microbiologia., Ctra. Majadahonda-Pozuelo, Km 2.5,
Majadahonda. Madrid. 28220, SPAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCAAGGAGAAGCGCTACGACCTGGCCCGCTGGGCCGGTACAAGGTGAACAAGAAGCTGG
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9
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                                                                                                                                                                                                                                                           tuberculosis"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 124.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mycobacterium tuberculosis partial beta subunit, isolate 1763-97.
                                                                                                                                                                                                                                                      /organism="Mycobacterium
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                                                                                                                                                                                                                                                                                    /db_xref="taxon:1773"
                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                        /isolate="1417-97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58.3%;
77.6%;
                                                                                                                                                                                                                                                                                                                                                    /gene="rpoB"
                  tuberculosis complex.
                                                                                                                            (bases 1 to 610)
Corynebacterineae;
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                                                                                                             Unpublished
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                                                                                                                                          Herrera, L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                         source
                                               AUTHORS
TITLE
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Matches
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ORIGIN
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                                 REFERENCE
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MTU318813
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AUTHORS
TITLE
                                                                                                                                          AUTHORS
                                                                                                                                                                                                                                                                                                        gene
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                                                                                                                            REFERENCE
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KEYWORDS
SOURCE
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Gaps 9 253

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/translation="robeAllolyrklrPgEPPTKESAQTLLENLFFKERRYDLARVGR
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HFGNRRLRYVGELIOWOIRVGMSRMERVYRERMTQDVEATPRTLINIRPVVAAIKE
FFGTSQLSQFMDQNNPLSGLTHKRRLLALGPGGLSRERAGLEVRDV"
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Mycobacterium tuberculosis partial rpoB gene for RNA polymerase
AJ318817
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Molecular analysis of rifampin-resistant Mycobacterium tuberculosis
isolated in Spain (1996-2001). Description of new alleles into rpob
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Mycobacterium tuberculosis.
Mycobacterium tuberculosis.
Mycobacterium tuberculosis.
Mycobacterium tuberculosis.
Mycobacterium tuberculosis.
Gorynebacterium, Actinobacteriae, Actinobacteriums, Mycobacterium tuberculosis.
Corynebacterinese; Mycobacteriaceae; Mycobacterium tuberculosis complex.
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       Majadahonda-Pozuelo,
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                                                                                                                                      /organism="Mycobacterium tuberculosis'
/isolate="2540-97"
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    618 // Approprime Approprime Appropries / Approprime 
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Pred. No. 4.9e-12;
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Nacional Microbiologia., Ctra. Maj
Majadahonda. Madrid. 28220, SPAIN
Location/Qualifiers
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FFGTSQPSQFMQONNULSGLTHKRRLSALGPGGLSRERAGLEVRDV"

192 c 207 g 95 t
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Submitted (07-AUG-2001) Herrera L., Servicio Bacteriologia, Centro
Nacional Microbiologia., Ctra. Majadahonda-Pozuelo, Km 2.5,
Majadahonda. Madrid. 28220, SPAIN
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RNA polymerase beta subunit; rpoB gene.
RNA polymerase beta subunit; rpoB gene.
Mycobacterium tuberculosis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriam
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                                                                                                                                                                                                                                                                                          DB 1;
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                                                                                                                                                                                                                                                                                     Score 124.8; DB 1
Pred. No. 4.9e-12;
0; Mismatches 42
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1. .618
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/codon_start=1
                                   /gene="rpoB"
                                                                                                                                                                                                                                                                                      58.3%;
ilarity 77.6%;
Conservative
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Herrera, L.
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/product="RNA polymerase beta subunit"
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AAIKEFFGTSQLSQFMONNPLSGRITYRRRLSALGFGGLSRERAGLEVRDV"
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gene for RNA bolvmerser
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Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium
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/protein_id="CAC87033.1"
/db_xref="GI:22208409"
                                                                                                                                                                                             Score 124.8; DB 1
Pred. No. 4.9e-12;
0; Mismatches 42
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rpoB
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Mycobacterium tuberculosis.
Mycobacterium tuberculosis
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                                                                                                                                                                                                         Best Local Similarity 77.6
Matches 166; Conservative
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KEFFGTSQLSQFMDQNNPLSGLTHKRRMFALGPGGLSRERAGLEVRDVHPSH*
198 c 210 g 101 t
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                                                                                                                                                                                                                                                                                                                                                                                                              MTU318821 639 bp DNA circular BCT 09-AUG-2002 Mycobacterium tuberculosis partial rpoB gene for RNA polymerase beta subunit, isolate 1071-98.
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Molecular analysis of rifampin-resistant Mycobacterium tuberculosis
isolated in Spain (1996-2001) Description of new alleles into rpob
gene and review
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (07-AUG-2001) Herrera L., Servicio Bacteriologia, Centro Nacional Microbiologia, Ctra. Majadahonda-Pozuelo, Km 2.5, Majadahonda. Madrid, 28220, SPAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RNA polymerase beta subunit; rpoB gene.
Mycobacterium tuberculosis.
Mycobacterium tuberculosis
Bacteria; Actinobacteria; Actinobacterium; Actinomycetales;
Corynebacterineae; Mycobacteriam
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/isolate="1071-98"
                                                                       Score 124.8; DB 1;
Pred. No. 4.9e-12;
0; Mismatches 42;
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AJ318821.1 GI:22208418
                                                                       58.3%;
ilarity 77.6%;
Conservative
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Score 124.8;

58.3%;

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                                                                                                                                                                                                                                                                                                                                                                             [ (bases 1 to 970)
Persing, D.H., Hunt, J.J., Young, K.K.Y., Felmlee, T.A., Roberts, G.D. and Whelan, A.Christian.
Detection of a genetic locus encoding resistance to rifampin in mycobecterial cultures and in clinical specimens
Patent: US 5643723-A 1 01-JUL-1997;
                                                                                                              214
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                                                  GTCTTGGCGGTGCCAACCCGGCTCTGGTGACTGCCACCACGACGAGGAAGACGTCG 120
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                                    TCAAGGAGAAGCGCTACGACCTGGCCCGCGTGGGCCGGTACAAGGTGAACAAGAAGCTGG
                                                                                                             161 GGCTGCATGTCGCCGAGCC-----CATCACGTCGTCGACGCTGACCGAAGAAGACGTCG
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Mycobacterium tuberculosis
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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             Indels
                                                                                                                                                                                                                                                                              linear
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77.6%; Pred. No. 4.6e-12;
Live 0; Mismatches 42
Pred. No. 4.9e-12;
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                                                                                                                                                                                                                                                                         970 bp
Sequence 1 from patent US 5643723.
150706
150706.1 GI:2472409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="unknown"
302 c 330 q
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Local Similarity 77.6%;
es 166; Conservative
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Mycobacterium; Mycobacterium tuberculosis complex.

1 (bases 1 to 3534)

Bergeron, M. G., Boissinot, M., Huletsky, A., m Nard, C., Ouellette, M., Picard, F.J. and Roy, P. H.

Highly conserved genes and their use to generate probes and primers for detection of microorganisms
Patent: WO 0123604-A 2072 05-APR-2001;
Infectio Diagnostic (I.D.I.) INC. (CA)

Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (11-JUL-1994) Paul Imboden, Institute for Medical Microbiology, University of Berne, Friedbuehlstrasse 51, Berne, 3010, Switzerland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 GTCTTGGCGGTGCCAACCCGGCTCTGGTGACTGCCACCACGCTCACCGAGGAAGACGTCG 120
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Mycobacterium tuberculosis
Mycobacterium tuberculosis
Bacteria: Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae;
Mycobacterium; Mycobacterium tuberculosis complex.
I (bases 1 to 3853)
Imboden, P., Troller, R., Marchesi, F., Telenti, A., Bodmer, T.,
Cole, S., Schopfer, K. and Burkart, T.
The rpob gene of Mycobacterium tuberculosis
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Actinomycetales; Corynebacterineae; Mycobacteriaceae;
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1. .3853
/organism="Mycobacterium tuberculosis"
                                                                                                                                                                                                                                                                   /organism="Mycobacterium tuberculosis"
                                                                                                                                                                                                                                                                                                                                                                                                                    Score 124.8; DB 6;
Pred. No. 3.9e-12;
0; Mismatches 42;
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/db_xref="taxon:1773"
1081 c 1188 q
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576. .>3853
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/gene="rpoB"
576. .>3853
/gene="rpoB"
/codon_start=1
/transl_table=11
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Best Local Similarity 77.6%;
Matches 166; Conservative
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Imboden, P.
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Mycobacterium tuberculosis CDC1551, section 50 of 280 of the complete genome.
AE006964 AE000516
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GLFCERIFGPFRDWECYCGKYKRVRFKGIICERCGVEVTRAKVRRERMGHIELAAPVT
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1534 c 1691 g 890 t
                                                                                                                                                                                      /translation="MLEGCILADSROSKTAASPSPSRPOSSSNNSVPGAPNRVSFAKL
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MSLSFSDPRFDDVKAPVDECKDKDMTYAAPLEVTAEFINNNTGEIKSQTVFWGDFPMM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 GTCTTGGCGGTGCCAACCCGGCTCTGGTGACTGCCACCACGCTCACCGAGGAAGACGTCG 120
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                                                                                                                      /product="RNA polymerase beta-subunit"
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                                                                                      /evidence-experimental
                                                                                                         /transl_table=11
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1065. .4598
/gene="rpob"
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/gene="rpoC"
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/gene="rpoC"
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RDTVGVRIDKRRQPVTVLLKALGGMTSEQTYERFGFSEIMRSTLHSVGTLHSCHYGEDFMM
FEKGTPFIINGTERVTORVDEATTPOPLINIFRYDLARVORTHSKUNKTRCHTSSTLT
REDVARVNTEEVTRYDOGVSGTTTPPGTLINIRRVVAANIFRTSSTLT
RRALSALGPGGLSRERAGLEVRDVHPSHVGRWCPTETPEGPNIGLIGSLSVYARNUP
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ANQCPTUDAGNRVAATAAIPLELENDARRALMGANUPGRANUPGTC
ANQCPTUDAGNRVAATAAIPLEGHDARRALMGANULATAINWEGTT
ANGCPTUDAGNRVAATAAIPLEGENTARDRALMGANULATAINGWGANUPGTT
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DILVGKVTPKGETELTPEERLLRAIFGERAREVRDTSLKVPHGESGRVTIGIRVESRED
EDELPAGOVNELVYAQRKRSSGDSGWTONGRONGNISCHILANISDEVLADLDERGTPVRIGEL
LUNTHGVPRRNNIGQILETHGGGLESGWWUDAARGYPDELLEAQPPNIIN
KLHHLVDDRIHARSTGPYSMITGQPLGCKAQFGGRRECWAANGARGPPPAATIGELL
RELHAUDDKIHARSTGPYSMITGQPLCGKAQFGGRRECWAANGARGAPPATIGELL
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Mycobacterium tuberculosis (strain Rv) DNA.
Mycobacterium tuberculosis
Bacteria: Actinobacteria; Actinobacteriam Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium
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58.3%; Score 124.8; DB 1; Length 3853;
Best Local Similarity 77.6%; Pred. No. 3.9e-12;
Matches 166; Conservative 0; Mismatches 42; Indels 6;
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1 (bases 1 to 5084)
Miller, L.P., Crawford, J.T. and Shinnick, T.M.
The rooB gene of Mycobacterium tuberculosis
Antimicrob. Agents Chemother. 38 (4), 805-811 (1994)
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1065. .4598
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STPVFDGAQEAELQGLLSCTLPNRDGDVLVDADGKAMLFDGRSGEPFPYPVTVGYMYI
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LTIKSDDTVGRVKVYEAIVKGENIPEPGIPESFKVLLKELQSLCLNVEVLSSDGAAIE
LREGEDEDLERAAANLGINLSRNESASVEDLA"
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          Mycobacterium tuberculosis CDC1551.

Mycobacterium tuberculosis CDC1551.

Mycobacterium tuberculosis CDC1551.

Actinomycetales: Actinobacteriae.

Actinomycetales: Corynebacterineae; Mycobacteriaceae;

Mycobacterium; Mycobacterium tuberculosis complex.

[ pases 1 to 19352]

Fleischmann, R.D., Alland, D., Eisen, J.A., Carpenter, L., White, O., Peterson, J., DeBoy, R., Oddson, R., Gwinn, M., Haft, D., Hickey, E., Kolonay, J.E., Nelson, W.C., Umayam, L.A., Ermolaeva, M., Salzbergs, S.L., Delcher, A., Utterback, T., Weidman, J., Khouri, H., Gill, J., Mikula, A. and Bishai, W.

Whole genome comparison of Mycobacterium tuberculosis clinical and
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Submitted (25-APR-2001) The Institute for Genomic Research, 9712 Medical Center Dr. Rockville, MD 20850, USA

Location/Qualifiers
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/strain="CDC1551"
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3744. 7504
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/gene="MT0695"
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/gene="MT0696"
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                                                                                                                                                                                                                                                                                                                                                 AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDS
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KEYWORDS
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IQAFEPMLVEGEATOLHEVEZETRADESCONNELLESAEGAEARALELESTRADES
IQAFEPMLVEGEATOLHEVEZETRADESCONNELLESAEGAEARALESSUNIL
SPAGGREPLAMPELDAWTGLYTITPVPEDTGETOPAGGDHPETGYVESPEATIAAADR
GULSVRAKIKVRLTQLRPPYELEELFGHSGWOPGDAWMAETTLGRWFNELLPLGYP
FVNKOMHKKVORAAIINDLAERYPMIVVAQTVDKLKDAGFWAAFRSGVTVSMADVLVPP
RKREILDHYEBRARKVEROFORGALHHDERNEALDEIWKEATDEGVGOLKEHYPDDNP
ITTIVDSGATGNFTOTRILAGMKGLYTNPKGEFIPRPVKSSFREGLTVLEYFINTHGA
RKGIADTALEFTADSGYLTRRLVDVSQDYIVRHDCOFREGITVELAERAPDGTLIRDP
ITTIVDSGATGNFTOTRILAGWGLYTNPKGEFIPRPVKSSFREGLTVLEYFINTHGA
RKGIADTALEFTADSGYLTRRLVDVSQDYIVRHDCOPERGITVETFHQGGVGEDITGCLPR
VOELFEARVPRGKAPIADVCRVYKLEDGEROFULNAGTFHQGGVGEDITGCLPR
VOELFEARVPRGKAPIADVCRVKLEDGERFYKITIVPDDGGEEVYVDKISKRORLRV
KHEDGSERVLSDOHVEVGQLMEGSADPHEVLRYOGPREWOITLVREVOEVEVRAGG
VSIHDKHIEVIVRQMLRRVTIIDSGSFFFLEGSLIDRAEFEARNRRVVAEGGEPAAGR
PVLMGITKASLATDSWLLSAAASQCETTRYLTDAAIRGAAVPLDDYGYSDYR" /product-"hydrolase/esterase, putative"

/protein_de=_aAK44925.1"

/db_xref="f1:1880222"

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SIFAAIGVVSGTQLDPCQSPRPVSVHIHGTADPLVRYHGGPGGFARIDGPPPDLN LRDVI RNGKGGKKLRALKRLKVVAAFQOSGNSPMGMVLDAVPVI PPELRPMVQLDGGR RASDLANDLY RRVI NRNNRLKRLIDLGAPEI IV VNREKRHLGSSVDALHOGRRGRPVT GPGRRPLKSLSDLLKGKGGRFGVOLLGKRYDVSGRSV IVVGPDLKLHQCGLPKLMALE LFKPFVWKRLVDLNHAONI KSAKRWVERQRPQVWDVLEEVI AEHPVLLNRAPTLHRLG /product-"AP endonuclease, family 2" Protein_id="AAK4924.1" /db_xref="GI:13880221" /translation="MLIGSHVSPTDPLAAAEAEGADVVQIFLGNPQSWKAPKPRDDAA ALKAATLPIYWHAPYLINLASANNRYRIPSRKILQETCAAAADIGAAAVIVHGGHVAD
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LDTGHTWAAGAEALTDAVDRIKAITGRIDLWHCNDSRDEAGSGRDRHANLGSGGIDPDL
LVAAVKAAGAPVICETADQGRKDDIAFLRERTGS" AVEDQRDGELEARAQKLEADLAELEAEGAKADARRKVRDGGEREMRQIRDRAQRELDR LEDIWSTFTKLAPKQLIVDENLYRELVDRYGEYFTGAMGAESIQKLIENFDIDAEAES /trans.ation="MFDSAAAITNPGHAWASAWERSGLLECVAGLDEQPFGEFTADKL NPDRGSSRRVPRRQADGGIATHVERGGGQRQSGGQAGVVPQRMHGFPALAWQDRLIHH HIWYFKGVPSRLGYLLDLAPKDLEKIIYFAAYVITSVDEEMRHNELSTLEAEMAVERK and ed by yeue="mivoss".

/note="This region contains an authentic frame shift an is not the result of a sequencing artifact; identified | Glimmer2; putative; conserved hypothetical protein, authentic frameshift"

10167. 10925
/gene="wr0699"

10167. #10925
/gene="wr0699"

/note="identified by match to PFAM protein family HWM PF01261" þ 10957. 11799 /gene-*MT0700" 10957. 11799 /gene-*similar to GB:U00012 PID:466863; identified sequence similarity; putative" /gene="MT0697" /note="ldentified by Gl1mmer2; putative" /codon_start=1 /transl_table=11 /product="hypothetical protein" /protein_id="AAKK4923.1" /db_xref="GI:13880220" GEQTONRIAQAFRVRFCVCSPT" complement(7691. .8065) complement(8058. .9972) complement(7691. .8065) /codon_start=1 /transl_table=11 /transl_table=11 /gene="MT0697" /codon_start=1

gene

CDS

gene

CDS

gene

CDS

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IFULAGAPOGLSCELLPRINGER OF THE STATE OF THE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation-"MSDTHVVTNQVPPLENYNPASSPVLIEALIQEGGQMGLDEVNEV
GAISASCQAGMGELADRNRPILHTHANAYTYRDEVEYDPAYHBLMRFATHGHHAAP
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DPELKPATTKAGITAGMSWTEKQGGSDVRAGTTQATPNADGSYSLTGHKWFTSARMC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ELSALVERADLDPGVHVILVSGRGGGFCAGFDLSAYABGGSSSTGGGGAYQGTVLLDGKT
QAVHILPNOPWDPMIDYQWMSRFVRGFASLWHADKPPVVKIHGYCVAGGTDIALHADQ
TAAADAKILYGYPPTRVWGVPAGLWAHRLGDORAKRLLFTGDCITGAQAAEWGLAVEA
PEPADLDERTERLVARIAALPVNOLIMVKLALNSALLQQGVATSRWYSTVFDGAARHT
PEGHAFVADAVEHGFRDAVRRRDEPFGDYGRQASRV
AFWREVNRCGALDTTTEGPVTTSGATCADNRRVVLLTVDDAGHRWPSFATQTLWRFFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="enoyl-CoA hydratase/isomerase family protein"
/protein_id="AAK44927.1"
/db_xref="GI:13880224"
/translation="MTHAIRPVDFDNLKTMTYEVTGRIARITFNRPEKCNAIIADTPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1;
                                                                                                                                                                                                                                                             /note="similar to SP:P33224 GB:L20915 PID:457172
PID:457174 PID:537028; identified by sequence similarity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1064 TCAAGGAGAAGCGCTACGACCTGGCCCGCGTCGGTCGCTATAAGGTCAACAAGAAGCTCG 1123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1178 FGGCCACCATCGAATATCTGGTCCGCTTGCACGAGGTCAGACCACGATGACGTTCCGG 1237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTCTTGGCGGTGCCAACCCGGCTCTGGTGACTGCCACCACGCTCACCGAGGAAGACGTCG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCGCCACCATCGGGTACCTGGTGCGCCTGCACGAGGCCCAGACCACGATGACCGCCCCCG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="acyl-CoA dehydrogenase, putative"
/protein_id="AAK44926.1"
/db_xref="GI:13880223"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 124.8; DB 1;
Pred. No. 3.1e-12;
0; Mismatches 42;
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/product="hypothetical protein"
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                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=1
/transl_table=11
                                                                               11859. .13487
/gene="MT0701"
11859. .13487
/gene="MT0701"
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al Similarity 77.6%;
166; Conservative
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Best Local (
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Details of M. tuberculosis sequencing at the Sanger Centre are available on the World Wide Web.

(URL, http://www.sanger.ac.uk/Projects/M_tuberculosis/) CDS have been renumbered from the original cosmid submissions but the old gene designations are in brackets after the new gene numbers. Gene prediction was based on a Hidden Markov Model of TB genes implemented in TBparse (Krogh) supplemented with visual inspection of positional base preference in codons, especially where there is an increase in the observed/expected third position q + c.

CAUTION: In some cases we may not have predicted the correct intitation codon. Where possible we choose an initiation codon (atg, qt, or ttg) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most upstream
                                                                                                                                                                                                                           Bacteria; Firmicutes; Actionbacteria; Actinobacteridae;
Actionbycetales; Corynebacterineae; Mycobacteriaceae;
Mycobacterium; Mycobacterium tuberculosis complex.

I (bases 1 to 1977)
Cole. S.T., Brosch, R., Parkhill, J., Garnier, T., Churcher, C.,
Harris, D., Gordon, S.V., Eiglmeler, K., Gas, S., Barry III, C.E.,
Tekaia, F., Badcock, K., Basham, D., Brown, D., Chillingworth, T.,
Connor, R., Davies, R., Devlin, K., Feltwell, T., Gentles, S.,
Hamlin, N., Holroyd, S., Hornsby, T., Jagels, K., Kroph, A., McLean, J.,
Moule, S., Murphy, L., Oliver, S., Osborne, J., Quali, M. A.,
Rajandream, M. A., Rogers, J., Rutter, S., Seeger, K., Skelton, S.,
Squares, S., Sqares, R., Sulston, J.E., Taylor, K., Whitehead, S. and
Barrell, B. G.
Deciphering the biology of Mycobacterium tuberculosis from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Rv0654, (MTC1376.22), len: 501. unknown, FASTA score: Q53353 LIGNOSTILBENE-ALPHA,BETA-DIOXYGENASE (485 and ) Opt:280 z-score: 330.1 E(): 2.3 = 11, (28.5% identity in 523 anaverlap). Also similar to M. tuberculosis protein MTCX21C12.07c (29.5% identity in 522 an overlap).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (11-JUN-1998) Submitted on behalf of the Mycobacterium tuberculosis sequencing and mapping teams, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CBIO 15A Unite de Genetique Moleculaire Bacterienne, Institut Pasteur, 28 rue du Docteur Roux, 75724 Paris Cedex 15, France E-mall: parkhill@sanger.ac.uk on Jun 27, 1998 this sequence version replaced 91:2143285.
             BCT 03-AUG-2001
                                              complete genome; segment 32/162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="agga, possible rbs upstream of Rv0654"
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/strain-"H37Rv"
                linear
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/db_xref-"GI:2143307"
                DNA
19770 bp
Mycobacterium tuberculosis H37Rv
295972 AL123456
295972.1 GI:3261790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complete genome sequence
Nature 393 (6685), 537-544 (1998)
                                                                                                                                                                         Mycobacterium tuberculosis H37Rv
                                                                                                                                                                                                       Mycobacterium tuberculosis H37Rv
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68. .1573
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 (bases 1 to 19770)
Parkhill, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1. .19770
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
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         LOCUS
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KEYWORDS
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ORGANISM
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REFERENCE
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/db_xref="SPTREMBL:006785"

RESULT 15 MTCI376

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complement(3691.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         //Journal Action (1976.21), len: 359, abc transporter, FASTA score: YRBE ECOLI P45393 hypothetical abc transporter atp-binding (269 aa) opt: 644 z. score: 721.8 E(): 3.4e-33 (38.5% identity in 244 aa overlap); contains PS00017 AFP/GTP-binding site motif A, PS00211 ABC transporters family signature, highly similar to M. leprae MKL_MYCLE P00765 possible ribonucleotide transport app. (347 aa) opt: 2021 z-score:2244.4 E(): 0, (92.2% identity in 335 aa overlap). Also similar to many otherM. tuberculosis ABC transporters eg. MTCY253:24 (33.6% identity in 241 aa overlap).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=1
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RLPYAWNESYSPARVGYWFREGGNEDVRWFDIEPCYYYHPLNAYSECRNGAEVLVLDVV
RYSRWFDRDRRGPGGOSRPSLMFTINLATGAVTACRDDRAGEPRINETLVGGPHR
FAYTVGIEGGFLVGAGAALSTPLYXTOCCYTGSSTVASLDPDLLIGENVFVPRNSSRRAE
DDGILMGYGWHRGRDEGOLLLLDAQTLESIATVHLPQRVPMGFHGNWAPTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /transl_table=11
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/gene="Rv0657c"
complement(3530, .3685)
/gene="Rv0657c"
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1585. off
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Complement(3761...3090)

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complement(3761...4477)

/gene="Rv0658c"

complement(3761...4477)

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complement(3761...4477)

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/de="Rv0658c"

/de="Rv06678c"

/de="Rv0678c"

/de="Rv0678c"
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Complement(1480...483)
Complement(1753...5061)
Gene="Rv0659c"
Complement(4753...5061)
Gene="Rv0659c"
(MTC1376.17), len: 102; unknown, similar to Yw28_MYCTU (0.10867 hypothetical 12.3 kd protein cy39.28 (114 aa), fasta scores; opt: 144 z-score: 213.2 E():
MYCY059.22 (32.7% identity in 107 aa overlap, Also similar to Andrea (1250...)
/db_xref="SPTREMBL:006782"
/translation="MSVTQIDLDDEALADVMRIAAVHTKKEAVNLAMRDYVERFRRIE
ALARSRE"
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LVSELELTAVENRVESDCVVNFDNIHTLPRTAFRRRITRLSPARLHEACQTLRASTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10818 GGCTGCATGTCGGCGAGCC-----CATCACGTCGTCGACGACGAGAAGAAGACGTCG 10871
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complement(5048. .5293)
/gene="Rv0660c"
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Db 10932 GCGCCTCGAGGTGCCGGTGGAAACCGACGACAT 10965

Search completed: November 13, 2002, 01:25:30 Job time : 681.07 secs

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OM nucleic

Run on:

rotal number

Minimum Maximum Database

Searched:

Sequence:

Title:

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B1914449 603179425
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BEZ15908 HV_CEDOUO
B1722737 1031063H0
AL509174 AL509174
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BM479096 AGENCOUNT
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AL053113 DTGS0P111
BG55697 BM1_40_G0
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BG3228B1 EM1_16_G0
BG3228B1 EM1_16_G0
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BG3228B1 FML1666
BG32695 TAEL1566
BG24605 TAEL1566
BG36099506 1030011E0
AU067540 AU067540
AU065740 AU065750
BGC09956 Mus muscu
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           UI-H-COO-
603179425
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Murugasu-Oei,B., Tay,A. and Dick,T.
Upregulation of stress response genes and ABC transporters in anaerobic stationary-phase Mycobacterium smegmatis
MOI. Gen. Genet. 262 (4-5), 677-682 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mycobacterium smegmatis
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mycobacterium Laboratory
Institute of Molecular and Cell Biology
No Medical Drive, Singapore 117609, Republic of Singapore
Tel: 65 874 3011
Fax: 65 779 1117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: mcbbom@imcb.nus.edu.sg
Insert Length: 1282 Std Error: 0.00
Seg primer: T3 Forward; T7 Backward.
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                                                               AL509174
AL509174
BL2995346
BC415787
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BC41580
BM100319
AV104150
BC66613
BC666613
BC66
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BQ246063
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BQ809506
AQ936743
BG321153
AU067540
AU051760
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                           BI914649
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1. .1282
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A1770311.1 GI:6742680
                         source
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AI770311/c
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BJ233830 BJ238830
BG908023 TaLr1164F
BJ258518 BJ258518
BEA18320 SCL024 FO
BG907534 TaLr1160G
                                                                                                           (without alignments) 3037.202 Million cell updates/sec
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                                                                                              ; Search time 1109.13 Seconds
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              GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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                                                                                                                                                                                                                                                                            of hits satisfying chosen parameters:
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Maximum Match 100%
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BG908023
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                                                                     nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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9b_htc:*
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9b_est4:*
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BG908023
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                                                                                                                                                                                        // ACCE—"Vector: Landar State Merricoll were disrupted using a Mini bead beater (Biospec). RNA was isolated using the RNeasy protocol (Qiagen). Purified RNA was subjected to 2 rounds of digestion with RNase-free DNase I (Promega). DNase I was heat-inactivated at 75cC for 5 min. and removed by using RNeasy columns followed by phenol extraction and ethanol precipitation. The RNA preparations were confirmed to be free of genomic DNA contamination by carrying out PCR and RT-PCR using the Access kit (Promega) and primars specific for the histone-like protein gene hip (Lee et al., 1998). cDNA was synthesized using random hexamer primers (Promega) and Stratagene's cDNA synthesis kit. CDNA fragments were ligated into lambda 2AP II vector and packaged in vitro using Stratagene reagents.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BJ233830 Y. Ogihara unpublished cDNA library, Wh_e Triticum aestivum cDNA clone whe7g20 5', mRNA sequence.
BJ233830. GI:20050958
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="Mycobacterium anaerobic stationary phase library"
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/organism="Mycobacterium smegmatis"
/strain="mc2155"
/db_xref="taxon:1772"
                                                                                                                                                                   /lab_host="E. coli XL1-Blue MRF'"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Triticum aestivum"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 CCGAGGTGCCGGTTGAGACCGACGACAT 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCGAGGTTCCCGTCGAGGTCGACGACAT 29
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Location/Qualifiers
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/clone_lib="Y. Ogihara unpublished cDNA library, Wh_e"
/tissue_type="seed DPA10"
/dev_stage="seed DPA1
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Trittceae, Trittcum.

Trittceae, Trittcum.

Trittceae, Trittcum.

Toutier, S., Dong, G. and Walsh, A.

Wheat functional genomics - Thatcher Lrl cDNA library
Unpublished (2001)
Contact: Dr. Sylvie Cloutier
Cereal Research Centre, Agriculture and Agri-food Canada
195 Dafoe Rd, Winnipeg, MB, Canada R3T 2M9
Tel: (204) 983-4604
Email: scloutier@em.agr.ca
was cloned directionally, not all sequences generated with reverse
primer were from the S' end (same with forward primer and 3' end).
Average inset size is >2.2 kb
Plate: 164 row: F column: 05
Seq primer: M13 Reverse.

Location/Qualifiers
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/db_xref="taxon:4565"
/clone="TaLrl164F05"
/clone_lib="TaLrl"
/db_xref~"taxon:4565"
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BG908023.1 GI:14315686
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1. (bases 1 to 644)

2. (a) ogihara,Y. and Murai,K.

2. Expressed genes in Triticum aestivum

2. Unpublished (2002)

2. Contact: Tadasu Shin-i

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2. National Institute of Genetics

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3. Tel: 81-559-81-6855

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5. Fax: 81-559-81-6855

6. Fax: 81-559-81-6855

6. Fax: 81-559-81-6855

7. Tel: 81-559-81-6855

7. Tel: 81-559-81-6855
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//Olltivar="Chinese Spring"
//db_xref="taxon:4565"
//clone_"wh8d07"
//clone_lib="Y. Ogihara unpublished cDNA library, Wh_h"
//tissue_type="spike at heading date"
//dev_stage="Feekes' scale 10.5"
//dev_stage="Feekes" scale 10.5"
//dev
                   /dev_stage="14 Days old"
/lab_host="E. coli XLOLR"
/note="Vector: Lambda ZapII; mass excised in plasmid
vector pBx-CMV (Stratagene); Site_1: EcoRI; Site_2: XhOI;
mRNA obtained from wheat NIL Thatcher Lrl 24 hours after
incoulation with leaf rust pathogen Puccinia triticina
race BBB carrying the avirulence gene Avrl."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              684 bp mRNA linear EST 08-7 BJ258518 Y. Ogihara unpublished cDNA library, Wh_h Triticum aestivum cDNA clone whh8d07 5', mRNA sequence. BJ258518 1 GI:20081256 EST.
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0
                                                                                                                                                                                                                                                                                                                                             Length 649;
                                                                                                                                                                                                                                                                                                                                         22.6%; Score 47; DB 12; Length 64
57.0%; Pred. No. 0.97;
ive 0; Mismatches 65; Indels
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                                                                                                                                                                                                                                              130 t
/tissue_type="Leaf tissue"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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es 86; Conserv
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Best Local S
Matches 86
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Eukaryotta; Viridim plantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; Pooldeae; Triticeae; Triticum.

1 (bases | Triticum.

1 (bases | to 1013)

Anderson, O.A., Appels, R., Bailey, P., Blake, T., Close, T., Cloutier, S., Dubcovsky, J., Feuillet, C., Gale, M., Graner, A., Gustafson, P., Largidge, P., Lazo, G.Y., Jao, J., Jao, J., Joudrier, P., Langridge, P., Lazo, G.Y., Lin, J.J., McGulre, P., Oqihara, Y., Pecchioni, N., Qualset, C., Schuch, W., Selvaraj, G., Shariflou, M., Sorrells, M., Marburton, M. and Wenzel, G.

Expressed Sequence Tags for Species of the Triticeae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BE418320 1013 bp mRNA linear EST 24-JUL-2000 SCL024.F08R990724 ITEC SCL Wheat Leaf Library Triticum aestivum cDNA clone SCL024.F08, mRNA sequence.
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/culivar="Thatcher Lr1"
/db_xref="taxon:4565"
/clone="SCLO4.F08"
/clone=lib="ITEC SCL Wheat Leaf Library"
/tissue_type="young leaf"
/dev_stage="after 24 hour challenge with LR-AVR1"
/note="vector: Lambda ZAP: 1.0 Kbp average insert size."
a 237 c 271 g 223 t 36 others
performed in the OD Anderson lab (all other authors)." 180 a 178 c 190 g 136 t
                                                                                                                                                                                                                                             83 CACCAGCTCCACGCTGACCGAGGAAGACGTCGTCGCCACCATCGAGTACCTGGTCCGCCT 142
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Tel: 204 983 2340
Fax: 204 983 4604
Email: scloutier@em.agr.ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                               Length 684
                                                                                                                                                                  Indels
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                                                                                                          Score 47; DB 13
Pred. No. 0.97;
                                                                                                                                                               0; Mismatches
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BE418320.1 GI:9416166
                                                                                                       Query Match 22.6%;
Best Local Similarity 57.0%;
Matches 86; Conservative
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Triticum aestivum
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source
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BM987859/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; Pooideae;
Triticae; Triticum.

E 1 (bases 1 to 363)
S (loutler, S., Dong, G. and Walsh, A.
Wheat functional genomics - Thatcher Lrl cDNA library
Unpublished (2001)
Contact: Dr. Sylvie Cloutier
Cereal Research Centre, Agriculture and Agri-food Canada
195 Dafoe Rd, Winnipeg, MB, Canada R3T 2M9
Tel: (204) 983-4604
Email: Scloutiereem.agr.ca
was cloned directionally, not all sequences generated with reverse
primer were from the 5', end (same with forward primer and 3' end).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib= raus.
/tissue_type="Leaf tissue"
/dev_stage="leaf tissue"
/dev_stage="leaf"
/
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0
                                                                                                                                                                                                                                                                                                                    BG907534 363 bp mRNA linear EST 05-JUN-2001 Talr1160G09R Talr1 Triticum aestivum cDNA clone Talr1160G09 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            83 CACCAGCTCCACGCTGACCGAGGAAGACGTCGTCGCCACCATCGAGTACCTGGTCCGCCT 142
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CACCAGCTCCACGCTGACCGGGAAGACGTCGCCCCCACCATCGAGTACCTGGTCCGCCT 142
                                                       244 CAAGATCGCCAAGGACACCCGCAACGCCGCCACCTGCGCCATCAAGGTGCTCGACCGCAA 303
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Pred. No. 2;
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/db_xref-"taxon:4565"
/clone-"TaLrl160609"
/clone_lib-"TaLrl"
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                                                                                                                                                                                                                                                                                                                                                                                    mRNA sequence.
BG907534
BG907534.1 GI:14315210
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56.3%;
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BG907534
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RESULT 7

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UI-WOOD asx-f-09-0-UI.s1 WCI_CGAP_Sub9 Homo saplens CDNA clone IMAGE:5860361 3', mRNA sequence.
BM987859 BM987859.1 GI:19707248
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1 (bases 1 to 468)
Zhang, H., Weschke, W., Michalek, W., Stein, N. and Graner, A.
EST sequencing and analysis in barley (2002)
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BQ463007 468 bp mRNA linear EST 30-MAY-2002
HI02L18r HI Hordeum vulgare cDNA clone HI02L18 5-PRIME, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Vector: pBluescript SK+; Site_1: EcoRI (5'-end of CDNA); Site_2: XhoI (3'-end of CDNA); Due to a cloning artefact caused by the kit, in most cases the EcoRI site is NOT present, as well as the EcoRIadapter used for cloning. To excise the insert, restriction sites upstream EcoRI should be used (e.g. bamHI, Sali, PStI). NOTE: Also due to the cloning system used Blue/white selection for recombinats is not 100% reliable.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Hordeum vulgare"
/cultivar="Barke"
/cultivar="Barke"
/clone="H102LiB"
/clone="H102LiB"
/clone="H102LiB"
/dev.stage="female inflorescences"
/dev.stage="female inflorescences"
/lab_host="XL10-Gold"
/lab_host="XL10-Gold"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Stein Nils
Molecular Markers Group, Department Genbank
Institute of Plant Genetics and Crop Plant Research (IPK)
Corresstr. 3, 06466, Gatersleben, Germany
Tel: 039482-5522
Fax: 039482-5522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: stein@ipk-gatersleben.de
Insert Length: 468 Std Error:
Plate: 2 row: L column: 18
Seq primer: M13rev.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
1. .468
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Anote—"Organ: Darin; Vector: pCMV-SPORT6; Site_1: Not!; Site_2: ECORV (destroyed); RNA source anonymous pool of 3 fetal brains, female age 20 weeks, female age 24 weeks, and male age 26 weeks. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon directionally cloned (EcoRV site is destroyed upon O.7-3.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 017. Note: this is a NIMGC Library."
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                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 74).

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
         603179425F1 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5243431 5'
                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65 TACGACATCGCGTCGCTTGTGGGCCCACGAGTTCGAGCGGGTCATTGACCAGCACGGCTGC 124
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/db_xref="taxon:9606"
/clone="IMAGE:5243431"
/clone_lib="NHIMGC_121"
/lab_host="DHI0B"
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Location/Qualifiers
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                                    mRNA sequence.
B1914649
B1914649.1 G1:16178742
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TITLE
JOURNAL
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//Clone="IMAGE:586076"
//Lissue_type="mixed"
//Lissue:
//Lissues:

                                                                                                                                                                                                              Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Gapbs refmail nih.gov
Tissue Procurement: Dr. Jose Mercuende
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://fmage.llnl.gov
sequence: 6-67, >MLTIC#LTR/MalR
Seq primer: M13 FORWARD
POLYA-Ves:
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                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutherla: Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 479)
NCI-CGAP http://www.ncbl.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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TAG_TISSUB-Bladder Carcinoma
TAG_SEQ-AGAGC 132 g 111 t
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Best Local Similarity 54.9%; Pred. No. 2.3;
Matches 89; Conservative 0; Mismatches
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Contact: Wing RA
Clemson University Genomics Institute
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1 (bases 1 to 988)
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Development of a genetically and physically anchored EST resource for barley genomics: Blumeria infected incompatible (Mla6) seedling Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       //note="Organ: brain; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: ECORV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27 yo. Library is oligo-dr primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.5 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber this is an III—MGC Library.

**Table 1.** A state of the constructed of the clones and was constructed by C. Gruber this is an III—MGC Library.

**Table 1.** A state of the constructed by C. Gruber this is an III—MGC Library.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear EST 23-OCT-2001
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                                                                                                                                                                                                                          DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
Clone distribution: MGC clone distribution information can be
Clone distribution: MGC clone distribution information can be
thatp://image.llnl.gov
Plate: LLAMI1485 row: h column: 21
High quality sequence stop: 797.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   75 GATCCGATCACCAGCTCCACGCTGACCGAGGAGGACGTCGTCGCCACCATCGAGTACCTG 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   163 GAGGCCATCGCGCGCCTCATGCCCAAGGTCGTGCGCGTCCTGGAGATCCTGGAGGTGCTG 222
     1 (bases 1 to 898)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                         Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

The strain of the strausberg, Ph.D.

Tissue Procurement: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9666"
/clone="IMAGE:5194052"
/clone_lib="NHH-MGC_l14"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   dq 886
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Local Similarity 54.9%;
tes 89; Conservative
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TITLE
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/note-Notcor: lambda2AP; Site_1: ECOR1; Site_2: Xhol:
/note-Notcor: lambda2AP; Site_1: ECOR1; Site_2: Xhol:
C.I. 16151 (Mla6) plants were greenhouse grown in the R
Wise lab at Iowa State University, Ames, IA; 7 day old
green seedlings were challenged with isolate 5874 (AvrMla6)
) of Blumeria graminis f. sp. hordel, and leaves were
harvested 20 and 24 hr post-incoulation and snap frozen;
uninoculated leaves were harvested 20 hr post-incoulation
(Wel, Wise). In the TJ Close lab at the University of
California, Riverside, total RNA was prepared from each
sample pool, equal quantities of all three RNA pools were
combined, poly(A) RNA was purified from the mixture, one
primary unamplified cDNA library was made, and 1 million
pfu were in vivo excised to give pBluescript SK(-) cDNA
phagemids (Choi, Close). Phagemids were plated and picked
at the Clemson University Genomics Institute (CUGI) (Begum
, Palmer, Frisch, Atkins and Wing). Plasmid DNA
preparations, DNA sequencing and sequence analysis were
performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates
, Rambo, Maln). The sequence has been trimmed to remove
vector sequence and contains a minimum of 100 bases of
phred value 20 or above. For more details on library
preparation and sequence analysis see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        see Close TJ, Wing R, Kleinhofs A, Wise R (2001)
Genetically and physically anchored EST resources for
bariety genomics. Bariety Genetics Newsletter 31:29-30.
(http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)*
295 C 327 g 152 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:4513"
/clone="HV_CEb0001J22f"
/clone=1lb="HOrddeum vulgare seedling green leaf EST
/lsrary HVCDNA0005 (Blumeria challenged)"
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55.0%; Pred. No. 3.1;
tive 0; Mismatches 72;
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                                  100 Jordan Hall, Clemson, SC 29634, USA
                                                                                                                                                                                                                                                                                                                                1. .988
/organism="Hordeum vulgare"
                                                                                                                                                                                                                                                                                                                                                                                                             (Mla6)"
                                                                                                                                                                                                            Seq primer: AATTAACCCTCACTAAAGGG
High quality sequence stop: 596.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                         /cultivar-"CI16151
                                                                                                                                          Email: rwing@clemson.edu
Total hq bases = 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 55.0%
Matches 88; Conservative
Clemson University
                                                                     Tel: 864 656 7288
Fax: 864 656 4293
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ISM Hordeum vulgare

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Manollophyta; Liliopsida; Poales; Pooldeae;

Triticeae; Hordeum.

CE I (bases 1 to 686)

RS Michalek,W. Weschke,W., Pleissner,K.-P. and Graner,A.

EST sequencing and analysis in barley
Unpublished (2000)

Contact: Michalek W
Institute for Plant Genetics and Crop Plant Research
Corrensstr. 3, D-06466 Gatersleben, Germany
Email: michalekelpk gatersleben, Germany
Email: michalekelpk gatersleben.de, http://pgrc.ipk-gatersleben.de
Seq primer for 5'end.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /noce="Vector: plasmid pBK-CMV; Site_1: EcoRI; Site_2:
XhoI; mRNA was made from developing caryopsis (3.-15.DAP)
of spring bariely variety 'Barke', a high quality malting
variety. Cloning sites: EcoRI (5'-end of cDNA) and XhoI
(3'-end of cDNA). NOTE: Due to a cloning artefact caused
by the kit, in most cases the EcoRI site is NOT present,
as well as the EcoRI adapter. Average insert size is ikb
Sequence trimming: Vector sequences and sequence ends were
trimmed from the 5'-and 3'-end until a 50 bp window
contains less than two ambiguities. The maximum length was
set to 700 bp=
set to 702 gp 98 t 8 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ανοδ///1
nbxb0075L01f CUGI Rice BAC Library Oryza sativa genomic clone
nbxb0075L01f, DNA sequence.
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Oryza sativa.

Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Enhartoclodaes; Oryzeae; Oryza.

1 (bases 1 to 877)

Wing, R.A. and Dean, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism-"Hordeum vulgare"
/cultivar-"Barke"
/db_xref="taxon:4513"
/clone="HY10020v"
/clone="HY10020v"
/clone="HY10020v"
/i.:DAP)"
/tissue_type="developing caryopsis (3.-15.DAP)"
/lab_host="XLOLR"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /strain="Cc-1690 wild type mt+ 21gr"
/strain="Cc-1690 wild type mt+ 21gr"
/db.xref="taxon:3055"
/clone_lib="C. reinhardtii Cc-1690, Stress II (normalized
), Lambda 2ap II"
/note="Vector: pBluescript II SK-; Site_l: EcoRI; Site_2:
XhoI; Stress condition II library, constructed by John
Davies and Jeffrey McDermott, combines cDNAs from Cc-1690
cells grown to mid-log phase in TAP (NH4+ - containing)
and shifted to TAP - NO3* (2Afrs); H2 production
conditions (0, 12hr, 24hr) see Melis et al.,(2000) Plant
Phys. 122: 127-135; TAP + H202 (1, 12, 24 hr); TAP +
sorbitol (1, 2, 6, 24 hr); TAP + Containing)
sorbitol (1, 2, 6, 24 hr); TAP + Containing)
sorbitol (1, 2, 6, 24 hr); TAP + Containing)
sorbitol (1, 2, 6, 24 hr); TAP + Containing)
sorbitol (1, 2, 6, 24 hr); TAP + Containing and shifted from each sample, pooled and cDNA
synthesized. The cDNA was directionally cloned into lambda
Zap II (Stratagene) in the EcoRI (5) and XhoR (3)
sites: pBluescript II SK- plasmids were excised from the
lambda ZAP clones by superinfection with ExAssist
(Stratagene) phage. The library was normalized using
method 4 described in Bonaldo et al., (1996) Genome
Research 6: 791-806."
                                                                                                                                                                           Grossman, A. Chang, C. M., Davies, J., Harris, E., Hauser, C., Lefebvre forosman, A., Chang, C. -W., Davies, J., Harris, E., Hauser, C., Lefebvre , P., Mobermott, J.P., Shrager, J., Silflow, C. and Stern, D. Analyses of the Chlamydomonas reinhardtii Genome: A Model, Unicellular System for Analyzing Gene Function and Regulation in Unpublished (2001)
Contact: Charles Hauser DCMB box 91000
Duke University
Durham, NC 27708-1100
Tel: 919 613 8177
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                                                                                                     Chlamydomonas reinhardtii
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: chauser@duke.edu.
  BI722737
BI722737.1 GI:15698432
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                                                                                                                                                                                                                                                                                                                                                                                                                                      /strain="Japonica"
/strain="Japonica"
/cultivar="Nipponbare"
/cultivar="Nipponbare"
/db_ref="taxon:4530"
/clone="lib="CuGI Rice BAC Library"
/clone="lib-"cuGI Rice BAC Library Rice In Library Rice Rice In R
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Chlamydomonadaceae; Chlamydomonas.
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A BAC End Sequencing Framework to Sequence the Rice Genome Unpublished (1998)
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Tel: 864 656 7288
Fax: 864 656 4293
                                                           Contact: Wing RA
Clemson University Genomics Institute
Clemson University
                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Oryza sativa"
                                                                                                                                                                                                                                    Email: rwing@clemson.edu
Seg primer: TAATAGGACTCACTATAGGG
Class: BAC ends
High quality sequence stop: 85.
Location/Qualifiers
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// Crganisma. Chlamydomonas reinhardtii...
// Strain="CC-1690 wild type mt+ 21gr"
// Abraref="texaon:3055"
// Clone_11b="C. reinhardtii CC-1690, Stress II (normalized
), Lambda Zap II...
// Lambda Zap II...
// Abraref="texaon:3055"
// Clone_11b="C. reinhardtii CC-1690, Stress II (normalized
), Lambda Zap II...
// Abraref="texaon:305"
// Abraref="texaon:305
Grossman, A., Chang, C.-W., Davies, J., Harris, E., Hauser, C., Lefebvre, P., McDermott, J.P., Shrager, J., Silflow, C. and Stern, D.
Analyses of the Chlamydomonas reinhardtii Genome: A Model,
Unicellular System for Analyzing Gene Function and Regulation in
Vascular Plants. Project: 1031
Unpublished (2001)
DCMB Box 91000
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Job time : 1134.63 secs
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Location/Qualifiers
1. .568
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Durham, NC 27708-1000
Tel: 919 613 8159
Fax: 919 613 8177
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Sequence 1, Appli
Sequence 3, Appli
Sequence 5, Appli
Sequence 7695, Ap
Sequence 1, Appli
Sequence 7738, Ap
Sequence 3, Appli
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Sequence 190, Ap
Sequence 7740, Ap
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1: /cgn2_6/ptodata/2/pubpna/USO7_PUBCOMB.seq:*

2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*

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4: /cgn2_6/ptodata/2/pubpna/USO6_NEW_PUB.seq:*

5: /cgn2_6/ptodata/2/pubpna/USO6_NEW_PUB.seq:*

6: /cgn2_6/ptodata/2/pubpna/USO8_NEW_PUB.seq:*

7: /cgn2_6/ptodata/2/pubpna/USO8_NEW_PUB.seq:*

8: /cgn2_6/ptodata/2/pubpna/USO8_NEW_PUB.seq:*

9: /cgn2_6/ptodata/2/pubpna/USO9_NEW_PUB.seq:*

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7690, Ap 21, Appl 109, App 111, App 7871, Ap 7, Appl1 3, Appli 1, Appli 560, App 7696, Ap Appl Appli Sequence Seq Sequence Sequence Sequence US-09-861-289-21 US-09-755-830-2 US-09-755-830-2 US-09-861-289-3 US-09-954-314-16 US-09-954-314-16 US-09-954-314-16 US-09-199-1314-21 US-09-199-1314-21 US-09-199-1314-7 US-09-199-1314-7 US-09-195-124-109 US-09-924-417-58 US-09-924-417-58 US-09-924-417-58 US-09-924-417-58 US-09-917-900-6 US-09-924-417-58 US-09-924-417-58 US-09-924-417-58 US-09-924-417-58 US-09-924-417-58 US-09-924-417-58 US-09-924-417-58 US-09-937-90-97-97-97-98 US-09-815-625-3 US-09-815-625-3 US-09-764-887-452 US-09-764-887-452 US-09-371-307-70 US-09-815-424-4071 US-09-815-424-4071 100 100 100 100 100 100 100 100 100 

## ALIGNMENTS

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GTCGGCGATCCGATCACCAGCTCCACGCTGACCGAGGAAGACGTCGTCGCCACCATCGAG 128
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                                                                                                            APPLICANT: STEPHAN, Hans
APPLICANT: KREUTER, Caroline
APPLICANT: KREUTER, Caroline
APPLICANT: HERMANN, Thomas
APPLICANT: FEFFERIE, Walter
APPLICANT: BINDER, Michael
TITLE OF INVENTION: NUCLECTIDE SEQUENCES WHICH CODE FOR THE rpsL GENE
FILE REFERENCE: 204209US0
CURRENT APPLICATION NUMBER: US/09/984,711
CURRENT FILING DATE: 2001-10-31
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PATENTIN VEXION 3.1
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Pred. No. 1.8e-12;
0; Mismatches 63;
                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Corynebacterium glutamicum
US-09-984-711-5
Sequence 5, Application US/09984711; Patent No. US20020119549A1
GENERAL INFORMATION:
APPLICANT: MOECKEL, Bettina
APPLICANT: BATHE, Brigitte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40.0%;
llarity 67.0%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LUCATION: (702)...(4196); OTHER INFORMATION:
US-09-984-711-5
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Matches 134; Conserv
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LENGTH: 5096
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Best Local 8
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RESULT 4
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Patent No. US2002015557A1

GENERAL INFORMATION:
APPLICANT: MOCKEL, BETTINA
APPLICANT: HANS, STEFAN
APPLICANT: HERMANN, THOMAS
APPLICANT: PFEFFERLE, WALTER
APPLICANT: PFEFFERLE, WALTER
APPLICANT: PFEFFERLE, WALTER
APPLICANT: BINDER, MICLEATIOR
APPLICANT: BINDER, MICLEOTIDE SEQUENCES WHICH CODE FOR THE rpsL GENE
FILE REFERENCE: 218472USOX
CURRENT APPLICATION NUMBER: US/10/075,460
CURRENT PFLING DATE: 2002-02-15
PRIOR FILING DATE: 2002-02-16
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-12-19
NUMBER OF SEQ ID NOS: 14
SEQ ID NO 5
LENGTH: 5099
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129 TACCTGGTCCGCCTGCACGAGGGCCAGCACACGATGACCGTCCCGGGCGGCGCACCGAGGTG 188
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Patent No. US20020119537A1

GENERAL INFORMATION:
APPLICANT: MOECKEL, Bettina
APPLICANT: HERMANN, Thomas
APPLICANT: HERMANN, Thomas
APPLICANT: BINDER, Malter
APPLICANT: BINDER, Malter
APPLICANT: The PROBLEM COME OF THE TOOL GENE
TITLE OF INVENTION: NUCLEOTIDE SEEQUENCES WHICH CODE FOR THE FOOL GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Pred. No. 1.8e-12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Corynebacterium glutamicum
                                                                                                    1755 CCAGTCGAGACCGATGACAT 1774
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                                                                             189 CCGCTTGAGACCGACGACAT 208
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Best Local Similarity 67.0%;
Matches 134; Conservative
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US-10-075-460-5
                                                                                                                                                                             RESULT 2
US-10-075-460-5
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Sequence 3, Application US/09887052
Patent No. US2002019537A1
GENERAL INFORMATION:
APPLICANT: MOCKEL, Bettina
APPLICANT: BATHE, Brigitte
APPLICANT: HERWANN, Thomas
APPLICANT: HERWANN, Thomas
APPLICANT: BINDER, Michael
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE rpoB GENE
FILE REFERENCE: 204212USOX
CURRENT APPLICATION NUMBER: US/09/887,052
CURRENT TILING DATE: 2001-06-25
PRIOR APPLICATION NUMBER: DE10107229:5
PRIOR PLICATION DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1695 TACCTGGTGCGTCTGCACGTGGTGAGCGCGTCATGACTTCTCCAAATGGTGAAGAGATC 1754
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Pred. No. 1.8e-12;
0; Mismatches 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 40.0%; Score 83.2; DB 10; Best Local Similarity 67.0%; Pred. No. 1.8e-12; Matches 134; Conservative 0; Mismatches 63;
FILE REFERENCE: 204212USOX
CURRENT APPLICATION NUMBER: US/09/887,052
CURRENT FILING DATE: 2001-06-25
PRIOR PPLICATION NUMBER: DE10107229.5
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PATENTIN VERSION 3.0
LENGTH: 5099
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                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Corynebacterium glutamicum
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Best Local Similarity 67.0°
Matches 134; Conservative
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; LOCATION: (702)...(4196)
US-09-887-052-3
                                                                                                                                                                                                                                                                                                                                       ; NAME/KEY: CDS
; LOCATION: (702)...(4196)
US-09-887-052-1
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Query Match 21.3%;
Best Local Similarity 55.1%;
Matches 87; Conservative
                        Zhang, Jie
Wang, Jian-Rui
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; LOCATION: (1612)..(2211)
US-09-816-828-9
                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
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US-09-815-242-7695
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: MOECKEL, Bettina
APPLICANT: HERWIN, Thomas
APPLICANT: HERWIN, Thomas
APPLICANT: HINGENIN, MUCLEOTIDE SEEQUENCES WHICH CODE FOR THE TPOB GENE
TITLE OF INVENTION: NUCLEOTIDE SEEQUENCES WHICH CODE FOR THE TPOB GENE
FILE REFERENCE: 204212USGX
CURRENT FILING DATE: 2001.06-25
PRIOR APPLICATION NUMBER: DE10107229.5
PRIOR FILING DATE: 2001.02-16
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PATENTIN UNIVERSIDATE
SEQ ID NO 5
LENGTH: 5099
                                                                                    1695 TACCTGGTGCGTCGCACGTGAGCGCGTCATGACTTCTCCCAAATGGTGAAGAGATC 1754
1635 GGTGGCGACCACGATGGTTTGATGATGATGATGAGGACATCGCAACCACCATCGAG 1694
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                                                                TACCTGGTCCGCCTGCACGAGGCCCACACACGATGACCGTCCCGGGCGCGCACCGAGGTG 188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Corynebacterium glutamicum
                                                                                                                                                                                                                                                                                             Sequence 5, Application US/09887052 Patent No. US20020119537A1
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Patent No. US20020150898A1
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APPLICANT: Tang, Y. Tom
APPLICANT: Should bing
APPLICANT: Asundi, Vinod
APPLICANT: Ren, Felyan
APPLICANT: Ren, Felyan
APPLICANT: Way, Aidong J.
APPLICANT: Way, Yunqing
APPLICANT: Way, Yunqing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; NAME/KEY; CDS
; LOCATION: (702)..(4196)
US-09-887-052-5
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US-09-816-828-9
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1984 ATGCCCAACGCGTGGGGCACGTGGACGACTGCCCAACGCGCTGTCCCCTGACGAC 2043
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Pred. No. 0.0066;
0; Mismatches 71; Indels 0;
APPLICANT: Wang, Jian-Rui
APPLICANT: Wang, Jian-Rui
APPLICANT: Wang, Jian-Rui
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. UG20020150898A1el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 791CIP2E
CURRENT APPLICATION NUMBER: US/09/816,828
CURRENT FILING DATE: 2001-03-22
PRIOR APPLICATION NUMBER: 09/770,160
PRIOR FILING DATE: 2001-01-26
PRIOR FILING DATE: 2000-04-18
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PL-Lgenes Version 2.0
SEQ ID NO 9
LENGTH: 2329
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APPLICANT: Cyskind, Judith W.
APPLICANT: Eyskind, Judith W.
APPLICANT: Trawlck, John D.
APPLICANT: Trawlck, John D.
APPLICANT: Trawlck, John D.
APPLICANT: Trawlck, John D.
APPLICANT: Tammoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELTTRA.011A
CURRENT APPLICATION NUMBER: 00/19,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR PRILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PRILING DATE: 2000-11-27
PRIOR PRILING DATE: 2000-12-27
PRIOR PRILING DATE: 2000-12-27
PRIOR FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2044 CTGCACGCCCACAAGCTTCGGGTGGACCCGGTCAACTT 2081
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Patent No. US20020061569A1
GEMERAL INFORMATION:
APPLICANT: Haselbeck, Robert
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46 TCAACAAGAAGCTCGGCCTGCACGTCGGCGATCCGATCACCAGCTCCACGCTGACCGAGG 105
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                                                                                                                                                                                  TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Identification of Essential Genes in FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT APPLICATION NUMBER: 00/10-03-21
CURRENT APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-36
PRIOR FILING DATE: 2000-10-23
PRIOR PRILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR PRILING DATE: 2000-10-22
PRIOR APPLICATION NUMBER: 60/255,931
PRIOR PELING DATE: 2000-12-22
PRIOR PELING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-10-2-16
NUMBER OF SQL ID NOS: 14110
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Best Local Similarity 54.3%; Pred. No. 0.39;
Matches 75; Conservative 0; Mismatches 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATE: LEVINE, et al.

TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
FILE REFERENCE: 802502-2005.1

CURRENT APPLICATION NUMBER: US/09/771,161A

CURRENT FILING DATE: 2001-01-26

PRIOR APPLICATION NUMBER: 13676

PRIOR FILING DATE: 2000-11-28

PRIOR FILING DATE: 2000-6-15

PRIOR FILING DATE: 2000-06-15

PRIOR FILING DATE: 2000-06-15

PRIOR FILING DATE: 2000-06-15

PRIOR FILING DATE: 2000-06-15

PRIOR FILING DATE: 2000-06-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                          Carr, Grant J.
Yamamoto, Robert T.
                                                   Ohlsen, Kari L.
Zyskind, Judith W.
Wall, Daniel
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                                                                                                                      Trawick, John D.
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; LOCATION: (1)...(1437)
US-09-815-242-7738
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SEQ ID NO 7738
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US-09-771-161A-4
                                                                                                                    APPLICANT:
APPLICANT:
                                                                                                APPLICANT:
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APPLICANT: Park, Chong-Hun; SAMYANG GENEX CORPORATION
TITLE OF INVENTION: CANCER DIAGNOSIS METHOD USING CELL GROWTH INHIBITING AND CELL DIF
TITLE OF INVENTION: EREOF
TITLE OF INVENTION: 1998-12-12
PRIOR FILING DATE: 1998-12-12
PRIOR FILING DATE: 1998-12-30
WUMBER: OF SEQ ID NOS: 3
SOFTWARE: KOPATIN 1.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  294 AGGAGGAGGGCGACATCGCGCTGCAGATCCATTTTACGCTGATCCAGGCTTTCTGCT 353
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                                                                                                                                                                                                                                                            Length 1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              137 CCGCCTGCACGAGGGCCAGCACACGATGACCGTCCCGGGGGGGCGCACCGA 184
                                                                                                                                                                                                                                                            Score 38.4; DB 10;
Pred. No. 0.2;
0; Mismatches 81;
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NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7695
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; Patent No. US20020061569A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/09879833
Patent No. US20020055107A1
                                                                                             TYPE: DNA ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match 17.9%;
Best Local Similarity 52.6%;
Matches 81; Conservative (
                                                                                                                                                                                                                                                            Query Match 18.5%;
Best Local Similarity 51.8%;
Matches 87; Conservative
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CORGANISM: HL60 cell line
US-09-879-833-1
                                                                                                                                                                                         ; LOCATION: (1)...(1998)
US-09-815-242-7695
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                                                                                                                                                                NAME/KEY: CDS
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                                                                       LENGTH: 1998
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APPLICANT: Bougueleret, Lydie
APPLICANT: Bougueleret, Lydie
APPLICANT: Jobert, Severin
TITLE OF INVENTION: FULL_LENGTH HUMAN CDNAS ENCODING POTENTIALLY SECRETED PROTEINS
FILE REPERENCE: 78, US3.REG
CURRENT APPLICATION NUMBER: US/09/731,872
CURRENT FILING DATE: 1990-12-08
PRIOR FILING DATE: 1999-12-08
PRIOR FILING DATE: 1999-12-08
PRIOR RELIGATION NUMBER: US 60/187,470
NUMBER OF SEQ ID NOS: 482
SOFTWARE: PATENT PRIOR
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APPLICANT: Dumas Milne Edwards, Jean Baptiste
APPLICANT: Dumas Milne Edwards, Jean Baptiste
APPLICANT: Dumas Milne Edwards, Jean Baptiste
APPLICANT: Bougueleret, Lydie
APPLICANT: Jobert, Severin
TITLE OF INVENTION: FULL-LENGTH HUMAN CDNAS ENCODING POTENTIALLY SECRETED PROTEINS
FILE REFERENCE: 78.053.REG
CURRENT APPLICATION NUMBER: US 60/131,872
CURRENT FILING DATE: 2000-12-08
PRIOR APPLICATION NUMBER: US 60/189,629
PRIOR APPLICATION NUMBER: US 60/187,470
PRIOR APPLICATION NUMBER: US 60/187,470
NUMBER OF SEQ ID NOS: 482
SOFTWARE: Patent.pm
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Pred. No. 0.51;
0; Mismatches 64;
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54.0%; Pred. No. 0.52;
tive 0; Mismatches 64;
                          APPLICANT: Dumas Milne Edwards, Jean Baptiste
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54.0%;
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Best Local Similarity 54.09
Matches 75; Conservative
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ORGANISM: Homo sapiens
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      GENERAL INFORMATION:
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; LOCATION: 86..505
US-09-731-872-229
                                                                                                                                                                                                                                                                                                                                                                                                         : NAME/KEY: CDS
; LOCATION: 3..368
US-09-731-872-190
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LENGTH: 526
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LENGTH: 654
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Sequence 3, Application US/09879833
Patent No. US20020055107A1
GENERAL INFORMATION:
CANCEN DIAGNOSIS METHOD USING CELL GROWTH INHIBITING AND CELL DIAGNOSIS METHOD USING CELL GROWTH INHIBITING AND PROMOTER TITLE OF INVENTION: FREDERIC SYG99601
CURRENT APPLICATION NUMBER: US/09/879,833
CURRENT FILING DATE: 1998-12-12
PRIOR PAPLICATION NUMBER: KR 54933
PRIOR FILING DATE: 1998-12-12
PRIOR FILING DATE: 1998-12-30
NUMBER OF SEO ID NOS: 3
SOFTWARE: KOPATIN 1.5
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                                                                                                                                                                                                                                     Length 2451;
                                                                                                                                                                                                                                                                             Indels
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                                                                                                                                                                                                                               Score 37.2; DB 10;
Pred. No. 0.4;
0; Mismatches 68;
                                                                                                                                             COCATION: (1)..(2451)
COTHER INFORMATION: "n" can be any nucleotide 'a', US-09-771-161A-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        175 GCGCACCGAGGTGCCGGTTGAGACCGACGACAT 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   148 AGGCCAGCACACGATGACCGTCCCG 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-731-872-190
; Sequence 190, Application US/09731872
; Patent No. US20020102604A1
SOFTWARE: PatentIn version 3.0 SEQ ID NO 4
                                                                                                                                                                                                                                 Query Match
Best Local Similarity 53.4%;
Matches 78; Conservative
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Matches 81; Conservative
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                                       LENGTH: 2451
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
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                                                                                                                             NAME/KEY: -
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                                                      86 CAGCICCACGCIGACCGAGGAAGACGICGICGCCACCAICGAGIACCIGGICCGCCIGCA 145
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                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: HASELDECK, Robert
APPLICANT: HASELDECK, Robert
APPLICANT: HASELDECK, Rari L.
APPLICANT: Wall, Janiel
APPLICANT: Trawick, Judith W.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Tarwick, John D.
APPLICANT: Tamancto, Robert T.
APPLICANT: Wall, H. HOWARD
TITLE OF INVENTION: Indentification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT FILING DATE: 2000-103-21
PRIOR FILING DATE: 2000-05-26
PRIOR PAPLICATION NUMBER: 60/207, 727
PRIOR APPLICATION NUMBER: 60/207, 727
PRIOR APPLICATION NUMBER: 60/25, 625
PRIOR PLING DATE: 2000-11-27
PRIOR PELING DATE: 2000-10-33
PRIOR FILING DATE: 2000-11-27
PRIOR PELING DATE: 2000-11-27
PRIOR PELING DATE: 2000-10-33
PRIOR FILING DATE: 2000-10-33
PRIOR PLING DATE: 2000-10-33
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                                                                                                                                                                                                                                                                                                                                                                                       Sequence 7740, Application US/09815242 Patent No. US20020061569A1
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ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                 321 AGTACGTGTGTCAGCAGAC 339
                                                                                                                                                                              142 TGCACGAGGGCCAGCACAC 160
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US-09-815-242-7740
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RESULT 15 US-09-960-352-5073

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Sequence 5073, Application US/09960352
Patent No. US20020137139A1
GENERAL INFORMATION
GENERAL INFORMATION
APPLICANT: Warren, Wesley C.
APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
TITLE OF INVENTION: MUSCLER AND FAT DEPOSITION
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT APPLICATION NUMBER: US/09/960,352
SED ID NO 573
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                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INCRMATION: Clone ID: 22-LIB3058-020-Q1-K1-F9
US-09-960-352-5073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17.4%; Score 36.2; DB 10;
ilarity 49.2%; Pred. No. 0.63;
Conservative 0; Mismatches 98;
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Best Local Similarity
Matches 95; Conserv
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Sequence 1, Appl
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Sequence 3, Appl
Sequence 3, Appl
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Sequence 31, Appl
Sequence 31, Appl
Sequence 31, Appl
Sequence 31, Appl
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Sequence 57, Appl
Sequence 57, Appl
Sequence 4, Appli
Sequence 2, Appli
Sequence 1, Appli
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Sequence 1, Appli
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2286.857 Million cell updates/sec
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                                                                                                                            November 12, 2002, 15:56:36; Search time 27.8936 Seconds
                                                                                                                                                                                                                                              1 tcaaggagaagcgctacgac........ccggttgagaccgacgacat 208
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2: /cgn2_6/ptcdata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptcdata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptcdata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptcdata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptcdata/1/ina/PcTuS_COMB.seq:*
                 GenCore version 5,1.3
Copyright (c) 1993 - 2002 Compugen Ltd
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US-08-313-185-57
US-09-082-614A-57
US-09-029-603-4
US-09-103-840A-2
US-09-103-603-1
US-08-476-519-10
US-08-476-519-1
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-08-461-379A-31
-08-462-390B-31
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US-08-804-227C-7

US-08-804-138-1

US-09-382-106-1

US-09-382-106-1

US-08-138-104-79

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US-09-103-840A-2
US-09-103-840A-1
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-08-465-585C-31
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Maximum Match 100%
Listing first 45 summaries
                                                                                         - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 2000000000
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APPLICANT: Persing, David H.
APPLICANT: Persing, David H.
TITLE OF INVENTION: Detection of a Genetic Locus Encoding
TITLE OF INVENTION: Resistance to Rifampin in Mycobacterial Cultures and J
TITLE OF INVENTION: Clinical Specimens
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schwegman, Lundberg & Woessner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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Sequence 1, Sequence 7, A
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPOTER: IBM PC Compatible
COMPOTER: IBM PC COMPATIBLE
COMPOTER: IBM PC COMPATIBLE
COMPOTER: IBM PC COMPATIBLE
CORRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/250,030
FILING DATE: 26-May-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MULLING, AND M.
REGISTRATION NUMBER: 33,977
REFERENCE/DOCKET NUMBER: 150.105US1
TELEPRANICATION INFORMATION:
TELEPRANICATION INFORMATION INFORMATION INF
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US-08-797-831A-3
US-08-461-379A-11
US-08-461-379A-11
US-08-462-390B-11
US-08-462-390B-11
US-08-463-074B-11
US-08-403-852D-4
US-08-403-852D-4
US-08-201-84B-1
US-08-201-84B-1
US-09-231-81B-1
US-09-231-81B-1
US-09-231-81B-1
US-09-42B-517-1
US-09-103-840A-1
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US-08-250-030-1
; Sequence 1, Application US/08250030
; Patent No. 5643723
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 970 base pairs
         1036
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US-08-250-030-1
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RESULT 4
US-09-082-614A-57
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                 GCCTGCACGTCGGCGATCCGATCACCAGCTCCACGCTGACCGAGGAAGACGTCGTCGCCA 120
                                                                  CCATCGAGTACCTGGTCCGCCTGCACGAGGCCAGCACGATGACCGTCCCGGGCGGCG 180
                                                                                    61 GCCTGCACGTCGGCGATCCGATCACCAGCTCCACGCTGACCGAGGAAGACGTCGTCGCCA 120
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                                                                                                                                                                                                                                                                                 APPLICANT: Mayo Foundation for Medical Education and Research
APPLICANT: and Hoffmann-La Roche Inc.
TITLE OF INVENTION: Detection of a Genetic Locus Encoding
TITLE OF INVENTION: Resistance to Rifampin
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schwegman, Lundberg & Woessner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 970;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING STATES COMPOLING OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06790 FILING DATE: 26-MAY-1995 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               80.0%; Score 166.4; DB 5;
87.5%; Pred. No. 4e-30;
tive 0; Mismatches 26;
                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Schwegman, Lundberg & Woessner
STREET: 3500 IDS Center
CITY: Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORREY/AGENT INFORMATION:
NAME: Raasch, Kevin W.
REGISTRATION NUMBER: 35,651
REFERENCE/DOCKET NUMBER: 150.105W01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-339-031
TELEFAX: 612-339-3061
                                                                                                                                                     181 CCGAGGTGCCGGTTGAGACCGACGACAT 208
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                                                                                                                                                                                                                                                    Sequence 1, Application PC/TUS9506790 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 612-339-3061
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 970 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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Best Local Similarity
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PCT-US95-06790-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
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61 GCCTGCACGTCGGCGATCCGATCACCAGGTCCACGCTGACCGAGGACGTCGTCGCCA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                       APPLICANT: Young, Douglas
APPLICANT: Zhang, Ying
APPLICANT: Honore, Nadine
APPLICANT: Telenti, Amalio
APPLICANT: Bodmer, Thomas
TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
TITLE OF INVENTION: in Mycobacterium Tuberculosis
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 3447;
                                                                                                                                                                                                                                                                                                                                                                                                                                SUFTWARE: PATENTIN PC-DOS/MS-DOS
SUFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/313,185
FILING DATE: 12-OCT-1994
ATTONEY/AGENT TEATS
                                                                                                                                                                                                                                                                             Finnegan, Henderson, Farabow, Garrett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 142.4; DB 2
Pred. No. 1.4e-24;
0; Mismatches 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02356.0068-00000
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Sequence 57, Application US/08313185 Patent No. 5851763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 0235
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4400
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 3447 base pairs
                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 2005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Meyers, Kenneth J. REGISTRATION NUMBER: 25,146
                                                                                                                                                                                                                                                                                                                1300 I Street, N.W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE: DNA (genomic) US-08-313-185-57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 80.3%;
                                                     APPLICANT: Heym, Beate
APPLICANT: Cole, Stewart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 167; Conservative
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                Dunner
                                                                                                                                                                                                                                                                                                                                       CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                 USA
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APPLICANT: Schupp, Thomas
APPLICANT: Schupp, Thomas
APPLICANT: Breal, Natalie
APPLICANT: Detenhader, Jurg
APPLICANT: Dropet, Christine
APPLICANT: Pospiech, Andreas
TITLE OF INVENTION: Staurosporin Biosynthesis Gene Clusters
FILE REFERENCE: 4-20555/A/PCT;
CURRENT APPLICATION NUMBER: US/09/029,603
CURRENT APPLICATION NUMBER: PCT/EP96/03643
EARLIER APPLICATION NUMER: PCT/EP96/03643
EARLIER FILING DATE: 1996-08-19
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
SEQ ID NO 4
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Streptomyces longisporoflavus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 2, Application US/09103840A
; Patent No. 6294328
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Best Local Similarity 60.79
Matches 99; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_RNA
LOCATION: (1747). (2553)
OTHER INFORMATION: ORF
FEATURE:
NAME/KEY: misc_RNA
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LOCATION: (5071)..(6085)
CTHER INFORMATION: ORF
US-09-029-603-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: (2593)..(4011)
OTHER INFORMATION: ORF
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LOCATION: (4013)..(4999)
OTHER INFORMATION: ORF
                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: (378)..(1665)
OTHER INFORMATION: ORF
                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_RNA
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US-09-103-840A-2/c
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                                                     APPLICANT: Heym, Beate
APPLICANT: Cole, Stewart
APPLICANT: Young, Douglas
APPLICANT: Zhang, Ying
APPLICANT: Thenti, Amalio
APPLICANT: Honore, Nadine
APPLICANT: Bodner, Thomas
TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
TITLE OF INVENTION: In Mycobacterium Tuberculosis
CORRESPONDENCE: 66
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 3447;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                          ADDRESSEE: Finnegan, Henderson, Farabow, Garrett
ADDRESSEE: Dunner
                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-00S/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/082,614A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 142.4; DB 3;
Pred. No. 1.4e-24;
0; Mismatches 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 02356.0068-00000
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 CCGAGGTGCCGGTTGAGACCGACGACAT 208
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APPLICATION NUMBER: US 08/313,185
FILING DATE: 12-OCT-1994
ATTONIEY/AGENT INFORMATION:
Sequence 57, Application US/09082614A
Patent No. 6124098
                                                                                                                                                                                                                                                                                                                 1300 I Street, N.W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 68.5%;
Best Local Similarity 80.3%;
Matches 167; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 3447 base pairs
                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy COMPUTER: IBM PC COMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                    Washington
                  Patent No. 6124098
GENERAL INFORMATION:
APPLICANT: Heym, E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-082-614A-57
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US-09-029-603-4
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1017 GAGGTGGACCGCGCGCGCGACGACCGCACGATCTGCTCACCCTCCTCGTCCGCGCC 1076
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APPLICANT: FLEISCHMAN, Robert D.

APPLICANT: HITE, Owen R.

APPLICANT: WHITE, Owen R.

APPLICANT: VENTER, Claire M.

APPLICANT: VENTER, John C.

TITLE OF INVENTION: UNB SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM TITLE OF INVENTION: TUBERCILLOSIS
FILE REFERENCE: 24366-20007.00

CURRENT APPLICATION NUMBER: US/09/103,840A

CURRENT FILING DATE: 1998-06-24

NUMBER OF SEQ ID NOS: 2
                                                                                                              18 GACCTGGCCCGGGTAGGCCGCTACAAGGTCAACAAGAAGCTCGGCCTGCACGTCGGCGAT 77
23.9%; Score 49.8; DB 4; Length 6085; 60.7%; Pred. No. 0.0022; tive 0; Mismatches 62; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                  1137 ACCGCGCCACGAGACCACCACCACTGCCTCGCCAGGGCGG 1179
                                                                                                                                                                                                                                                                                                                                             137 -CCGCCTGCACGAGGCCCAGCACGATGACCGTCCCGGGCGG 178
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Sequence 4, Application US/09029603

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NAME: BOTHER, GRACE L.
REGISTRATION NUMBER: 32,963
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPRA: (314)537-7286
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/476,519
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/281902
FILING DATE: 28-JUL-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 9
PCT-US95-09323-10
; Sequence 10, Application PC/TUS9509323
                                                                                                                                                                                                                           Sequence 10, Application US/08476519 Patent No. 5750876
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STRANDEDNESS: double
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US-08-476-519-10
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                                                                                                                                                                                                                       OTHER INFORMATION: CDC 1551
OTHER INFORMATION: "n" bases at various positions throughout the sequence
OTHER INFORMATION: represent a, t, c or g
0S-09-103-840A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        130 ACCTGGTCCGCCTGCACGAGGGCCAGCACGATGACCGTCCCGGGCGGCGCACCGAGGTGC 189
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                                                                                                                                                                                                                                                                                                                                                                                                                          Length 4403765;
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APPLICANT: Schupp, Thomas
APPLICANT: Begel, Nataliae
APPLICANT: Bigel, Nataliae
APPLICANT: Bigel, Nataliae
APPLICANT: Bospiech, Andreas
TITLE OF INVENTION: Stauchoperin Biosynthesis Gene Clusters
FILE REFERENCE: 4-20555/A/PCT
CURRENT APPLICATION NUMBER: US/09/029,603
CURRENT APPLICATION NUMBER: PCT/FEP96/03643
EARLIER APPLICATION NUMBER: PCT/FEP96/03643
EARLIER FILING DATE: 1996-08-19
SOFTWARRE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 2122
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Pred. No. 0.073;
0; Mismatches 85; Indels
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: LOCATION: (1)..(2122)

: OTHER TO OTHER TOWN Product = 2.1 kb region

US-09-029-603-1
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ORGANISM: Streptomyces longisporoflavus
FEATURE:
                                                                                                           TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
FEATURE:
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52.5%;
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ilarity 52.4%;
Conservative
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 4403765
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Best Local Similarity 52.5
Matches 94; Conservative
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Best Local Similarity
Matches 100; Conserva
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US-09-029-603-1
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1338 CGAGTGGAACGGCCTCTACCGCGACGCGCTGCGCAAGAAGAAGAACAAGCTCGGCGTGGA 1397
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GENERAL INFORMATION:
APPLICANT: Barry, Gerard F.
APPLICANT: Kishore, Ganesh M.
APPLICANT: Krohn, Bradley M.
TITLE OF INVENTION: No. 5750876el Isoamylase Gene, Compositions
TITLE OF INVENTION: Containing It and Methods of Using Isoamylases
NUMBER OF SEQUENCES: II
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                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Grace L. Bonner. Monsanto Company, E
STREET: 700 Chesterfield Parkway No. 5750876th
CITY: St. Louis
STATE: Missouri
                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
PCT-US95-09323-1
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Best Local Similarity 52.9%;
Matches 90; Conservative
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TYPE: nucleic acid
STRANDEDNESS: double
  PRIOR APPLICATION DATA:
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PCT-US95-09323-1
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APPLICANT: Barry, Gerard F.
APPLICANT: Kishore, Ganesh M.
APPLICANT: Kishore, Ganesh M.
APPLICANT: Krohn, Brady M.
TITLE OF INVENTION: No. 5750876el Isoamylase Gene, Compositions
TITLE OF INVENTION: Containing It and Methods of Using Isoamylases
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Grace L. Bonner, Monsanto Company, BB4F
STREET: 700 Chesterfield Parkway No. 5750876th
                                    Novel Isoamylase Gene, Compositions
Containing It and Methods of Using Isoamylases
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                                TITLE OF INVENTION: Novel Isoamylase Gene, Compositions TITLE OF INVENTION: Containing It and Methods of Using Isonumber OF SEQUENCES: 11
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/09323
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80; Indels
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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Pred. No. 0.12;
0; Mismatches
                                                                                                                                                                                                                                                          CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/281902
FILING DATE: 28-JUL-1994
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 2244 base pairs
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Patent No. 5750876
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52.9%;
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MEDIUM TYPE: Floppy disk
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Best Local Similarity 52.9
Matches 90; Conservative
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STRANDEDNESS: double
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CLASSIFICATION: 800
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STREET: 700 C...
CITY: St. Louis
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17 CGACCTGGCCCGGGTAGGCCGCTACAAGGTCAACAAGAAGCTCGGCCTGCACGTCGGCGA 76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Novel Isoamylase Gene, Compositions
TITLE OF INVENTION: Containing It and Methods of Using Isoamylases
NUMBER OF SEQUENCES: 11
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
APPLICATION NUMBER: PCT/US95/09323
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 2334;
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Best Local Similarity 52.9%; Pred. No. 0.13;
Matches 90; Conservative 0; Mismatches 80; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                80; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 42; DB 1;
Pred. No. 0.13;
0; Mismatches
FILING DATE: 28-UL-1994

FILING DATE: 28-UL-1994

ATTORNEY/GERT INFORMATION:
NAME: BONNET. Grace L.
REGISTRATION NUMBER: 32,963

REFERENCE/DOCKET NUMBER: 38-21(13577)A

TELECOMMUNICATION INFORMATION:
TELEFRANCE (314)537-7286

TELEFRANCE (314)537-7286

TELEFRANCE (314)537-7286

TELEFRANCE (314)537-7286

TYPE: 314)537-6047

INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 234 base pairs

TYPE: nucleic acid stress pairs

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/281902
FILING DATE: 28-JUL-1994
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application PC/TUS9509323 GENERAL INFORMATION:
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us-09-697-123b-1.rni

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Db 175086 G 175086
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US-08-387-942C-1
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Patent No. 629438

GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: FRASER, Claire M.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM FILE OF INVENTION: UNMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTHER INFORMATION: CDC 1551
GTHER INFORMATION: "n" bases at various positions throughout the sequence is OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Db 175195 GCGGTCGCCAACTACGACACGCCCACCGAGGGCGCGGCGAGGAACATCATCAAGACC 175254
                          81 ATCACCAGCTCCACGCTGACCGAGGAAGACGTCGTCGCCACCATCGAGTACCTGGTCCGC 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               141 CTGCACGAGGCCAGCACCATGACCGTCCCGGGCGGCACCGAGGTGCCGGTTGAGACC 200
77 TCCGATCACCAGCTCCACGCTGACCGAGGAAGACGTCGTCGCCACCATCGAGTACCTGGT 136
                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: FLEISCHANN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: WHITE, Owen R.
APPLICANT: WHITE, Owen R.
APPLICANT: VENAER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM TITLE OF INVENTION: TUBERCULOSIS FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT APPLICATION NUMBER: US/09/103,840A
SOFTWARE: PALEALIN VOR: 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 19.3%; Score 40.2; DB 4; Length 4403765; Best Local Similarity 51.4%; Pred. No. 0.55; Matches 93; Conservative 0; Mismatches 88; Indels 0;
                                                                                                                     137 CCGCCTGCACGAGGCCAGCACCACGATGACCGTCCCGGGCGGCGCACCGAGG 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                  Sequence 2, Application US/09103840A Patent No. 6294328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 2
LENGTH: 4403765
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US-09-103-840A-2
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                                                                                                                                                                                                                                                                                                                                   DD 174966 GGGCCGGTTCGGCGATGGCCGATGACGTCGCCGAGATTCGCGACAAGGGGGGCCGG 175025
                                                                                                                                                                                                                                                                                                         81 ATCACCAGCTCCACGCTGACCGAGGAAGACGTCGTCGCCACCATCGAGTACCTGGTCCGC 140
                                                                                                                                                         Gaps
                                                                                                                                                                                                      21 CTGGCCCGGGTAGGCCGCTACAAGGTCAACAAGAAGCTCGGCCTGCACGTCGGCGATCCG 80
                                                                                                                                                                                                                                                                                                                                                                                                          141 CTGCACGAGGCCCACCACACGATGACCGTCCCGGGCGGCACCGAGGTGCCGGTTGAGACC
                                                                                                   Length 4411529;
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                                                                                                                                                       Indels
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APPLICANT: VALLA, SVEIN
APPLICANT: SKJAK-BRAEK, GUDMUND
APPLICANT: SKJAK-BRAEK, GUDMUND
APPLICANT: LARSEN, BJORN
TITLE OF INVENTION: DNA COMPOUNDS COMPRISING SEQUENCES
TITLE OF INVENTION: BKOODING MANNURONAN C-5-EPIMERASE
CORRESPONDENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP STREET: P.O.BOX 747
CITY: FALLS CHURCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                   Score 40.2; DB 4;
Pred. No. 0.55;
0; Mismatches 88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DAYR:
APPLICATION NUMBER: US/08/387,942C
FILING DATE: 09-MAY-1995
CLASSIFICATION: 435
ATORNEY/AGENT INFORMATION:
NAME: MURBHY JR, GERALD M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1809-106P
TELECHONE: 703-205-8000
TELECHONE: 703-205-8050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORCANISM: Azotobacter vinelandii
STRAIN: E
) ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 703-205-8050
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                   19.3%;
ilarity 51.4%;
Conservative
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TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity
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NAME/KEY:
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LOCATION:
FEATURE:
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; LOCATION:
US-08-804-227C-7
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FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                            137 CCGCCTGCACGAGGCCAGCACACGATGACCGTCCCGGGCGGCGCCGAGGTGCCGGTTGA 196
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                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                 DB 2; Length 12588;
                                                                                                                                                                                                                             Ouery Match 18.8%; Score 39.2; DB 2; Length 1 Best Local Similarity 50.5%; Pred. No. 0.62; Matches 95; Conservative 0; Mismatches 93; Indels
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Sequence 7, Application US/08804227C

Sequence 7, Application US/08804227C

Parent No. 5876991

CENERAL INFORMATION:
APPLICANT: DeHoff, Bradley S.
APPLICANT: Kubstoss, Stuart A.
APPLICANT: Sottech, Kimberly L.
TITLE OF INVEWTION: POLYKETIDE SYNTHASE GENES
CORRESSPONDENCES 115
CORRESSPONDENCE ADDRESS:
ADDRESSEE: THOMAS G. PLANT 1501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTER: USA

21P: 46285

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM COMPATIBLE

OPERATING SYSTEM: MS-DOS

SOFTWARE: ASCI(DOS) Text only

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/804,227C

FILING DATE: FEDRUARY 21, 1997

CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Plant, Thomas, G.
REGISTRATION NUMBER: 35,784
REFERENCE/DOCKET NUMBER: x-8231
TELECOMUNICATION INFORMATION:
TELEPHONE: 317-276-2459
INFORMATION FOR SEO ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: LILLY CORPORATE CENTER CITY: INDIANAPOLIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 44377 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                           CDS
9973..12588
                                                                                                         CDS
6702..9695
                                                       CDS
2227..6438
   CDS
290..1951
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NAME/KEY:
LOCATION:
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FEATURE:
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LOCATION:
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US-08-387-942C-1
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DD 43485 CGAGGAGGCGCGATGCGCTCGACGCGGGGGGGGGGGGCGACGCCGTCGTGCAGGAGGAGGG 43426
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62 CCTGCACGTCGGCGATCCGATCACCAGGTCGACGAGGAAGACGTCGTCGCCAC 121
                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 CAAGGAGAAGCGCTACGACCTGGCCCGGGTAGGCCGCTACAAGGTCAACAAGAAGCTCGG 61
                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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Pred. No. 0.75;
0; Mismatches 70; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     122 CATCGAGTACCTGGTCCGCCTGCACGAGGGC 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Search completed: November 12, 2002, 18:08:49
Job time: 4510.89 secs
MOLECULE TYPE: DNA (genomic) FEATURE:
                                                                                                                                                                                                                                                                                                                                                                  Query Match 18.8%;
Best Local Similarity 53.6%;
Matches 81; Conservative (
                                                                                                                                                                                                                                                                                       CDS
36155..41830
                                                                                                    CDS
14046..20036
                                                                                                                                                             CDS
20110..31284
                                                                                                                                                                                                                         CDS
31329..36071
                                          CDS
350..14002
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November 12, 2002, 15:44:35; Search time 136.222 Seconds (without alignments) 3438.621 Million cell updates/sec
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N. Losticseq_101002;

SIDS2/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*

SIDS2/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*

SIDS2/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*

SIDS2/gcgdata/geneseq/geneseqn-embl/NA1984.DAT:*

SIDS2/gcgdata/geneseq/geneseqn-embl/NA1984.DAT:*

SIDS2/gcgdata/geneseq/geneseqn-embl/NA1986.DAT:*

SIDS2/gcgdata/geneseq/geneseqn-embl/NA1987.DAT:*

SIDS2/gcgdata/geneseq/geneseqn-embl/NA1987.DAT:*

SIDS2/gcgdata/geneseq/geneseqn-embl/NA1987.DAT:*

SIDS2/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:*

SIDS2/gcgdata/geneseq-geneseqn-embl/NA1999.DAT:*

SIDS2/gcgdata/geneseq-geneseqn-embl/NA1999.DAT:*
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208
1 tcaaggagaagcgctacgac......ccggttgagaccgacat 208
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2185239 seqs, 1125999159 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IDENTITY_NUC Gapop 10.0 , Gapext 1.0
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length: 2000000000
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Maximum DB seq
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Searched:
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			Description	Mycobacterium gord	Mycobacterium gord	Mycobacterium aviu	Mycobacterium gord	Mycobacterium mari	Mycobacterium gord	Mycobacterium ulce	Mycobacterium fort	Mycobacterium intr
SUMMARIES			ID		AAS05203	AAS05215	AAS05202	AAS05211	AAS05204	AAS05210	AAS05219	AAS05220
			8	22	22	22	22	22	22	22	22	22
			Length	208	208	208	208	208	207	208	208	202
	æ	Query	re Match Length DB 1	100.0	93.8	91.5	85.4	85.4	84.2	83.1	81.5	80.8
			Score	208	195.2	190.4	177.6	177.6	175.2	172.8	169.6	168
		Result	No.	1	7	m	4	5	9	7	80	6

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27-OCT-2000; 2000WO-KR01223.
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Best Local Simi
Matches 200;
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                            fragment is 1 of 24 roob gene fragments (AAS05201-AAS05224) from
fragment is 1 of 24 roob gene fragments (AAS05201-AAS05224) from
various Mycobacterial species. These roops gene fragments can be used
in the diagnosis and identification of Mycobacterium species using a
novel PCR-restriction fragment length polymorphism analysis (PRA)
method. The method comprises obtaining a restriction fragment length
polymorphism (RPLP) pattern of the 24 roob gene fragments: isolating,
amplifying and digesting the DNA fragment from the microorganism to
be identified and comparing the RFLP patterns from the Known rpob gene
fragments with the unidentified fragment. The roob gene fragments
are useful to identify a wide range of Mycobacterium species, e.g. for
diagnosis or to obtain epidemiological and pathogenesis information for
selection of appropriate therapies, including M. tuberculosis, M. leprae
and non-tuberculous mycobacteria (NTM) encountered in subjects infected
with human immunodeficiency virus (HTV). Analysis of the roob gene
fragments is rapid, precise, simple and cost effective (only 1 PCR
required), and can differentiate between many species in a single
tests. Also described are oligonuclectide probes (AAS05227-AAS05242) for
detecting specific Mycobacterial species.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCCTGCACGTCGGCGATCCGATCACCAGCTCCACGCTGACCGAGGAAGACGTCGTCGCCA 120
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                                                                                                                                                                                                                                                                                                                            Length 208;
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                                                                                                                                                                                                                                                                                                                            100.0%; Score 208; DB 22;
100.0%; Pred. No. 8.9e-36;
ative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                     Sequence 208 BP; 46 A; 71 C; 65 G; 26 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mycobacterium gordonae type III.
            Claim 1; Page 40; 50pp; English
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                                                                                                                                                                                                                                                                                                                                         Local Similarity 100.
les 208; Conservative
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The present sequence for Mycobacterium gordonae type III rpoB gene fragment is 1 of 24 rpoB gene fragments (AAS05201-AAS05224) from various Mycobacterial species. These rpoB gene fragments can be used to the diagnosis and identification of Mycobacterium species using a novel PCR-restriction fragment length polymorphism analysis (PRA) method comprises obtaining a restriction fragment length polymorphism (RFLP) pattern of the 24 rpoB gene fragments; isolating, amplifying and digesting the DNA fragment from the microorganism to be identified and comparing the RFLP patterns from the known rpoB gene fragments with the unidentified fragment. The rpoB gene fragments are useful to identify a wide range of Mycobacterium species, e.g. for diagnosis or to obtain epidemiological and pathogenesis information for selection of appropriate therapies, including M. tuberculosis, M. leprae and non-tuberculous mycobacteria (NTM) encountered in subjects infected with human immunodeficiency virus (HTV). Analysis of the rpoB gene frequired), and can differentiate between many species in a single experiment, including those difficult to distinguish by usual blochemical dates in a society of a particular disconding procies.
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                                                                 New DNA fragments from the rpoB gene of mycobacteria, useful for diagnosis and identification of many mycobacterial species by restriction fragment length polymorphism
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 208 BP; 46 A; 69 C; 63 G; 30 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         detecting specific Mycobacterial species.
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                                                                                                                                                                                                                       Claim 1; Page 41; 50pp; English.
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WPI; 2001-300520/31.
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                                                                                                                                                                                                                                                         The present sequence for Mycobacterium avium rpoB gene
fragment is 1 of 24 rpoB gene fragments (AASO5201-AASO524) from
various Mycobacterial species. These rpoB gene fragments can be used
to the diagnosis and identification of Mycobacterium species using a
novel PCR-restriction fragment length polymorphism analysis (PRA)
method. The method comprises obtaining a restriction fragment length
colymorphism (RFLP) pattern of the 24 rpoB gene fragments isolating,
amplifying and digesting the DNA fragment from the microorganism to
be identified and comparing the RFLP patterns from the known rpoB gene
fragments with the unidentified fragment. The rpoB gene fragments
fragment of appropriate therapies, including M. tuberculosis, M. leprae
selection of appropriate therapies, including M. tuberculosis, M. leprae
and non-tuberculous mycobacteria (NTM) encountered in subjects infected
with human immunodeficiency virus (HTW). Analysis of the rpoB gene
fragments is rapid, precise, simple and cost effective (only 1 PCR
required), and can differentiate between many species in a single
experiment, including those difficult to distinguish by usual blochemical
tests. Also described are oligonucleotide probes (AASO5227-AASO5242) for
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                                                                                                                                                      New DNA fragments from the rpoB gene of mycobacteria, useful for diagnosis and identification of many mycobacterial species by restriction fragment length polymorphism
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                                                                                     Park HJ;
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0; Mismatches 11; Indels
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91.5%; Score 190.4; DB 22;
Best Local Similarity 94.7%; Pred. No. 5e-32;
Matches 197; Conservative 0; Mismatches 11;
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                                                                                     Kim Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       detecting specific Mycobacterial species.
                                                                                     Cho S,
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                                                    (ERUM-) ERUME BIOTECH CO LTD
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                                                                                     Park YK, Bai G,
                                                                                                                       WPI; 2001-300520/31.
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tragment is 1 of 24 rpob gene fragments (AASO5201-AASO524) from various Mycobacterial species. These rpob gene fragments can be used in the diagnosis and identification of Mycobacterium species using a novel pCR-restriction fragment length polymorphism species using a movel pCR-restriction fragment length polymorphism analysis (PRA) method comprises obtaining a restriction fragment length polymorphism analysis (PRA) method comparises obtaining a restriction fragment length polymorphism (RFLP) pattern of the 24 rpob gene fragments; isolating, amplifying and digesting the DNA fragment from the microorganism to be identified and comparing the RFLP patterns from the known rpob gene fragments with the unidentified fragment. The rpob gene fragments for useful to identify a wide range of Mycobacterium species, e.g. for diagnosis or to obtain epidemiological and pathogenesis information for selection of appropriate therapies, including M. tuberculosis, M. leprac and non-tuberculous mycobacteria (NTW). Analysis of the rpob gene fragments is rapid, precise, simple and cost effective (only 1 PCR required), and can differentiate between many species in a single experiment, including those difficult to distinguish by usual blochemical tests. Also described are oligonucleotide probes (AASO5227-AASO5242) for detecting specific Mycobacterial species.
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                                                                                                                                                                                                                                                                                       Kim Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 208 BP; 45 A; 62 C; 73 G; 28 T; 0 other;
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                                                                                                                                                                                                                                                                                       Cho
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                                                                                                                                                                                                                                                                                       Kim S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 40; 50pp; English
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                                                                                                                                                                                                            (ERUM-) ERUME BIOTECH CO LTD.
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                                                                    27-OCT-2000; 2000WO-KR01223.
                                                                                                                                        99KR-0046795.
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                                                                                                                                                                                                                                                                                       Bai G,
                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-300520/31.
                                                                                                                                                                                                                                                                                       Park YK,
03-MAY-2001
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                                                                                                                                                                                                                                                                                       Lee H,
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AAS05204 standard; DNA; 207 BP.

(first entry)

07-SEP-2001

AAS05204;

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frep present sequence for Mycobacterium marinum rpoB gene fragment is 1 of 24 rpoB gene fragments (AASO5201-AASO5224) from various Mycobacterial species. These rpoB gene fragments can be used in the diagnosis and identification of Mycobacterium species using a novel PCR-restriction fragment length polymorphism analysis (PRA) method. The method comprises obtaining a restriction fragment length polymorphism (RRLP) pattern of the 24 rpoB gene fragments; isolating, amplifying and digesting the DNA fragment from the microorganism to be identified and comparing the RRLP patterns from the known rpoB gene fragments with the unidentified fragment. The rpoB gene fragments are useful to identify a wide range of Mycobacterium species. Gor diagnosis or to obtain epidemiological and pathogenesis information for selection of appropriate therapies, including M. tuberculosis, M. leprae and non-tuberculous mycobacteria (NTM) encountered in subjects infected with human immunodeficiency virus (HTW). Analysis of the rpoB gene fragments is rapid, precise, simple and cost effective (only 1 PCR required), and can differentiate between many species in a single experiment, including those difficult to distinguish by usual blochemical tests. Also described are oligonucleotide probes (AASO5227-AASO5242) for detecting specific Mycobacterial species.
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                                        Non-tuberculous mycobacteria; rpoB gene fragment; NTM; HIV; PRA; RFLP; PCR-restriction fragment length polymorphism analysis; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    New DNA fragments from the rpoB gene of mycobacteria, useful for diagnosis and identification of many mycobacterial species by
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Pred. No. 2.7e-29;
0; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                      Cho S, Kim Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 208 BP; 45 A; 69 C; 68 G; 26 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               restriction fragment length polymorphism
Mycobacterium marinum rpoB gene fragment.
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                                                                                                                                                                                                                                                                                                                                                      Park YK, Bai G, Kim
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Best Local Similarity 90.9%;
Matches 189; Conservative
                                                                                                       Mycobacterium marinum.
                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-300520/31.
                                                                                                                                              WO200131061-A1.
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The present sequence for Mycobacterium gordonae type IV rpoB gene fragment is 1 of 24 rpoB gene fragments (AAS05201-AAS05224) from various Mycobacterial species. These rpoB gene fragments can be used in the diagnosis and identification of Mycobacterium species using a novel PCR-restriction fragment length polymorphism analysis (PRA) method comprises obtaining a restriction fragment length polymorphism (RFLP) pattern of the 24 rpoB gene fragments; isolating, amplifying and digesting the DNA fragment from the microorganism to be identified and comparing the RFLP patterns from the known rpoB gene fragments with the unidentified fragment. The rpoB gene fragments

C fragments with the unidentified fragment. The rpoB gene fragments

are useful to identify a wide range of Mycobacterium species, e.g. for diagnosis or to obtain epidemiological and pathogenesis information for selection of appropriate theraptes, including M. tuberculosis, M. leprae and non-tuberculous mycobacteria (NTM) encountered in subjects infected with human immunodeficiency virus (HIV). Analysis of the rpoB gene frequired), and can differentiate between many species in a single required), and can differentiate between many species in a single experiment, including those difficult to distinguish by usual blochemical archive machine experience.
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                                                                                                                                                      HIV; PRA; RFLP;
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                                                                                                                                                Non-tuberculous mycobacteria; rpoB gene fragment; NTM; PCR-restriction fragment length polymorphism analysis;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Park
                                                                                                            Mycobacterium gordonae type IV rpoB gene fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Kim Y,
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Cho S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           detecting specific Mycobacterial species.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Lee H, Park YK, Bai G, Kim S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 41; 50pp; English.
                                                                                                                                                                                                         Mycobacterium gordonae type IV
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                                                                                                                                                                                                                                                                                                                        27-OCT-2000; 2000WO-KR01223
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181 CCGAGGTGCCGGTTGAGACCGACGACAT 208

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RESULT 6 AAS05204

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us-09-697-123b-1.rng

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Non-tuberculous mycobacteria; rpoB gene fragment; NTM; HIV; PRA; RFLP; PCR-restriction fragment length polymorphism analysis; ds.
                       CCATCGAGTACCTGGTCCGCCTGCACGAGGGCCAGCACGATGACCGTCCCGGGCGCA 180
                                           Mycobacterium fortuitum rpoB gene fragment.
                                                                                                                     181 TCGAGGTGCCGGTCGAGACCGACGACAT 208
                                                                                                 CCGAGGTGCCGGTTGAGACCGACGACAT 208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Mycobacterium fortuitum.
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AAS05219
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                                                                                                                                                                                                                                                                       method. The method comprises obtaining a restriction fragment length polymorphism (RFLP) pattern of the 24 rpoB gene fragments isolating, amplifying and digesting the DNA fragment from the microorganism to be identified and comparing the RFLP patterns from the known rpoB gene fragments with the unidentified fragment. The rpoB gene fragments or comparing a wide range of Mycobacterium species, e.g. for diagnosis or to obtain epidemiological and pathogenesis information for selection of appropriate theraples, including M. tuberculosis, M. leprae and non-tuberculous mycobacteria (NTM) encountered in subjects infected with human immunodeficiency virus (HTV). Analysis of the rpoB gene fragments is rapid, precise, simple and cost effective (only 1 pcR required), and can differentiate between many species in a single experiment, including those difficult to distinguish by usual biochemical to the standard of described are oligonucleotide probes (AASO5227-AASO5242) for
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                                                                                                                                                                                                                                                                     Non-tuberculous mycobacteria; rpoB gene fragment; NTM; HIV; PRA; RFLP; PCR-restriction fragment length polymorphism analysis; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kim Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 172.8; DB 22
Pred. No. 2.8e-28;
0; Mismatches 22;
                                                                                                                                                                                                                                 Mycobacterium ulcerans rpoB gene fragment.
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180 CCGAGGTTCCGGTGGAGCCGACGT 207
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                                                                                                                 BP
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Matches 186; Conservative
                                                                                                                                                                                                                                                                                                                            Mycobacterium ulcerans.
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                                                                           RESULT 7
                                                                                               AAS05210
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Park HJ;

Kim Y,

Cho S,

Bai G, Kim S,

99KR-0046795.

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The present sequence for Mycobacterium fortultum rpoB gene fragment is 1 of 24 rpoB gene fragments (AAS05201-AAS05224) from various Mycobacterial species. These rpoB gene fragments can be used in the diagnosis and identification of Mycobacterium species using a novel PCR-restriction fragment length polymorphism analysis (PRA) method comprises obtaining a restriction fragment length polymorphism (RFLP) pattern of the 24 rpoB gene fragments isolating, amplifying and digesting the DNA fragment from the microorganism to be identified and comparing the RFLP patterns from the Known rpoB gene fragments with the unidentified fragment. The rpoB gene fragments are useful to identified and comparing the RFLP patterns from the Known rpoB gene are useful to identify a wide range of Mycobacterium species, e.g. for diagnosis or to obtain epidemiological and pathogenesis information for selection of appropriate therapies, including M. tuberculosis, M. leprae and non-tuberculous mycobacteria (NTM) encountered in subjects infected with human immunodeficiency virus (HTV). Analysis of the rpoB gene frequired), and can differentiate between many species in a single experiment, including those difficult to distinguish by usual blochemical abstract in an encountered are oligonuclectide probes (AAS05227-AAS05242) for abstract in a shorter in a second and an additional and an additional and an additional are oligonuclectide probes (AAS05227-AAS05242) for abstract in a second and additional additional additional and additional and additional additional and additional additional and additional a
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                          for
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New DNA fragments from the rpoB gene of mycobacteria, useful f
diagnosis and identification of many mycobacterial species by
restriction fragment length polymorphism
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                                                                                                                                                                                                                                                                   Claim 1; Page 46; 50pp; English.
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Matches 184; Conservative
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GCCTGCACGTCGGCGATCCGATCACCAGCTCCACGCTGACCGAGGAAGACGTCGTCGCCA 120

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Tragment is 1 of 24 rpoB gene fragments (AAS05201-AAS0524) from various Mycobacterial species. These rpoB gene fragments can be used in the diagnosis and identification of Mycobacterium species using a novel PCR-restriction fragment length polymorphism analysis (PRA) method comprises obtaining a restriction fragment length polymorphism analysis (PRA) pattern of the 24 rpoB gene fragment; isolating, amplifying and digesting the DNA fragment from the microorganism to be identified and comparing the RELP patterns from the microorganism to be identified and comparing the RELP patterns from the known rpoB gene fragments with the unidentified fragment. The rpoB gene fragments with the unidentified fragment. The rpoB gene fragments or to obtain epidemiological and pathogenesis information for selection of appropriate therapies, including M. tuberculosis, M. leprae and onstuberculosus mycobacteria (NTM) encountered in subjects infected with human immunodeficiency virus (HIV) Analysis of the rpoB gene fragments is rapid, precise, simple and cost effective (only 1 PCR required), and can differentiate between many species in a single experiment, including those difficult to distinguish by usual biochemical tests. Also described are oligonucleotide probes (AAS05227-AAS05242) for detecting specific Mycobacterial species.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HIV; PRA; RFLP;
                                                      61 GCCTGCACGTCGGCGATCCGATCACCAGCTCCACGCTGACCGAGGAAGACGTCGTCGCCA 120
                                                                            121 CCATCGAGTACCTGGTCCGCCTGCACGAGGCCAGCACGATGACCGTCCCGGGCGGCA 180
                                                                                                                                                    for
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diagnosis and identification of many mycobacterial species by
restriction fragment length polymorphism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Park HJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Non-tuberculous mycobacteria; rpoB gene fragment; NTM; PCR-restriction fragment length polymorphism analysis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kim Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                Mycobacterium intracellulare rpoB gene fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cho s,
                                                                                                                                                                                                                              181 TCGAGGTCCCGGTCGAGGTGGACGAT 208
                                                                                                                                                                                                        181 CCGAGGTGCCGGTTGAGACCGACGACAT 208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 46; 50pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mycobacterium intracellulare,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-OCT-2000; 2000WO-KR01223.
                                                                                                                                                                                                                                                                                                                                     AAS05220 standard; DNA; 205
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                                                                                                                                                                                                                                                                                                    RESULT 9
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Sequence 205 BP; 44 A; 69 C; 67 G; 25 T; 0 other;

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The present sequence for Mycobacterium kansasii rpoB gene
fragment is 1 of 24 rpoB gene fragments (AASO5201-AASO5224) from
various Mycobacterial species. These rpoB gene fragments can be used
in the diagnosis and identification of Mycobacterium species using a
novel PCR-restriction fragment length polymorphism analysis (PRA)
method romerises obtaining a restriction fragment length
polymorphism (RFLP) pattern of the 24 rpoB gene fragments isolating,
amplifying and digesting the DNA fragment from the microorganism to
be identified and comparing the RFLP patterns from the known rpoB gene
fragments with the unidentified fragment. The rpoB gene fragments
are useful to identify a wide range of Mycobacterium species, e.g. for
diagnosis or to obtain epidemiological and pathogenesis information for
selection of appropriate therapies, including M. tuberculosis, M. leprae
and non-tuberculous mycobacteria (NTM) encountered in subjects infected
with human immunodeficiency virus (HIV). Analysis of the rpoB gene
fragments is rapid, precise, simple and cost effective (only 1 PCR
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                                                                                                                                        61 GCCTGCACGTCGGCGATCCGATCACCAGGTCCACGCTGACCGAGGAAGACGTCGTCGCCA 120
                                                                                                                                                          CCATCGAGTACCTGGTCCGCCTGCACGAGGGCCAGCACGATGACCGTCCCGGGGGGCA 180
                                                                                                                                                                                                                                    Gaps
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                                                                                          1 TCAAGGAGAAGCGCTACGACCTGGCCCGGGTAGGGCCGCTACAAGGTCAACAAGAAGCTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New DNA fragments from the rpoB gene of mycobacteria, useful for diagnosis and identification of many mycobacterial species by restriction fragment length polymorphism -
                                            ë
         Length 205;
                                        Indels
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       DB 22;
80.8%; Score 168; DB 2;
llarity 91.3%; Pred. No. 3e-27;
Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mycobacterium kansasii rpoB gene fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Park YK, Bai G, Kim S, Cho S,
                                                                                                                                                                                                                                                                                181 CCGAGGTGCCGGTTGAGACCGACGACAT 208
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                                                                                                                                                                                                                                                                                                                                                                                                         AAS05208 standard; DNA; 208 BP.
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   Query Match
Best Local Similarity
Matches 190; Conserv
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required), and can differentiate between many species in a single experiment, including those difficult to distinguish by usual biochemical tests. Also described are oligonucleotide probes (AAS05227-AAS05242) for detecting specific Mycobacterial species.
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                                                                                                                                                                                                                                                                                                                                                                                                                             HIV; PRA; RFLP;
ds.
                                                                                                                                                                   61 GCCTGCACGTCGGCGATCCGATCACCAGCTCCACGCTGACCGAGGAAGACGTCGTCGCCA 120
                                                                                                                                                                               121 CCATCGAGTACCTGGTCCGCCTGCACGAGGGCCAGCACGATGACCGTCCCGGGCGGCA 180
                                                                                                      Gaps
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                                                                                                                                                                                                                         1 TCAAGGAGAAGCGCTACGACCTGGCCCGGGTAGGCCGCTACAAGGTCAAGAAGCTCG
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                                                                                Length 208;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Park HJ;
                                                                            Score 168; DB 22; Length 2
Pred. No. 3e-27;
0; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                            Non-tuberculous mycobacteria; rpoB gene fragment; NTM; PCR-restriction fragment length polymorphism analysis;
                                                      Sequence 208 BP; 51 A; 65 C; 65 G; 27 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kim Y,
                                                                                                                                                                                                                                                                                                                                                                                                       Mycobacterium tuberculosis rpoB gene fragment.
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                                                                                                                                                                                                                                                                     181 CCGAGGTGCCGGTTGAGACCGACGAT 208
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                                                                             80.8%;
88.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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                                                                                                  Matches 183; Conservative
                                                                                         Similarity
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                                                                               Ouery Match
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                                                                                         Best Local
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are useful to identify a wide range of Mycobacterium species, e.g. for diagnosis or to obtain epidemiological and pathogenesis information for selection of appropriate therapies, including M. tuberculosis, M. leprae and non-tuberculous mycobacteria (NTM) encountered in subjects infected with human immunodeficiency virus (HIV). Analysis of the rpoB gene fragments is rapid, precise, simple and cost effective (only 1 PCR required), and can differentiate between many species in a single experiment, including those difficult to distinguish by usual biochemical tests. Also described are oligonuclectide probes (AASO5227-AASO5242) for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCATCGAGTACCTGGTCCGCCTGCACGAGGCCCAGCACGATGACCGTCCCGGGCGGCA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCCTGCACGTCGGCGATCCGATCACCAGCTCCACGCTGACCGAGGAAGACGTCGTCGCCA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 TCAAGGAGAAGCGCTACGACCTGGCCCGGGTAGGCCGCTACAAGGTCAACAAGAAGCTCG
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                                                                                                                                                                                                                                                                                                                                                                                             Length 208;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                26; Indels
                                                                                                                                                                                                                                                                                                                                                                                         DB 22;
                                                                                                                                                                                                                                                                                                                                   Sequence 208 BP; 46 A; 62 C; 67 G; 33 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 6.5e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                      80.0%; Score 166.4;
87.5%; Pred. No. 6.5
                                                                                                                                                                                                                                                                         detecting specific Mycobacterial species.
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                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 87.5
Matches 182; Conservative
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Claim 1; Page 45; 50pp; English.

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novel PCR-restriction fragment length polymorphism analysis (PRA)
method. The method comprises obtaining a restriction fragment length
polymorphism (RFLP) pattern of the 24 rpoB gene fragments; isolating,
amplifying and digesting the DNA fragment from the microorganism to
fragments with the unidentified fragment. The rpoB gene fragments
fragments with the unidentified fragment. The rpoB gene fragments
are useful to identify a wide range of Mycobacterium species, e.g. for
diagnosis or to obtain epidemiological and pathogenesis information for
selection of appropriate therapies, including M. tuberculosis, M. leprae
and non-tuberculous mycobacteria (MTM) encountered in subjects infected
with human immunodeficiency virus (HIV). Analysis of the rpoB gene
fragments is raphd, precise, simple and cost effective (only 1 PCR
required), and can differentiate between many species in a single
experiment, including those difficult to distinguish by usual blochemical
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Non-tuberculous mycobacteria; rpoB gene fragment; NTM; HIV; PRA; RFLP; PCR-restriction fragment length polymorphism analysis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCATCGAGTACCTGGTCCGCCTGCACGAGGCCAGCACGATGACCGTCCCGGGCGGCA 180
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                                                                                                                                                                                                                                                                                                                           Score 166.4; DB 22; Length 208;
Pred. No. 6.5e-27;
0; Mismatches 26; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Park
                                                                                                                                                                                                                                                                                            Sequence 208 BP; 46 A; 62 C; 67 G; 33 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kim Y,
                                                                                                                                                                                                                                                           detecting specific Mycobacterial species.
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                                                                                                                                                                                                                                                                                                                           Query Match 80.0%;
Best Local Similarity 87.5%;
Matches 182; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mycobacterium bovis.
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The present sequence for Mycobacterium bovis rpoB gene
fragment is 1 of 24 rpoB gene fragments (AAS05201-AAS05224) from
various Mycobacterial species. These rpoB gene fragments can be used
in the diagnosis and identification of Mycobacterium species using a
in the diagnosis and identification of Mycobacterium species using a
novel pCR-restriction fragment length polymorphism analysis (PRA)

method. The method comprises obtaining a restriction fragment length

complifying and dispering the DNA fragment from the microorganism to
be identified and comparing the RFLP patterns from the microorganism to
be identified and comparing the RFLP patterns from the known rpoB gene
fragments with the unidentified fragment. The rpoB gene fragments
are useful to identify a wide range of Mycobacterium species, e.g. for
clasmosis or to obtain epidemiological and pathogenesis information for
selection of appropriate therapies, including M. tuberculosis, M. leprae
and non-tuberculous mycobacteria (NTW) encountered in subjects infected
with human immunodeficiency virus (HIV). Analysis of the rpoB gene
fragments is rapid, precise, simple and cost effective (only 1 PCR
required), and can differentiate between many species in a single
comparison of appropriate difficult to distinguish by usual blochemical
tests. Also described are oligouncleotide probes (AAS05227-AAS05242) for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 208;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 208 BP; 46 A; 62 C; 67 G; 33 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 87.5%; Pred. No. 6.5e-27
Matches 182; Conservative 0; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 166.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mycobacterium celatum rpoB gene fragment.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mycobacterium celatum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200131061-A1
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AAS05217
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"primer DDIDHL"

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                                                                                                                                                                          misc_feature
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        The present sequence for Mycobacterium celatum rpoB gene fragment is 1 of 24 rpoB gene fragments (AAS05201-AAS05224) from various Mycobacterial species. These rpoB gene fragments can be used in the diagnosis and identification of Mycobacterium species using a novel PCR-restriction fragment length polymorphism analysis (PRA) can ethod. The method comprises obtaining a restriction fragment length polymorphism (RFLP) pattern of the 24 rpoB gene fragments; isolating, amplifying and digesting the DNA fragment from the microorganism to be identified and comparing the RFLP patterns from the known rpoB gene fragments with the unidentified fragment. The rpoB gene fragments

Tragments with the unidentified fragment. The rpoB gene fragments

are useful to identify a wide range of Mycobacterium species, e.g. for diagnosis or to obtain epidemhological and pathogenesis information for selection of appropriate therapies, including N. tuberculosis, M. leprae and non-tuberculous mycobacteria (NFW) encountered in subjects infected with human immunodeficiency virus (HIV). Analysis of the rpoB gene fragments is rapid, precise, simple and cost effective (only 1 PCR required), and can differentiate between many species in a single experiment, including those difficult to distinguish by usual biochemical cests.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tuberculosis; disease diagnosis; oligonucleotide; DNA primer; PCR; polymerase chain reaction; DNA amplification; rpoB locus; TB; ss.
                       New DNA fragments from the rpoB gene of mycobacteria, useful for diagnosis and identification of many mycobacterial species by restriction fragment length polymorphism
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                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match 80.0%; Score 166.4; DB 22; Length 208; Best Local Similarity 87.5%; Pred. No. 6.5e-27; Matches 182; Conservative 0; Mismatches 26; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mycobacterium tuberculosis rpoB gene DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                            Sequence 208 BP; 48 A; 71 C; 64 G; 25 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                  detecting specific Mycobacterial species
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/note~ "primer FENLFF"
226..243
/*tag~ b
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                                                                          Claim 1; Page 45; 50pp; English
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WPI; 2001-300520/31
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Detection of Mycobacterium tuberculosis – by amplifying sample DNA
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note= "M. tuberculosis signature nucleotide"
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/note- "M. tuberculosis signature nucleotide"
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/note= "M. tuberculosis signature nucleotide"
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'note= "M. tuberculosis signature nucleotide"
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/note= "primer NMQRQ-1"
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/note= "primer NMQRQ-2"
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/note= "primer rpo105"
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'note= "primer rpo397"
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/note= "primer rpo273"
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/note= "primer DDIDH"
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/note- "primer rpo95"
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'note= "primer rpo293'
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/note= "primer KY292"
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                                                                      This oligonucleotide DNA primer is specific for Mycobacterium tuberculosis, and may be used to amplify a sample DNA by targeting a portion of the gene encoding rpoB. The 1st several bases comprise a nonhybridizing tail consisting of filler bases followed by a restriction site incorporated to facilitate cloning using the amplicon at a later date, if desired. The remaining bases hybridize to bacterial rpoB DNA. The method provides for the detection of M. tuberculosis and the concurrent determination of its drug susceptibility, particularly to rifamycin. The method can provide often greater than 95% sensitivity and 100% specificity. The biological sample is a fluid or tissue sample from a human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 GCCTGCACGTCGGCGATCCGATCACCAGCTCCACGCTGACCGAGGAAGACGTCGTCGCCA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 CCATCGAGTACCTGGTCCGCCTGCACGAGGCCAGCACACGATGACCGTCCCGGGCGGCA 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       with a primer set that targets portions of the gene encoding rpoB.
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80.0%; Score 166.4; DB 17; Length 970;
Best Local Similarity 87.5%; Pred. No. 6.3e-27;
Matches 182; Conservative 0; Mismatches 26; Indels 0;
                                                                                                                                                                                                                                                                                                                 Sequence 970 BP; 182 A; 302 C; 330 G; 156 T; 0 other;
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Job time : 142.222 secs
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MTU318818
Mycobacterium tuberculosis partial rpoB gene for RNA polymerase beta subunit, isolate 1415-97.
Mycobacterium tuberculosis
AJ318818
AJ318818.1 GI:22208412
RNA Polymerase beta subunit; rpoB gene.
Mycobacterium tuberculosis.
Mycobacterium tuberculosis
Bacteria; Actinobacteria; Actinobacterium tuberculosis
Corymbbacterines.
Mycobacterium tuberculosis
Corymbbacteria; Actinobacteriae; Actinomycetales;
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AJ318813 Mycobacte
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AL034492 Streptomy
AL391588 Streptomy
AL724413 Oryza sat
AL64658 Raistonia
AL597786 Sinorhizo
AE247649 Coniothyr
AE004747 Pseudomon
AL023861 Streptomy
AL665949 Oryza sat
AL663013 Oryza sat
                                                                                                                      AJ318818 Mycobacte
score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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AK096697
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MSU24494
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MLB1790G
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       version 5.1.3
- 2002 Compugen Ltd.
                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                       2054640 seqs, 14551402878 residues
                                                         nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Copyright (c) 1993
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/transl_table=11
/product="RRM polymerase beta subunit"
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Molecular analysis of rifampin-resistant Mycobacterium tuberculosis isolated in Spain (1996-2001). Description of new alleles into rpob gene and review
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Molecular analysis of rifampin-resistant Mycobacterium tuberculosis
isolated in Spain (1996-2001). Description of new alleles into rpoB
gene, and review
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Mycobacterium tuberculosis.
Bacteria; Actinobacteria; Actinobacteria; Actinomycetales;
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                                                                                                                                                                           Direct Submission
Submitted (07-ANG-2001) Herrera L., Servicio Bacteriologia,
Nacional Microbiologia, Ctra. Majadahonda-Pozuelo, Km 2.5,
Majadahonda. Madrid. 28220, SPAIN
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MTU318813

Mycobacterium tuberculosis partial rpoB gene for RNA polymerase
AJ318813

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Molecular analysis of rifampin-resistant Mycobacterium tuberculosis isolated in Spain (1996-2001). Description of new alleles into rpob gene and review
                                                                     Servicio Bacteriologia, Centro lahonda-Pozuelo, Km 2.5,
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Submitted (07-AUG-2001) Herrera L., Servicio Bacteriologia, Centro
Nacional Microbiologia., Ctra. Majadahonda-Pozuelo, Km 2.5,
Majadahonda. Madrid. 28220, SPAIN
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Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              139
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Direct Submission
Submitted (07-ANG-2001) Herrera L., Servicio Bacterio
Nacional Microbiologia., Ctra. Majadahonda-Pozuelo, Km
Majadahonda. Madrid. 28220, SPAIN
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                     /organism="Mycobacterium tuberculosis"
/1solate="1417-97"
/db_xref="taxon:1773"
1. .610
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Pred. No. 1.5e-16;
0; Mismatches 26;
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ilarity 87.5%;
Conservative 0
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Herrera, L.
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Gaps

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Length Indels 120 214

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FFGTSGLSQFOLSOFTHERLALGPGGLSRERAGLEVRDV"

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Molecular analysis of rifampin-resistant Mycobacterium tuberculosis isolated in Spain (1996-2001). Description of new alleles into rpob
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Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium
tuberculosis complex.
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                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (07-AUG-2001) Herrera L., Servicio Bacteriologia,
Nacional Microbiologia., Ctra. Majadahonda-Pozuelo, Km 2.5,
Majadahonda. Madrid. 28220, SPAIN
Location/Oualifiers
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                                                                                                                                                                                                                                                     Score 166.4; DB 1;
Pred. No. 1.5e-16;
0; Mismatches 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mycobacterium tuberculosis partial rpoB
beta subunit, isolate 2348-98.
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RNA polymerase beta subunit; rpoB gene.
Mycobacterium tuberculosis.
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<1. .>618
/gene="rpoB"
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Matches 182; Conservative
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Unpublished
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                                                                                                                                                                                                                                                       Query Match
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AUTHORS
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KEYWORDS
SOURCE
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AJ318815
AJ318815.
RNA polymerase beta subunit; rpoB gene.
Mycobacterium tuberculosis.
Mycobacterium tuberculosis.
Macobacterium tuberculosis.
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RLRTVGELIONOIRVGMSRMERVVREMTTQDVEAITPQTLINIRPVVAAIKEFFGTS
0201 g 99 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (07-AUG-2001) Herrera L., Servicio Bacteriología, Centro Nacional Microbiología, Ctra. Majadahonda-Pozuelo, Km 2.5, Majadahonda. Madrid. 28220, SPAIN Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  80 TCAAGGAGAAGCGCTACGACCTGGCCCGCGTCGGTCGCTATAAGGTCAACAAGAAGCTCG 139
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                                                                                                                                                                                                                                                                                                                                                                     616;
                                                                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                                                                                                                                         26; Indels
/organism="Mycobacterium tuberculosis"
/isolate="1763-97"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Mycobacterium tuberculosis"
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/db_xref="taxon:1773"
                                                                                                                                                                                                                                                                                                                                                               Score 166.4; DB 1;
Pred. No. 1.5e-16;
0; Mismatches 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 CCGAGGTGCCGGTTGAGACCGACGACAT 208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="rpoB"
<1. .>618
                                                                          /gene="rpoB"
                                                                                                                                                                                                                                                                                                                                                               tch 80.0%;
al Similarity 87.5%;
182; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tuberculosis complex.
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Herrera, L.
                                                                                            .>615
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Best Local S
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DEFINITION
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KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                         BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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AUTHORS
TITLE
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AUTHORS
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circular BCT 09-AUG-2002 gene for RNA polymerase

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Query Match
Best Local Similarity
Matches 182; Conserv
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/translation="TDEALLDIYRKLRPGEPPTKESAQTLLENLFFKEKRYDLARVGR
YKVNKKLGLHVGEPITSSTLTEEDVVATIEYLVRLHEGOTIMTVPGGVEVPVETDDID
HFGNRRLRTVGELIONOIRVGMSRMERVVREEMTTQDVEATTPOTLINIRPVVAAIKE
FFGTSQPSOFMGQNPLSGLTHRRLSALGPGGLSRERAGLEVRDV"
192 c 95 t
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/product="RNA_polymerase beta subunit"
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AAIKEFFGTSQLSQEMOONNPLSGLYKRRLSALGPGGLSRERAGLEVRDV"
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Molecular analysis of rifampin-resistant Mycobacterium tuberculosis
stolated in Spain (1996-2001). Description of new alleles into rpoB
gene and review
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Corynebacterineae: Mycobacteriaceae; Mycobacterium; Mycobacterium
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Nacional Microbiologia., Ctra. Majadahonda-Pozuelo, Km 2.5,
Majadahonda. Madrid. 28220, SPAIN
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/isolate="1058-97"
/db_xref="taxon:1773"
                                                                                                                                            26;
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0; Mismatches 26
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Mycobacterium tuberculosis.
Mycobacterium tuberculosis
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Mycobacterium tuberculosis partial rpoB gene for RNA polymerase beta subunit, isolate 1255-98.
AJ318816. G1:22208408
RNA polymerase beta subunit; rpoB gene.
Mycobacterium tuberculosis.
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Molecular analysis of rifampin-resistant Mycobacterium tuberculosis
isolated in Spain (1996-2001). Description of new alleles into rpos
gene and review
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/db_xref="G1:2208409"

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/kranslation="VGTDEALDIYRKRPATCOPEALTPQTLINIRPVVAAI

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Submitted (07-407-2001) Herrera L., Servicio Bacteriologia, Centro
Nacional Microissologia, Ctra. Majadahonda-Pozuelo, Km 2.5,
Majadahonda. Madrid, 28220, SPAIN
Location/Qualiflers
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Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium
tuberculosis complex.
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       Length 633;
                                                   Indels

    637 / Organism="Mycobacterium tuberculosis" /isolate="1255-98"

         DB 1;
    Score 166.4; DB 1
Pred. No. 1.5e-16;
0; Mismatches 26
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/gene="rpoB"
/codon_start=1
80.0%;
ilarity 87.5%;
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PAT 07-0CT-1997

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Actinomycetales; Corynebacterineae; Mycobacteriaceae;
Mycobacterium; Mycobacterineae; Mycobacteriaceae;
I (bases I to 334)

Bergeron, M.G., Boissinot, M., Huletsky, A., m Nard, C., Ouellette, M.,
Picard, F.J. and Roy, P.H.

Highly conserved genes and their use to generate probes and primers
for detection of microorganisms
Patent: WO 0123604-A 2072 05-APR-2001;
Infectio Diagnostic (I.D.I.) INC. (CA)

Location/Qualifiers
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Persing, D.H., Hunt, J.J., Young, K.K.Y., Felmlee, T.A., Roberts, G.D. and Whelan, A.Christian.
and Whelan, A.Christian.
Detection of a genetic locus encoding resistance to rifampin in mycobacterial cultures and in clinical specimens
Patent: US 5643723-A i 01-JUL-1997;
Location/Qualifiers
                    GCCTGCACGTCGGCGATCCGATCACCAGCTCCACGCTGACCGAGGAAGACGTCGTCGCCA 120
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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Sequence 2072 from Patent W00123604.
AX111339
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Sequence 1 from patent US 5643723.
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150706.1 GI:2472409
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Best Local Similarity 87.5%;
Matches 182; Conservative
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/transl_table=11
/product="RNA polymerase beta subunit"
/product="RNA polymerase beta subunit"
/product="C1:22208419"
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GRYKVNKKLGHVGEPTTSSTLTEDVVATIEYLVRHHEGGTTMTVGGVEPPDTD
IDHFGNRRLRTVGELIONQIRVGRSRMERVVRERMTTQDVEAITPOTLINIRPAVAAI
KEFFGTSQLSQFMVQNNPLSGLTQKRRLSALGPGGLSRERAGLEVRDVHPSHS"
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Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium
tuberculosis complex.
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AJ318821 GI:22208418
RNA polymeraeche.
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                                                                                                                                           121 CCATCGAATATCTGGTCCGCTTGCACGAGGTCAGACCACGATGACCGTTCCGGGCGGCG
                101 TCAAGGAGAAGCGCTACGACCTGGCCCGCGTCGGTCGCTATAAGGTCAACAAGAAGCTCG
                                                                      121 CCATCGAGTACCTGGTCCGCCTGCACGAGGCCCAGCACGATGACCGTCCCGGGCGGCA
                                                  61 GCCTGCACGTCGGCGATCCGATCACCAGCTCCACGCTGACCGAGGAAGACGTCGTCGCCA
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    639
/organism="Mycobacterium tuberculosis"

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-rhes 26;
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Pred. No. 1.5
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<1. .>639
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ilarity 87.5%;
Conservative
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Mycobacterium tuberculosis H37Rv RNA-polymerase beta subunit (rpoB)
012205
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                                                                                                                                                                                                                              Direct Submission
Submitted (11-1994) Paul Imboden, Institute for Medical
Microbiology, University of Berne, Friedbuehlstrasse 51, Berne,
3010, Switzerland
                                                                                                                                                                                            61 GCCTGCACGTCGGCGATCCGATCACCAGCTCCACGCTGACCGAGGAAGACGTCGTCGCCA 120
                                                                                                                                         Gaps
                                                                                                                            1 TCAAGGAGAAGCGCTACGACCTGGCCCGGGTAGGCCGCTACAAGGTCAACAAGAAGCTCG 60
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Actinomycetales; Corynebacterineae; Mycobacteriaceae;
Mycobacterium; Mycobacterium tuberculosis complex.
1 (bases 1 to 383)
Imboden, P., Troller, R., Marchesi, F., Telenti, A., Bodmer, T., Cole, S., Schopfer, K. and Burkart, T.
The room gene of Mycobacterium tuberculosis
Unpublished
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                                                                          DB 6; Length 3534;
                                                                /organism="Mycobacterium tuberculosis"

    3853 _____/organism="Mycobacterium tuberculosis"

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1081 c 1188 g
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576. .>3853
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             /strain="Rv"
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/gene="rpoB"
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                                                                        Ouery Match 80.0%;
Best Local Similarity 87.5%;
Matches 182; Conservative
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Imboden, P.
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MTU12205
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FGFIE IPPRKVVDGVVSDGIVYLTADEEDRHVVAQANSPIDADGRFVEPRVLVRRKAG
EVETVPESEUDYMDVSPRQWSVATAMIPFELEBDANRALLGANMQRONPLVRSEAP
LVGTGABELRAAIDATSSSQESGYIEEVSADVITVMHDNGTRRTYRRKFARSCHHGTC
ANQCPIVDAGDRVBAGQVIADGPCTDDGEMALGKNLLVAIMPWEGHNYEDAIILSNRL
VEDDVLTSIHIEBHEIDARDTRKLAGEETTRDIPHIS ISBEVLADDLBERGINYEDAIILSNRL
VEDDVLTSIHIEBHEIDARDTRKLAGEETTRDIPHIS ISBEVLADDLBERGINYERGAEVNDG
DILVGKYTPKGETETTPEERLLKAIFGERGREVNDTSLKVPHGESGKVIGIRVESRED
EDELPAGVNELVRYVYAQKRKISDGDKLAGRHGKNKGVIGKILPVEDMPITLINTHQVPRRNNIGGILETHLGWCARBKKVOTOGKARALPDELLEAGPNDI
TINTHQVPRAGALGGLLSCTLENREGDVLVDAGKARMLSDELLEAGPNAIVS
TRHHLYDDKIHARSTGPYSMITQQPLGGKAQFEGGREGEMECWAMQAYGAAYTLQELL
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MSRMERVVRERNTTQDVEAITPQTLINIRPVVAAIKEFFGTSQLSQFMDQNNPLSGLT
HKRRLSALGPGGLSRERAGLEVRDVHPSHYGRMCPIETPBGPNIGLIGSLSVYARVNP
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127989.
RNA polymerase beta-subunit; rpoB gene.
Mycobacterium tuberculosis (strain Rv) DNA.
Mycobacterium tuberculosis
Mycobacterium tuberculosis
Actinobacteria; Actinobacteria; Actinobacteria; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium
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1 (bases 1 to 5084)
Miller,L.P., Crawford,J.T. and Shinnick,T.M.
The rpoB gene of Mycobacterium tuberculosis
Antimicrob. Agents Chemother. 38 (4), 805-811 (1994)
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1. .5084
/organism="Mycobacterium tuberculosis"
/strain="Rv"
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Pred. No. 1e-16;
0; Mismatches 26;
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/protein_id-"AAA21416.1"
/db_xref-"GI:468334"
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1065. .4598
/gene="rpoB"
1065. .4598
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/gene="rpoB"
/codon_start=1
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Best Local Similarity 87.5%;
Matches 182; Conservative
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LVGTGWELRAAIDAATSSQESGVIEEVSADYITVWHDNGTRRTYRWRKFARSNHGTC
ANOCPTVDAGDRVEAGQYIACCGAEGTRATYRWRKFARSNHGTC
ANOCPTVDAGDRVEAGQYIACCGAEGTRAD PNISDEVLADLDERGIVURIARLYSIL
BLEDAGVYDFRIGAEGTRAD PNISDEVLADLDERGIVURIGAEVRD
DILVGKVTPKGETELTPERILLRAIFGERAREVRDTSLKVPHGESGKVIGIRVFSRED
EDELPAGVNELVRVYAQKRKISDGDKLAGRHGKKOYDGKLLVFUEDWPPLADCTPVDI
ILNTHGVPRRNNIGGILETHLGWCAHSGWKVDARKPOWAARLPDELLEAHANAIVS
TPVFDGAQCAAGAELGGLLGCTLPNNGDVLVDADGKSMEPGRSCEPFPYVVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="MLDVNFFDELRIGLATAEDIRQWSYGEVKKPETINYRTLKPEKD
GLFCERIFFOFRDWECYGKYKRVFRFKGIICERGGVEYTRAKVRRERMGHIELAAPVT
HWYFKGVPSRLGYLELEKIIYFAAYVITSVDEEMRHNEL"
1534 c 1691 g 890 t
                                                                           EEDVVATIELLYRLEGGTTWIVEGVEVPVETDIOHEGNRRELETVGELIONORSCH
MSRKERVVRERMTTODVEATTWIVEGVEVPVAAIKEFGTSGLSGFWDQNNFLSGLT
MSRKERVALGEGGLSRERAGLEVROWHENYGANGVEIETPEGTSGLSGFWDQNNFLSGLT
FRELSALGEGGLSRERAGLEVROWHENYGENGVEIETPEGSPUIGLIGSLSVYARVND
FGFIETPYRKVVDGVYSDEIVITAADEEDRHWVAQANSPIDADGRFVEPRUIVRRKAG
EVEYVPSSEVDYMDVSPRQMVSVATAMIPFLEHDDANRALMGANMQRQAVPLVRSEAP
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Mycobacterium tuberculosis CDC1551, section 50 of 280 of the
                        RDTVGVRIDRKRRQPVTVLLKALGWTSEQIVERFGFSEIMRSTLEKDNTVGTDEALLD
IYRKLRPGEPPTKESAQTLLENLFFKEKRYDLARVGRYKVNKKLGLHVGEPITSSTLT
                                                                                                                                                                                                                                                                                                                                                                                                                                    KLHHLVDDKIHARSTGPYSMITQQPLGGKAQFGGQRFGEWECWAMQAYGAAYTLQELL
TIKSDDTVGRVKVYEAIVKGENIPEPGIPESFKVLLKELQSLCLNVEVLSSDGAAIEL
FEKGTFIINGTERVVVSQLVRSPGVYFDETIDKSTDKTLHSVKVIPSRGAWLEFDVDK
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1 (bases 1 to 1935)

Fleischmann, R.D., Alland, Eisen, J.A., Carpenter, L., White, O., Peterson, J., DeBoy, R., Dodson, R., Gwinn, M., Haft, D., Hickey, E., Kolonay, J.F., Nelson, W.C., Umayam, L.A., Ermolaeva, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1966 TCAAGGAGAAGCGCTACGACCTGGCCCGCGTCGGTCGCTATAAGGTCAACAAGAAGCTCG 2025
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Actinomycetales, Corynebacterineae, Mycobacteriaceae,
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/codon_start=1
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/procein_id="AAA2141.1"
/db_xref="GI:537608"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGEDEDLERAAANLGINLSRNESASFEDLA"
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/gene="rpoC"
4641. .>5084
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AE006964
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LEDIWSTFTKLAPKQLIVDENLYRELVDRYGEYFTGAMGAESIQKLIENFDIDAEAES
LRDVIRNGGCGKKLRALKKVVAAPCOSGNSPMGWYLDAVPYIPPELRPWYQLDGGR
FASDLANDLYRRVINRNRKLKLIDLGAPEIIVNNEKRALQESVDALFDNGRRGRPYT
GPGNPELKSLSDLLKGKQGFRQNLLGKRNDYSGRSVIVVGPQLKLHQCGLFRLMALE
LEKPFWKRLVDLHAQNIKSAKRMYERQFPOWWVLEEVIABHPHRLG
IQAFEPMLVEGKAIQLHPLVCEAFNADFDGDQMAVHLPLSAEAQAEARILMLSSNNIL
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GLFCEKIFGPTRDWECYCGKYKRVRFKGIICERCGYEVTRAKVRRERMGHIELAAPVT
HIWYFKGVPSRLGYLLDLAPKDLEKIIYFAAYVITSYDEEMRHNELSTLEAEMAVERK
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Salzberg,S.L., Delcher,A., Utterback,T., Weidman,J., Khouri,H., Alll,J., Mikula,A. and Bishai,W. Whole genome comparison of Mycobacterium tuberculosis clinical and laboratory strains
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PID:149992; identified by sequence similarity; putative" /codon_start=1
                                                                                                                                                                                                                           Eleischmann, R.D., Alland, D., Eisen, J.A., Carpenter, L., White, O., Fleischmann, R.D., Alland, D., Eisen, J.A., Carpenter, L., White, O., Peterson, J., DeBoy, R., Dodson, R., Gwinn, W., Haft, D., Hickey, E., Kolonay, J.E., Nelson, W.C., Umayam, L.A., Ermolaeva, M., Salzberg, S.L., Delcher, A., Utterback, T., Weidman, J., Khouri, H., Gill, J., Mikula, A. and Bishai, W.

Submitted (25-APR-2001) The Institute for Genomic Research, 9712 Medical Center Dr. Rockville, MD 20850, USA
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/strain="CDC1551"
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/codon_start=1
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/gene="MT0696"
3744. .7694
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163. .3699
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/gene="MT0695"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FKHEDGSERVLSDGDHVEVGQQLMEGSADPHEVLRVQGPREVQTHLVREVGEVTRAGG
SYSHDKHLEVTVRQMLRRYTIDGSGPFELPGSLIDBAEFEABIRRVVASGGEPBAAGR
PVLMGITKASLATDSMLSAASFQETFELPGSLIDBAEFEABIRRVASGGEPBAAGR
GINRYRNIAVQPTEEARAAAYTIPSYEDQYYSPDFGAATGAAVPLDDYGYSDYR"
Comptement (7691. .8065)
SPASGRPLAMPRLDMVTGLYYLTTEVPEDTGEYQPASGDHPETGVYSSPAEAIMAADR
GVLSVRAKTKVRLTQLRPPYELEAELEGHSGMOGDDAMMAETTGRYMENBLLEPLGYP
FVNKQMHKKVQART INDLABERYDM IVVAQTVDKLKDAGFYMATRSGVTVSMADVLVPP
RKKEILDHYEERADKVEKQFQRGALNHDERNEALVEIWKEATDEVGQALREHYPDDNP
                                                                                                                                                                                                      IITIVDSGATGNFTQTRTLAGMKGLVTNPKGEFIPRPVKSSFREGLTVLEYFINTHGA
RKCLADTALRTADSGYLTRRLVDVSQDVIVREHDCQTERGIVVELAERAPDGTLIRDP
YIETSAYARTLGTDAVDEAGNVIVERGQDLGDPEIDALLAAGITQVKVRSVLTCATST
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MGGGCGGFRARENDDLGFVRAVVADTAINNYSIDARVYYCHGANGATMYSTLACUT
SIFAAIGVVSGTQULDPCQSPRPVSUYHHGTADPLVRYHGGPGAFAIDGPPVPDLN
AFWREVNRCGALDTTTEGPVTTSGATCADNRRVVLLTVDDAGHRWPSFAIQTLWRFFA
                                                                                                                                                                                                                                                                                                                                                                      GVCATCYGRSMATGKLVDIGEAVGIVAAQSIGEPGTQLTMRTFHÖGGVGEDITGGLPR
VQELFEARVPRGKAPIADVTGRVRLEDGERFYKITIVPDDGGEEVVYDKISKRQRLRV
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PID:457174 PID:537028; identified by sequence similarity;
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10957. .11799
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/note="Similar to GB:U00012 PID:466863; identified by
/codence slmilarity; putative"
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/note="ldentified by Glimmer2; putative"
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10167. .10925
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11859. .13487
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DPELKPATTKAGITAGWSWTEKQGGSDVRAGTTQATPNADGSYSLTGHKWFTSAPWCD
IFLVLAQAPGGLSCELLPRRVLPDGTRRRWFLQRLKKDKLGNHAANSSEVEYDGAAWLV
GEGGRGVPTIIEMVNLTRLDCALGSATSMRTGLTRAVHHAQHRRAFGAYLIDQPLMRN
VLADLAVEARAATTYAMRWAGATDNAYRGNEFFBALLRRIGLAARKYWVCKRSTAHAAE
ALECLGGNGYVEDSGMPRLYREAPLMGIWEGSGNVSALDTLRAMATRPACVEVLEDEL
ARSAQODPRLICGHVERLRRPGCDLDTTGYRARKTAEDICLALQGSLLVRRGHPAVAEA
FLATRLGGGWGGAYGTMPAGLDLAPILERALVKG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="mtherpednikthmyvevtgriarltenrpekgnaliadppl
Elsalverablopgvyvilvsgregegreagpplsaraegssstggggayggyvldgky
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Viaaadakigypptrwgvpaaglwahrlgdorakrilftgdcitgaqaabwglavba
Pepalldberterlyariaalpvvqlimvklalnsallqogvatsrmystvfdgaarht
Peghavadavehgfrdavrrdbepegdygrqasrv"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mycobacterium tuberculosis H37Rv complete genome; segment 32/162. 295972 AL123456 295972.1 GI:3261790
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="enoyl-CoA hydratase/isomerase family protein"
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/db_xref="GI:13880224"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1124 GGCTGCATGTCGGCGAGCCCATCACCATCGTCGTCGTCGACGAAGAAGACGTCGTGGCCA 1183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1184 CCATCGAATATCTGGTCCGCTTGCACGAGGGTCAGACCACGATGACCGTTCCGGGCGGCG 1243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 GCCTGCACGTCGGCGATCCGATCACCAGCTCCACGCTGACCGAGGAAGACGTCGTCGCCA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 CCATCGAGTACCTGGTCCGCCTGCACGAGGGCCAGCACCACGATGACCGTCCCGGGCGGCA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Mycobacterium tuberculosis H37Rv
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium tuberculosis complex.
                                                                                                                                                                                                                                                                                                                                                                                                         /note="similar to GP:3885480; identified by similarity; putative"
/codon_start=1
/transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14439. .15161
/gene="MT0703"
/note="identified by Gl1mmer2; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=1
/transl_table=11
/product="hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        80.0%; Score 166.4; DB 87.5%; Pred. No. 7.7e-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCGAGGTGCCGGTGGAAACCGACGACAT 1271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 CCGAGGTGCCGGTTGAGACCGACGACAT 208
                                                                                                                                                                                                                                                                                                                                 /gene="MT0702"
13498. .14436
/gene="MT0702"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="MT0703"
14439. .15161
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                                                                                                                                                                                                                                                                                                               13498.
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Best Local Similarity
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ACCESSION
VERSION
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MTCI376
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Complement(3530. .3685)
/gene="Rv0657c"
/note="Rv0657c"
/note=
                                                                                                              /note="RV0655, (MTC1376.21), len: 359, abc transporter,
FASTA score: YRBF_ECOLI P45393 hypothetical abc
FASTA score: YRBF_ECOLI P45393 hypothetical abc
E(1): 3.4e.33 (38.5% identity in 244 as overlap); contains
PS00017 ATP/GTP-binding site motif A, PS00211 ABC
transporters family signature, highly similar to M. leprae
MKL_MYCLE P30769 possible ribonucleotide transport atp-
(347 as opt: 2021 z-score:2244.4 E(): 0, (92.2% identity
in 335 as overlap). Also similar to many otherM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product-"hypothetical protein Rv0655"
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/db_xref="GI:214308"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PGEISGGMRKRAGLARALVLDPQIILCDEPDSGLDPVRTAYLSQLIMDINAQIDATIL
TYTHNINIARTVPDMGMLFKKHLVMEGPREVLLTSDEPVVROFLNGRRIGPIGMSEE
KDEATWAEEQALLDAGHHAGGVEEIEGVPPQISATPGMPERRAVARRQARVREMLHTL
PKKAQAAILDDLEGTHKYAVHEIGO*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RTLFGVLFQDGALFGSMNLYDNTAFPLREHTKKKESEIRDIVMEKLALVGLGGDEKKF
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/gene="Rv0656c"
/note="Rv0656c, (MTCI376.20, unknown), len: 127 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="PS00017 ATP/GTP-binding site motif A"
2074. 218
/gene="Rv655"
/note="Rv655"
/note="PS00211 ABC transporters family signature"
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/note="possible RBS upstream of Rv0657c"
complement(3761. .4477)
/gene="Rv0658c"
/gene="Rv0658c"
/note="Rv0658c"
/note="Rv0658c"
/note="Rv0658c"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                identity in 241 aa overlap)"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref-"SPTREMBL:006782"
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/gene="Rv0656c"
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/db_xref="G1:2143304"
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/transl_table=11
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                                              1585. .2664
/gene="Rv0655"
/note="Rv0655,
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/gene="Rv0655"
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                                              CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Details of M. tuberculosis sequencing at the Sanger Centre are available on the World Wide Web.

(URL, http://www.sanger.ac.uk/Projects/M_tuberculosis/) CDS have been renumbered from the original cosmid submissions but the old gene designations are in brackets after the new gene numbers. Gene prediction was based on a Hidden Markov Model of TB genes implemented in TBparse (Krogh) supplemented with visual inspection of positional base preference in codons, especially where there is an increase in the observed/expected third position G + C.

CAUTION: In some cases we may not have predicted the correct initiation codon. Where possible we choose an initiation codon (atg, qtg, or ttg) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most upstream
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission

Submitted (11-JUN-1998) Submitted on behalf of the Mycobacterium tuberculosis sequencing and mapping teams, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA Unite de Genetique Moleculaire Bacterienne, Institut Pasteur, 28 rue du Docteur Roux, On Jun 27, 1998 this sequence Version replaced gi:2143285.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Rv0654, (MTC1376.22), len: 501. unknown, FASTA
core: 053353 LIGNOSTILERNETA-LPHA, PETA-LDIOXYEENASE (485
aa) opt:280 z-score: 330.1 E(): 2.38-11, (28.5% identity
in 523 aaoverlap). Also similar to M. tuberculosis protein
MTCY21C1. O7C (29.5% identity in 522 aa overlap)"
//codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YVV YDLPVTFDPMQVVPASVPRWLORPARLVIQSVIGRYR FDPFIALGNRWGGHSD
RLPYAWNESYPARVGVMPREGGNEDVRWFDIEPCYVYHPLAAYSECRNGAEVLVLDVV
RYSRMFDRDRRGFGGDSRPSLDRWTINATGATAERDDRAOEFPRINETLVGGPHR
FAYTVGIEGGFLVGAGALSTPLXQDCVTGSSTVASLDPDLLIGEWYFVPNSSARAE
DDGILMGYGWHRGRDEGQLLLLDAQTLESIATVHLDQRVPMGFHGNWAPTT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MTTAQAAESQNPYLEGFLAPVSTEVTATDLPVTGRIPEHLDGRY
LRNGPNPVAEVDPATYHWFTGDAMVHGVALRDGKARWYRNRWVRTPAVCAALGEPISA
RPHPRTGIIEGGPNTNVLTHAGRTLALVEAGVVNYELTDELDTVGPCDFDGTLHGGYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AHPQRDPHTGELHAVSYSFARGHRVQYSVIGTDGHARRTVDIEVAGSPMMHSFSLTDN
                             Cole, S.T., Brosch, R., Parkhill, J., Garnier, T., Churcher, C.,
Harris, D., Gordon, S.V., Eiglmeier, K., Gas, S., Barry III, C.E.,
Harris, D., Gordon, S.V., Eiglmeier, K., Gas, S., Barry III, C.E.,
Connor, R., Badocock, K., Basham, D., Ebrown, D., Chillingworth, T.,
Hamlin, N., Holroyd, S., Hornsby, T., Jagels, K., Krogh, A., McLean, J.,
Moule, S., Murphy, L., Oliver, S., Osborne, J., Quail, M.A.,
Rajandream, M.A., Rogers, J., Rutter, S., Seeger, K., Skelton, S.,
Barrell, B.G.
                                                                                                                                                                                                                                                                                                                                                                                                     Deciphering the biology of Mycobacterium tuberculosis from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="agga, possible rbs upstream of Rv0654"
68. .1573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Mycobacterium tuberculosis H37Rv"
/strain="H37Rv"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product-"hypothetical protein Rv0654"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref-"SPTREMBL:006785"
                                                                                                                                                                                                                                                                                                                                                                                                                                               complete genome sequence
Nature 393 (6685), 537-544 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:83332"
/clone="1376"
57. .61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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68. .1573
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (bases 1 to 19770)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    . 2664
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Parkhill, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         source
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AUTHORS
TITLE
JOURNAL
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MEDLINE
PUBMED
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REFERENCE
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Mycobacterium smegmatis. Mycobacterium smegmatis
                                                                                                                                                                                                                                                                                                                                                      2 (bases 1 to 3752)
Hetherington, S.V.
Direct Submission
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                                                                                                                                     Mycobacterium.
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Best Local Similarity
Matches 178; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ø
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ORIGIN
                                          ORGANISM
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                                                                                                                                                               REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement (4480 . .4483)
/note="possible RBS upstream of Rv0658c"
complement (4753 . .5061)
/gene="Rv0659c"
complement (4753 . .5061)
/gene="Rv0659c"
/note="Rv0659c, (MTC1376.17), len: 102; unknown, similar
to YW28_MYCTU 010867 hypothetical 12.3 kd protein cY39.28
(114 aa), fasta scores; opt: 144 z-score: 213.2 E():
7.3e-05, 30.88 identity in 107 aa overlap. Also similar to
MTCY09F9.22 (32.7% identity in 101 aa overlap)"
                                                                                                                                                  /codoi_state_1
//transl_table=11
/product="hypothetical protein Rv0658c"
/product="hypothetical protein Rv0658c"
/product="hypothetical protein Rv0658c"
/db_xref="c1:2143303"
/db_xref="spTREMBL:006781"
/db_xref
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MSU24494 3752 bp DNA linear BCT 02-MAR-2000 Mycobacterium smegmatis DNA polymerase (rpob) gene, complete cds. U24494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /Lranslation="MRRGELWFAATPGGDRPVLVLTRDPVADRIGAVVVVALTRTRRG
LVSELELTAVENRVPSDCVVNFDNIHTLPRTAFRRITRLSPARLHEACQTLRASTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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probablemembrane protein, similar to YPRB_ECOLI P33774 hypotherical24.3 kd protein (urf 1) (217 aa), fasta scores, opt: 174 z-score: 215.8 E(): 5.3e-05, (25.6% identity in 223 aa overlap). Also similar to MTCY359.10 (28.7% identity in 178 aa overlap)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10758 TCAAGGAGAAGGCCTACGACCTGGCCCGCGTCGGTCGCTATAAGGTCAACAAGAAGAAGCTCG 10817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10818 GGCTGCATGTGGGCGAGCCCATCACGTCGTCGACGAAGAAGAAGACGTGGCCA 10877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 GCCTGCACGTCGGCGATCCGATCACCAGCTCCACGCTGACCGAGGAAGACGTCGCCA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCATCGAGTACCTGGTCCGCCTGCACGAGGCCCAGCACGATGACCGTCCCGGGCGGCA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 TCAAGGAGAAGCGCTACGACCTGGCCCGGGTAGGCCGCTACAAGGTCAACAAGAAGCTCG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /transl_table=11
/product_"hypothetical protein Rv0659c"
/protein_id="CAB09387.1"
/db_xref="G1:2143302"
/db_xref="SPTREMBL:006780"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 166.4; DB 1;
Pred. No. 7.7e-17;
0; Mismatches 26;
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complement(5048. .5293)
/gene="Rv0660c"
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ilarity 87.5%;
Conservative
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Best Local Similarity
Matches 182; Conserv
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ACCESSION
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KEYWORDS
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LOCUS
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VLNIGOILETHLGMGAKAGWNIDVLACVPDWASKLPEELYSAPADSTVATPVPDGAOE
GELAGLLGSTLPNRDGEVWVNADGKATLFDGRSSGEPFPYPVTVGYMYILKLHHLVDD
KIHARSTGPYSMITQQPLGGKAQFGGQRFGEMECWAMQAYGAAYTLQELLTIKSDDTV
GRVKVYEAIVKGENIPEPGIPESFKVLLKELQSLCLNVEVLSSDGRAIEMRDGDDEDL
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                                                                                                                                                                                                                                                  Submitted (11-APR-1995) Seth V. Hetherington, Infectious Diseases,
St. Jude Children's Research Hospital, 332 N. Lauderdale, Memphis,
TN 38101, USA
                                                           1 (bases 1 to 3752)
Hetherington,S.V., Watson,A.S. and Patrick,C.C.
Sequence and analysis of the rpoB gene of Mycobacterium smegmatis
Antimicrob. Agents Chemother. 39 (9), 2164-2166 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1068 TCAAGGAGAAGGCTACGACCTGGCCCTGTGGGCCGTTACAAGGTCAACAAGAAGCTGG 1127
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae;
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    .3752
/organism="Mycobacterium smegmatis"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="DNA polymerase"
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                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
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/gene="rpob"
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/gene="rpob"
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Sequence 57, Appl
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Sequence 32, Appl
Sequence 33, Appl
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Sequence 120,
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/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
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/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
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                              GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd
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Maximum Match 100%
Listing first 45 summaries
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GENERAL INFORMATION:
APPLICANT: Persing, David H.
TITLE OF INVENTION: Detection of a Genetic Locus Encoding
TITLE OF INVENTION: Resistance to Rifampin in Mycobacterial Cultures and
TITLE OF INVENTION: Clinical Specimens
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                 Sequence 1, Appl 1
Sequence 13, Appl 1
Sequence 1, Appl 1
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT AFPLICATION DATA:
APPLICATION NUMBER: US/08/250,030
FILING DATE: 26-MAY-1994
CLLASSIFICATION: ANA-1994
CLLASSIFICATION: AND MERRICASSIFICATION: NAME: Mueting, Ann M. REGISTRATION: AND MERRICASSIFICATION NUMBER: 150.105US1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-339-031
TELEPHONE: 612-339-031
SEQUENCE CHARACTERISTICS:
LENGTH: 970 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
US-09-105-537-3
US-08-125-468-1
US-08-320-878-19
US-09-320-878-19
US-08-804-128-1
US-08-804-198-1
US-08-118-904-79
US-09-385-028-1
US-09-385-028-1
US-09-385-028-1
US-09-385-028-1
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US-09-385-028-1
US-08-332-643-41
US-08-332-643-41
US-08-332-643-41
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US-07-642-734C-1
US-08-439-009A-1
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Best Local Similarity 87.5%;
Matches 182; Conservative
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STREET: 3500 IDS Center
CITY: Minneapolis
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COMPUTER READABLE FORM:
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CORRESPONDENCE ADDRESS
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US-08-250-030-1
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US-09-082-614A-57
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APPLICANT: and Hoffmann-La Roche Inc.
TITLE OF INVENTION: Detection of a Genetic Locus Encoding
TITLE OF INVENTION: Resistance to Rifampin
NUMBER OF SEQUENCES: 15
ADDRESSEE: Schwegman, Lundberg & Woessner
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OFFRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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3500 IDS Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    150.105WO1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: PCT/US95/06790 FILLING DATE: 26-MAY-1995 CLASSIFICATION:
                                                                                                                              181 TCGAGGTGCCGGTGGAAACCGACGAT 208
                                                                                                                                                206 TCGAGGTGCCGGTGGAAACCGACGACAT 233
                                                                                                                                                                                                                                          Sequence 1, Application PC/TUS9506790 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Radsch, Kevin W.
REGISTRATION NUMBER: 35,651
REFERENCE/COCKET NUMBER: 150.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-339-0331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 612-339-3061
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  80.0%;
87.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 970 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                       Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; MOLECULE TYPE: DNA PCT-US95-06790-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
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                                                                                                                                                                                                                 RESULT 2
PCT-US95-06790-1
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COUNTRY:
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CITY: Mi
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Pred. No. 4.1e-27;
0; Mismatches 41; Indels 0;
                                                                                                                                      APPLICANT: Zhang, Ying
APPLICANT: Telenti, Amalio
APPLICANT: Telenti, Amalio
APPLICANT: Telenti, Amalio
APPLICANT: Rodmer, Thomas
TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
TITLE OF INVENTION: in Mycobacterium Tuberculosis
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                 ADDRESSEE: Finnegan, Henderson, Farabow, Garrett
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-00S/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 02356.0068-00000
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 TCGAGGTGCCGGTGGAAACCGACGACAT 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/313,185
FILING DATE: 12-OCT-1994
                 Sequence 57, Application US/08313185 Patent No. 5851763 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ 1D NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 3447 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , MOLECULE TYPE: DNA (genomic) US-08-313-185-57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68.5%;
80.3%;
                                                                            APPLICANT: Heym, Beate
APPLICANT: Cole, Stewart
APPLICANT: Young, Douglas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 80.31
Matches 167; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                            USA
US-08-313-185-57
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SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO) CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/329,350
FILING DATE: Herewith
                                                                                                                                                                                                                                                                                                                                                        Sterne, Kessler, Goldstein & Fox P.L.L.C. 1100 New York Avenue, N.W., Suite 600
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LOCATION: 233..838
OTHER INFORMATION: /product= "50K-cellulase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 04-DEC-1995,
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/020,840
FILING DATE: 28-JUN-1996
FILING DATE: 28-JUN-1996
FILING DATE: 16-OCT-1996
FILING DATE: 16-OCT-1996
FILING DATE: 16-OCT-1996
APPLICATION NUMBER: PCT/F196/00550
FILING DATE: 17-OCT-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: HEFWAITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/841,636
FILING DATE: 30-APR-1997
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 60/005,335
PRIOR APPLICATION DATA:
APPLICATION DATE: US 60/007,926
FILING DATE: U-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Melanocarpus albomyces
                                                                      Londesborough, John
                                                                                          APPLICANT: Vehmaanper Jari
APPLICANT: Haakana, Heli
APPLICANT: M ntyl, Arja
APPLICANT: Lantto, Ralja
APPLICANT: Elovainio, Minna
APPLICANT: Paloheimo, Marja
APPLICANT: Suominen, Pirkko
                                               Miettinen-Oinonen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Shea Jr., Timothy
REGISTRATION NUMBER: 41.306
REFERENCE/DOCKET NUMBER: 17
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 1894 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: DNA (genomic) ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : (202)371-2600
(202)371-2540
                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                       Washington
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                                                                                                                                                                                                                       THILE OF INVENTION: Rapid Detection of Antibiotic Resistance Title OF INVENTION: in Mycobacterium Tuberculosis HUMBER OF SEQUENCES: 66 CORRESPENDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                             ADDRESSEE: Finneyan, Henderson, Farabow, Garrett & ADDRESSEE: Dunner
STREET: 1300 i Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURKENT APPLICATION DATA:
APPLICATION NUMBER: US/09/082,614A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 02356.0068-00000
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 TCGAGGTGCCGGTGGAAACCGACGACAT 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/313,185
FILING DATE: 12-OCT-1994
ATTOKNEY/AGENT INFORMATION:
Sequence 57, Application US/09082614A
Patent No. 6124098
GENERAL INFORMATION:
APPLICANT: HEYM, BEALE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 5
US-09-329-350-32
: Sequence 32, Application US/09329350
                                                                                      APPLICANT: Cole, Stewart
APPLICANT: Young, Douglas
APPLICANT: Zhang, Ving
APPLICANT: Honore, Nadine
APPLICANT: Telent, Amalio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 57:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (202) 408-4000
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TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                     STREET: 1300 L St
CITY: Washington
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D.C
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                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                STATE:
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APPLICANT: Suominen, Pirkko TITLE OF INVENTION: NOVEL CELLULASES, THE GENES ENCODING THEM AND TITLE OF INVENTION: USES THEREOF 916..1596 NAME/KEY: exon LOCATION: 916.

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Sequence 1. Application US/09103840A
Patent No. 6294328
GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, ROBERT D.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN
TITLE OF INVENTION: DNA SEQUENCES
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/383,833
FILING DATE: 21-JUL-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Mycobacterium tuberculosis OTHER INFORMATION: H37Rv US-09-103-840A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
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60.8%;
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Best Local Similarity 55.5%;
Matches 71; Conservative
                                                                                                                                  Ouery Match 18.3%;
Best Local Similarity 60.8%;
Matches 62; Conservative (
  TYPE: DNA ORGANISM: Pseudorabies virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                         ; NAME/KEY: CDS
; LOCATION: (1)..(2742)
US-09-232-468A-1
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Matches 62; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                          5196516-7
;Patent No. 5196516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 4897
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                                                                                                                                      Query Match
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                                                                                                                                                             253 CGCGGCGCGCCATAAAACGAGTCCACCTGCAGATACATCGACGAGGAGTGTGGGC 312
                                                                                                                                      56 GCTGGGCCTGAACACCAATCATCCGATCACCACGACGACGCTGACCGAAGAAGACGTCGT 115
                                                                                                                                                                                                                  116 CGCCACCAFCGAGTATCTGGTCCGCCTFGCACGAGGCCCAGGCCACGATGACCGTGCCGGG 175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           107 AGACGTCGTCGCCACCATCGAGTATCTGGTCGCCTGCACGAGGGCCAGGCCACGATGAC 166
                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: AUDONNET et al.
TITLE OF INVENTION: POLYNUCLEOTIDE VACCINE FORMULA AGAINST PORCINE
TITLE OF INVENTION: REPRODUCTIVE AND RESPIRATORY PATHOLOGIES
FILE REFERENCE: 454313-2230
CURRENT APPLICATION NUMBER: US/09/232,468A
CURRENT FILING DATE: 1999-01-05
NUMBER OF SEO ID NOS: 54
SOFTWARE: PALENTIN Ver. 2.1
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0
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                                                         Length 1894;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: MCGONIGLE, BRIAN
APPLICANT: O'REEF, DANIEL
APPLICANT: O'REEF, DANIEL
TTTLE OF INVENTION: PLANT GLUTATHIONE-S-TRANSFERASE ENZYMES
FILE REFERENCE: CL-1128-A
CURRENT APPLICATION UNMBER: US/09/248,335
CURRENT FILING DATE: 1999-02-10
EARLIER APPLICATION NUMBER: 08/924,759
EARLIER APPLICATION NUMBER: 08/924,759
EARLIER APPLICATION NUMBER: 08/924,759
SARICER FILING DATE: 1997-September-05
NUMMER OF SEQ 1D NOS: 74
SOFTWARE: MICROSOIL WORD VERSION 7.0A
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                                                                                                Indels
                                                                                                61;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  313 GGGACGGGCCGGCCGTTCCGGCCGACCCTACGA 351
                                                         18.9%; Score 39.4; DB 4; 55.5%; Pred. No. 0.15;
; OTHER INFORMATION: /product.= "50K-cellulase"
US-09-329-350-32
                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                          US-09-248-335-53
. Sequence 53, Application US/09248335
. Patcut No. 6096504
. GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                1251 CGTCGTCGACGCCCGG 1267
                                                                             Best Local Similarity 55.59
Matches 76; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: maize US-09-248-335-53
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Rest Local Simil
Matches 84;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 53
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                                                             Query Match
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                                                                                                     2484 CATGAAGGCCCTGTACCCCGTCACGACGAAGACGCTCAAGGAGGAGGACGACGACGACGAGG 2543
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                                                                                62 CCTGAACACCAATCATCCGATCACCACGACGCTGACCGAAGAAGACGTCGTCGCCAC 121
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Score 38; DB 4; Length 2742;
Pred. No. 0.36;
0; Mismatches 40; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 4897;
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                                                                                                                                                                                                                                                                                                                                  APPLICANT: SCHREURS, CHRISTA S.; METTENLEITER, THOMAS C.; SIMON, ARTUR J.; LUKAS, NOEML; RZIHA, HANNS J.
TITLE OF INVENTION: PSEUDORABIES VIRUS VACCINE
NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2544 CGACGTGGACGAGGCCAAGCTGGACCAGGCCCGGGACATGAT 2585
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                                                                                                                                                                  122 CATCGAGTATCTGGTCCGCCTGCACGAGGGCCAGGCCACGAT 163
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Pred. No. 1.9;
0; Mismatches 57;
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Pred. No. 0.39;
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Secondary-Metabolite Biosynthesis Genes
From Actinomycetes, Method of Isolating Them, and Their
Use.
                                                                                    72 AATCATCCGATCACCACGACGACGCTGACCGAAGAAGACGTCGTCGCCACCATCGAGTAT 131
                                                                                                                                                                                                                    Gaps
                                                         12 CGCTACGACCTGGCCCGTGTCGGCCGATACAAGGTCAACAAGAAGCTGGGCCTGAACACC 71
                      ;
0
                  98; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Pinnegan, Henderson, Farabow, Garrett ADDRESSEE: Dunner STREET: 1300 I Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/681,953
FILING DATE: 30-JUL-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02481.1372-00000
  Pred. No. 1;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Piepersberg, Wolfgang
APPLICANT: Stockmann, Michael
APPLICANT: Taleghani, Kampiz Mansouri
APPLICANT: Taleghani, Kampiz Mansouri
APPLICANT: Taleghani, Kampiz Mansouri
APPLICANT: Grabley, Susanne
APPLICANT: Sichel, Petra
APPLICANT: Sichel, Petra
APPLICANT: Sichel, Petra
APPLICANT: Brau, Barbara
TITLE OF INVENTION: Secondary-Metabolite
TITLE OF INVENTION: From Actinomycetes,
NUMBER OF SEQUENCES: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/196,218
FILING DATE: 25-AUG-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 31, Application US/08681953
Patent No. 5710032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 31: SEQUENCE CHARACTERISTICS: LENGTH: 2634 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Ogden, Stasia L.
REGISTRATION NUMBER: 36,228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 02
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: DNA (genomic)
  49.28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RY: United States 20005-3315
Best Local Similarity 49.2
Matches 95; Conservative
                                                                                                                                                                                                                                                                                                                                     2377 GCGATCATCGGCG 2389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                              192 GTGGAAACCGACG 204
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LOCATION:
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From Actinomycetes, Method of Isolating Them, and Their
                                   Db 595867 ACTCACGCCACCATCACCGCGCGCTAACCGGCACCCTGGGCACCGTGGCGG 595808
                50 CANGAAGCTGGGCCTGAACACCAATCATCCGATCACCACGACGACGTGACCGAAGAAGA 109
                                                                                          110 COTCGTCGCCACCATCGAGTATCTGGTCCGCCTGCACGAGGCCAGGCCACGATGACCGT 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17.4%; Score 36.2; DB 1; Length 2634;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Z1P: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DUS/MS-DOS
SOFTWARE: PALENLIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Piepersberg, Wollqang
APPLICANT: StockMann, Michael
APPLICANT: Taleghani, Kampiz Manscuri
APPLICANT: Distler, Jurgen
APPLICANT: Grabley, Susanne
APPLICANT: Sichel, Petra
APPLICANT: Brau, Barbara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/196,218
FILING DATE: 25-AUG-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                            Sequence 31, Application US/08196218
Patent No. 5614619
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Ogden, Stasia L.
REGISTRATION NUMBER: 36,228
REFRENCE/DOCKET NUMBER: 0248
TELECOMMUNICATION INFORMATION:
TELEPAN: 202-408-4000
TELEFAX: 202-408-4400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1300 1 Street, N.W
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INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 2634 base pairs
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1561..2625
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
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416..1531
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                                                                                                                                                                                         1 111 11
0b 595807 GTC:GTCG 595800
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TITLE OF INVENTION:
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FEATURE:
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; LOCATION:
US-08-196-218-31
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TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
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55.5%;
                                                                                                                                                                                                                                                                     Query Match 17.2%;
Best Local Similarity 60.2%;
Matches 80; Conservative (
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Best Local Similarity 55.5%
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 734 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                    ) NAME/KEY: misc_feature
; LOCATION: 1...734
US-09-221-017B-1070
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SOFTWARE: Patentin Ver. 2.1
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                                                                                                                                    ANTI-SENSE: UNK
ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                       2197 CTCTACGACGCTACTGGAAGGACACCGGGAGGTCGAGGACGTCCTTGAGTGCAACAGC 2256
                                                                                                                                                                                                                                                                    72 AATCATCCGATCACCACGACGACGCTGACCGAAGAAGACGTCGTCGCCACCATCGAGTTAT 131
                                                                                                                                                                    Gaps
                                                                                                                                                                                                    12 CGCTACGACCTGGCCCGTGTCGGCCGATACAAGGTCAACAAGAAGCTGGGCCTGAACACC 71
                                                                                                                                                                                                                                                                                                                                     APPLICANT: ROSS, Bruce C.
TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF
NUMBER OF SEQUENCES: 1120
CORRESPONDENCE ADDRESS:
                                                                                                                                                                  0;
                                                                                                                                                                    Indels
                                                                                                                                                                  98;
                                                                                                                                 Score 36.2; DB 1;
Pred. No. 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OFFRATING SYSTEM: WINDOWS
SOFTWARE: FASTSEQ for WINDOWS
CURRENT APPLICATION DATA:
                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27340-20021.00
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FILING DATE: 23-DEC-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1070, Application US/09221017B Patent No. 6444799 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: MORRISON & FOERSTER STREET: 755 PAGE MILL ROAD CITY: PALO ALCO STATE: CA COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: MODFOY, GLADAYS H
REGISTRATION NUMBER: 32,430
REFERENCE/DOCKET NUMBER: 273
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP1182
FILING DATE: 31-DEC-1997
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: PP2911
FILING DATE: 09-APR-1998
                                                                                                                               17.4%;
ilarity 49.2%;
Conservative
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FILING DATE: 30-JAN-1998
PRIOR APPLICATION DATA:
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APPLICATION NUMBER: PCT/I
FILING DATE: 10-DEC-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 650-494-0792
TELEX: 706141
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1561..2625
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               CDS
416..1531
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                                                                                                                                                 Best Local Similarity
Matches 95; Conserv
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               NAME/KEY:
                               LOCATION:
                                                                 NAME/KEY:
                                                                               ; LOCATION:
US-08-681-953-31
                                                                                                                                    Query Match
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OTHER INFORMATION: "n" bases at various positions throughout the sequence
OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Db 597288 CACCCAGATGCACCTGGACGCCGGCCAGCAGGTATGGCTGATCACCGCTACCCCATACGA 597229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Db 597228 ACTCGCGCCCACCATCGCCCGCGCTCGGCCTAACCGGCGCCCTGGGCACCGTGGCCGA 597169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  110 CGTCGTCGCCACCATCGAGTATCTGGTCCGCCTGCACGAGGGCCAGGCCACGATGACCGT 169
                                                                                                                                                                                                                                                                                                                                                                                                      61 GCCTGAACACCAATCATCCGATCACCACGACGACGCTGACCGAAGAAGACGTCGTCGCCA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: PLEISCHMAN, Robert D.

APPLICANT: FRASER, CLAITE, Owen R.

APPLICANT: FRASER, CLAITE M.

APPLICANT: PROFIEE, JOHN C.

TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM

TITLE OF INVENTION: TUBERCULOSIS

FILE REPERENCE: 24366-220007,00

CURRENT APPLICATION NUMBER: US/09/103,840A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50 CAAGAAGCTGGGCCTGAACACCAATCATCCGATCACCACGACGACGACGAAGAAGA 109
                                                                                                                                                                                                                                                                                                                        1 TCAAGGAGAAGCGCTACGACCTGGCCCGTGTCGGCCGATACAAGGTCAACAAGAAGCTGG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 34.8; DB 4; Length 4403765;
Pred. No. 5.8;
0; Mismatches 57; Indels 0;
                                                                                                                                                                                                                                    9
                                                                                                                                                                             Length 734;
                                                                                                                                                                                                                                    47; Indels
                                                                                                                                                                       Score 35.8; DB 4;
Pred. No. 1.1;
                                                                                                                                                                                                                                 0; Mismatches
ORGANISM: PORYPHYROMONAS GINGIVALIS
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/09103840A Patent No. 6294328
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/codon_start= 19
/function= "gene eryA"
/product= "eryA ORF2 encoding modules 3 & 4 for
6-deoxyerythronolide B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature
LOCATION: 4471..5847
OCHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: beta-ketoacylACPsynhase domain of module"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature
LOCATION: 7165..9216
OCHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: dehydratase and encylreductase domains m"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature
LOCATIOn: 97.1482
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: beta-ketoacyl ACP synthase of module 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
LOCATION: 3406..3921
OTHER INFORMATION: /function- "approximate span of
OTHER INFORMATION: beta-ketoreductase domain of module 3"
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
LOCATION: 654.7026
OTHER INFORMATION: /function="approximate span of
OTHER INFORMATION: acyltransferase domain of module
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
LOCATION: 1693..267
LOCATION: 1693..267
LOCATION: /function= "approximate span of OTHER INFORMATION: acyltransferase domain module 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
LOCATION: 4171..428
COTHER INFORMATION: /tunction= "approximate span of
OTHER INFORMATION: acyl carrier domain of module 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: /function= "approximate span of OTHER INFORMATION: module 4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature
LOCATION: 19.4470
OTHER INFORMATION: /function= "approximate span
OTHER INFORMATION: module 3"
                                                                                                                                                                                                                                                                                                                                ORGANISM: Saccharopolyspora erythraea
STRAIN: NRRL 238
                                        4952.US.01
                                                                                                    TELEFAX: 708-938-2623
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 20235 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
             REGISTRATION NUMBER: 32652
REFERENCE/DOCKET NUMBER: 45
TELECOMBUNICATION INFORMATION:
TELEPHONE: 708-937-9396
TELEFAX: 708-938-2623
                                                                                                                                                                                                                            TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
Danckers, Andreas M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature
LOCATION: 4471..10722
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9433..9984
                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: 19.10722
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                         19..10722
                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: CDS
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                                                                                                                                                                                                                                                                      HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY:
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                                                                                                                                                                                                                                                                                                 ANTI-SENSE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .;
0
                                                                                                                                                             APPLICANT: Robison, Keith E.
TITLE OF INVENTION: Nucleic Acid Molecules Encoding Human Protease Homologs FILE REFERENCE: 5800-24, 035800/176965
CURRENT APPLICATION NUMBER: US/09/280,116A
CURRENT FILING DATE: 1999-03-26
NUMBER OF SEQ ID NOS: 268
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 120
LENGTH: 1366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  369 CTGCCTGGAGACTGCCTTCCGCCTGGACCTCGCCGCCGCCGCTGGAGCTCTCCGGAGA 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59 GGGCCTGAACACCAATCATCCGATCACCACGACGCTGACCGAAGAAGACGTCGTCGC 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        309 GGCCTGGCCACCTATGGACCNCGCGTCCGCACCGAGACCTACGGTGCTGCCTTCAC 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16.6%; Score 34.6; DB 4; Length 1366; 54.0%; Pred. No. 2.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC competible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/07/642,734C
FILING DATE: 17-JAN-91
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                      Sequence 120, Application US/09280116A
Patent No. 6331427
GENEKAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(1366)
COTHER INFORMATION: n = a, t, c or g
                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: zinc proteases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 54.0°
Matches 67; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Homo sapiens
    ub 597168 GTCGGTCG 597161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: US
ZIP: 60064-3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    179 GGTC 182
                                                                                    US-09-280-116-120
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OTHER INFORMATION: Affortclow "approximate span of OTHER INFORMATION: Affortclow "approximate span of OTHER INFORMATION: Data "Actoreductase of module 4"

NAME/KEY: MISS_CENTURE OF CALCIFICE domain of module 4"

NAME/KEY: 10733. 2023

OTHER INFORMATION: Actoritic domain of module 4"

NAME/KEY: 10733. 2023

OTHER INFORMATION: Actoritic domain of module 5 of OTHER INFORMATION: Actoritic domain of module 6 of OTHER INFORMATION: All processes domain of module 6 of OTHER INFORMATION: All processes domain of module 6 of OTHER INFORMATION: All processes domain of modu
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Score 34.2; DB 1; Length 20235; Pred. No. 4.2;

16.4%; 52.4%;

Query Match Best Local Similarity

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                                                    Db 17573 TGAGCCCGCACCCGGTGCTCACCGCGGCGGTGCAGGAGATCGCCGCGGGGCCGTGGCCA 17632
                                                                                                                          Db 17633 TCGGGTCGCTGCACCGCGGACGACGACGACCTGATCGCCGACTCGCCCGGGCGC 17692
                                64 TGAACACCAATCATCCGATCACCACGACGACGATGACCGAAGAAGACGTCGTCGCCACCA 123
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Indels
68;
 0; Mismatches
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                                                                                                                                                                                                   Db 17693 ACGTGCACGCCTGGCCGTGGAC 17715
                                                                                                                                                                               184 AGGTGCCGGTGGAAACCGACGAC 206
 75; Conservative
 Matches
                                                                                                           124
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us-09-697-123b-8.rnpb

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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November 12, 2002, 16:05:40 ; Search time 21.1607 Seconds (without alignments) 3487.380 Million cell updates/sec OM nucleic - nucleic search, using sw model Run on:

US-09-697-123B-8 208 Title: Periect score:

1 tcaaggagaagcgctacgac......ccggtggaaaccgacgacat 208 IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Scoring table: sedneuce:

320260 seqs, 177392727 residues Searched:

Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000 Minimum DB seq Maximum DB seq Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Published_Applications_NA:* Database

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9: 10: 11: 12: 13:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	4 4 5 5 5 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	Description	Sequence 5, Appli	Sequence 5, Appli	Sequence 1, Appli	Sequence 3, Appli	Sequence 5, Appli	Sequence 109, App	Sequence 111, App	Sequence 4001, Ap	Sequence	Sequence 1392, Ap	٠,	Sequence 7738, Ap	Sequence 32324, A	Sequence 15816, A	Sequence 43, Appl	Sequence 7920, Ap	Sequence 229, App	Sequence 7837, Ap	Sequence 4071, Ap
	4	91	US-09-984-711-5	US-10-075-460-5	US-09-887-052-1	US-09-887-052-3	US-09-887-052-5	US-10-062-254-109	US-10-062-254-111	US-09-815-242-4001	US-09-815-242-7946	US-09-294-093B-1392	US-09-880-107-3678	US-09-815-242-7738	US-09-864-761-32324	US-09-864-761-15816	US-09-923-779-43	US-09-815-242-7920	US-09-925-300-229	US-09-815-242-7837	US-09-815-242-4071
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	4	Match Length DB	5096	5099	5099	5099	5099	704	752	897	492	278	2693	1437	284	269	622	1266	1640	3522	4863
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		score	80	80	80	80	80	37.6	37.6	37.6	37	36.2	36.2	35.6	34.8	34.8	34.8	34.8	34.8	34.8	34
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58, Ap 02, Ap 0, App 0, App 1, App	App , Ap
4158, Ap 3102, Ap 280, App 280, App	529, 3950 115,
Sequence 4158, A Sequence 2102, A Sequence 280, App Sequence 190, App Sequence 1915, App Sequence 292, Ap	Sequence Sequence Sequence
US-09-815-242-4158 US-09-923-876-3102 US-09-925-598-280 US-09-989-722-280 US-09-989-722-280 US-09-989-723-280 US-09-989-723-280 US-09-989-723-280 US-09-989-723-280 US-09-989-723-280 US-09-991-163-280 US-09-991-163-280 US-09-991-163-280 US-09-991-163-280 US-09-991-163-280 US-09-991-163-280 US-09-991-280-193-280 US-09-989-721-280 US-09-989-721-280 US-09-815-242-7935 US-09-815-242-7935 US-09-815-242-7935 US-09-815-242-7935 US-09-816-289-9	US-09-954-456-529 US-09-880-107-3950 US-10-062-254-115
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	32.8 32.8 32.6
01222222220022222220002222222222222222	44 45 45
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## ALIGNMENTS

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GENERAL INCORANTION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: BATHE, Brigitte
APPLICANT: STEPHAN, Hans
APPLICANT: STEPHAN, Hans
APPLICANT: REUTZER, Caroline
APPLICANT: FEFETERE, Walter
APPLICANT: PFEFETERE, Walter
APPLICANT: BINDER, Michael
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE FPSL GENE
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE FPSL GENE
TITLE OF INVENTION NUCLEOTIDE SEQUENCES WHICH CODE FOR THE FPSL GENE
CURRENT APPLICATION NUMBER: US/09/984,711
PRIOR PRIOR PELLING DATE: 2001-10-31
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 6
SED TO NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9 AAGCGCTACGACCTGGCCCGTGTCGGCCGATACAAGGTCAACAAGAAGCTGGGCCTGAAC 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ب
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          38.5%; Score 80; DB 10; L 66.0%; Pred. No. 1.3e-12; tive 0; Mismatches 65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Corynebacterium glutamicum
; Sequence 5, Application US/099847111
; Patent No. US20020119549A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 38.5' Best Local Similarity 66.0' Matches 132; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION:
US-09-984-711-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 5
LENGTH: 5096
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FILE REFERENCE: 204212US0X
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Matches 132; Conserv
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LENGTH: 5099
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Sequence 5, Application US/10075460

Patent No. US2002015557A1

GENERAL INFORMATION:

APPLICANT: MOCKEL, BETTINA

APPLICANT: HANS, STEFAN

APPLICANT: HERNAN, THOMAS

APPLICANT: FREEFERLE, WALTER

APPLICANT: FREEFERLE, WALTER

APPLICANT: PREFFERLE, WALTER

APPLICANT: PREFFERLE, WALTER

APPLICANT: PREFFERLE, WALTER

APPLICANT: PREFFERLE, WALTER

APPLICANT: BINDER, MICHAEL

TITLE OF INVENTION: NUCLETILE SEQUENCES WHICH CODE FOR THE FPSL GENE

FILE REFERENCE: 210472USOX

CURRENT APPLICATION NUMBER: DE 10107230.9

PRIOR FILING DATE: 2001-02-16

PRIOR FILING DATE: 2001-12-19

PRIOR FILING DATE: 2001-12-19

NUMBER OF SEQ ID NOS: 14

SEQ ID NO S

LEAGTH: 5099
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                   69 ACCAATCATCGATCACCACGACGACGCTGACCGAAGAAGACGTCGTCGCCACCATCGAG 128
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Sequence 1, Application US/09887052
Palent No. US20020119537A1
GENERAL INFORMATION:
APPLICANT: BATHE, Bertina
APPLICANT: HERMANN, Thomas
APPLICANT: PFEFFERLE, Walter
APPLICANT: BINDER, Michael
TITLE OF INVENTION: NUCLEOTIDE SEEQUENCES WHICH CODE FOR THE rPOB GENE
 9 AAGGGGTACGACCTGGCCCGTGTCGGCCGATACAAGGTCAACAAGAAGCTGGGCCTGAAC 68
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Pred. No. 1.3e-12;
0; Mismatches 65
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66.0%;
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Matches 132; Conservative
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| LOCATION: (702)..(4196)
| O'THER INFORMATION:
| US-10-075-460-5
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US-09-887-052-1
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US-10-075-460-5
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APPLICANT: MOECKEL, Bettina

APPLICANT: MOECKEL, Bettina

APPLICANT: BATHE, Brighte

APPLICANT: PFEFFERLE, Walter

APPLICANT: PFEFFERLE, Walter

APPLICANT: BINDER, Michael

TITLE OF INVENTION: NUCLEOTIDE SEEQUENCES WHICH CODE FOR THE rPOB GENE

FILE REFERENCE: 204212USOX

CURRENT APPLICATION NUMBER: US/09/887,052

PRIOR APPLICATION NUMBER: DE10107229.5

PRIOR APPLICATION NUMBER: DE10107229.5

PRIOR FILING DATE: 2001-06-25

PRIOR FILING DATE: 2001-06-26

PRIOR FILING DATE: 2001-06-26
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                                                                                                                                                                                                                                                                                                                                                                            Length 5099;
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Pred. No. 1.3e-12;
0; Mismatches 65; Indels
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66.0%; Pred. No. 1.3e-12;
Live 0; Mismatches 65
CURRENT APPLICATION NUMBER: US/09/887,052
CURRENT FILING DATE: 2001-06-25
PRIOR APPLICATION NUMBER: DEL0107229.5
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PATENTIN VERSION 3.0
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Corynebacterium glutamicum
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66.0%;
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Best Local Similarity 66.09
Matches 132; Conservative
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; NAME/KEY: CDS
; LOCATION: (702)..(4196)
US-09-887-052-1
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CURRENT APPLICATION NUMBER: US/10/062,254
                                                                                                                                                                                            CURRENT FILING DATE: 2002-02-01
PRIOR APPLICATION NUMBER: 09/630,346
PRIOR PILING DATE: 2000-07-28
PRIOR PILING DATE: 2000-07-28
PRIOR PILING DATE: 1999-07-30
PRIOR FILING DATE: 1999-07-30
PRIOR FILING DATE: 1999-09-30
PRIOR PILING DATE: 1999-09-30
PRIOR APPLICATION NUMBER: 60/15699
PRIOR APPLICATION NUMBER: 60/15699
PRIOR PILING DATE: 1999-10-01
PRIOR PELING DATE: 1999-10-01
PRIOR FILING DATE: 1999-10-01
PRIOR FILING DATE: 1999-12-09
PRIOR FILING DATE: 1999-12-09
PRIOR PILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: 60/171054
PRIOR FILING DATE: 1999-12-17
PRIOR PELING DATE: 1999-12-21
PRIOR PELING DATE: 1999-12-21
PRIOR PELING DATE: 1999-12-21
PRIOR PELING DATE: 1999-12-22
PRIOR APPLICATION NUMBER: 60/173535
PRIOR APPLICATION NUMBER: 60/173535
PRIOR APPLICATION NUMBER: 60/173535
PRIOR PELING DATE: 1999-12-22
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Patent No. US20020138882A1
GENERAL INFORMATION:
APPLICANT: Cahoon, Edgar B
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56.5%;
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SOFTWARE: Mcrosoft Office 97
SEQ ID NO 109
LENGTH: 704
Morgante, Michele
                                         Odell, Joan
Rafalski, Antoni
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Best Local Similarity 56.5
Matches 70; Conservative
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ORGANISM: Zea mays
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US-10-062-254-109
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  69 ACCAATCATCCGATCACCACGACGACGCTGACCGAAGAAGACGTCGTCGCCACCATCGAG 128
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APPLICANT: BATHE, Brigite
APPLICANT: BERNANN, Thomas
APPLICANT: BERNANN, Thomas
APPLICANT: PFEFERLE, Walter
APPLICANT: BINDER, Michael
TITLE OF INVENTION: NUCLEOTIDE SEBQUENCES WHICH CODE FOR THE TPOB GENE
FILE REFERENCE: 204212USOX
CURRENT APPLICATION NUMBER: US/09/887,052
CURRENT FILING DATE: 2001-06-25
PRIOR FILING DATE: 2001-06-25
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PALENTIN VORSION 3.0
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Patent No. US20020138882A1
GENERAL INPORMATION:
APPLICANT: Cahoon, Edgar B
APPLICANT: Cahoon, Rebecca E
APPLICANT: Fanco, Saverio Carl
APPLICANT: Fang, Yiwen
APPLICANT: Lee, Jian-Ming
APPLICANT: Lee, Jian-Ming
APPLICANT: Li, Zhongsen
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                                                                                                                                                                                                                                                                                Sequence 5, Application US/09887052
Patent No. US20020119537A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : NAME/KEY: CDS
: LOCATION: (702)...(4196)
US-09-887-052-5
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Best Local Similarity
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LENGTH: 5099
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APPLICANT: Sakai, Hajime
APPLICANT: Zheng, Peizhong
APPLICANT: Zhu, Qun
TITLE OF INVENTION: Polynucleotides Encoding Proteins Involved In Plant Metabolism
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77 TCCGATCACCACGACGCTGACCGAAGAGGCGTCGTCGCCACCATCGAGTATCTGGT 136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 897;
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FILE REPERENCE: ELITRA.011A

CURRENT APPLICATION NUMBER: US/09/815,242

CURRENT APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR FILING DATE: 2000-05-23

PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-05-26
                                APPLICANT: Tandanto. Or NODELL I.

APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: PROMARYORES
FILE REPERENCE: ELITRA.011A
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/296,848
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/206,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-33
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-16
NUMBER OF SEQ. ID NOS: 14110
SOFTHARE: 2001-02-16
SOFTHARE: FASISED for Windows Version 4.0
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Pred. No. 0.14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 7946, Application US/09815242 Patent No. US20020061569A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pseudomonas aeruginosa
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Zyskind, Judith W.
Wall, Daniel
Trawick, John D.
Carr, Grant J.
Yamamoto, Robert T.
Carr, Grant J.
Yamamoto, Robert T.
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nilarity 51.2%;
Conservative
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APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
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Best Local Similarity
Matches 88; Conservat
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APPLICANT:
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APPLICANT: Zheng, Peelzhong
APPLICANT: Zhu, Oun
TITLE UP! INVENTION: PolynucleoLides Encoding Proteins Involved In Plant Metabolism
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/062,254
CURRENT APPLICATION NUMBER: 09/630,346
FRIOR APPLICATION NUMBER: 09/630,346
FRIOR APPLICATION NUMBER: 00/146511
PRIOR APPLICATION NUMBER: 00/156006
FRIOR APPLICATION NUMBER: 00/156006
FRIOR FILING DATE: 1999-09-20
FRIOR PLING DATE: 1999-09-20
FRIOR APPLICATION NUMBER: 00/15609
FRIOR APPLICATION NUMBER: 00/15787
FRIOR PLING DATE: 1999-10-01
FRIOR PLING DATE: 1999-10-01
FRIOR PLING DATE: 1999-10-01
FRIOR APPLICATION NUMBER: 00/15787
FRIOR FILING DATE: 1999-12-16
FRIOR FILING DATE: 1999-12-16
FRIOR FILING DATE: 1999-12-21
FRIOR PLING DATE: 1999-12-21
FRIOR APPLICATION NUMBER: 00/173535
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       296 regretraceacereacaregeeeechadaadaregeerreardaggagarereergg 355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 752;
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Pred. No. 0.14;
0; Mismatches 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4001, Application US/09815242 Patent No. US20020061569A1 GENERAL INFRMATION: APPLICANT: Haselbeck, Robert
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Zyskind, Judith W.
Wall, Daniel
Trawick, John D.
Cahoon, Rebecca E
Falco, Saverio Carl
Fang, Yiwen
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SOFTWARE: Microsoft Office 97
                                                                                                                                        Miao, Guo-Hua
Morgante, Michele
                                                                  Hantke, Sabine S.
Lee, Jian-Ming
Li, Zhongsen
                                                                                                                                                                                                                              Rafalski, Antoni
Sakai, Hajime
Zheng, Peizhong
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Best Local Similarity 56.5%
Matches 70; Conservative
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Odell, Joan
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CRCANISM: Zea mays
US-10-062-254-111
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356 TCGA 359
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APPLICANT:
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APPLICANT:
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              202 AFCGAAGTGGTCAAGCTGGTGGATCTGTCGGAAAGCGCCCATATCGAGCGCGAGCTGATG 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         142 CTGACCACCGTGGGGCACGATGAGGTGATCGAGCAGATCACCAAGAACCTCAACAAGCTG 201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17.4%; Score 36.2; DB 10; Length 278; 57.5%; Pred. No. 0.28; 1.ve 0; Mismatches 48; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. US20010051335A1 700344235H1
NAME/KEY: unsure
LOCATION: 158
                                                                                                                                                                                                                                                                                                                                                                                     Query Match 17.8%; Score 37; DB 10; Length 492; Best Local Similarity 51.5%; Pred. No. 0.19; Matches 85; Conservalive 0; Mismatches 80; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     262 CTGGTGAAGGTCAAGGCCACGGCGCCCACGCGCCCACGAGTCAAG 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             141 CTGCACGAGGCCCAGGCCACGATGACGGTGCCGGGGGGGTCGAG 185
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEG ID NOS: 14110
SUFTWARE: PASLSEO for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: a, t, c, g, or other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1392, Application US/09294093B
Patent. No. US20010051335A1
GENERAL INFORMATION:
APPLICANT:
Lalgudi, Rayhunath, V.
                                                                                                                                                                                                                                                        ORGANISM: Pseudomonas aeruginosa
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Matches 65; Conservative
                                                                                                                                                                                                                                                                                                                     ; LOCATION: (1)...(492)
US-09-815-242-7946
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                                                                                                                                                                                                                                                                                                    NAME/KEY: CDS
                                                                                                                                                                                   SEQ 1D NO 7946
LENGTH: 492
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LENGTH: 278
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                                                                                                                                                                                                                                                                               FEATURE:
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213 TGCCTGGTGGCGGTGACCATGCCGCTGGTGCTGCCTGGCTCGTCGGCCC 154
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US-09-880-107-3678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 2693;
                                                                                                                                                                                                           APPLICANT: Society, Joseph G.
APPLICANT: Scherf, Uwe
APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
FILE REFERENCE: 44321-5028-WO
CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR FILING DATE: 2000-06-14
PRIOR FILING DATE: 2000-06-14
PRIOR FILING DATE: 2000-06-14
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APPLICANT: Cart, Grant J.
APPLICANT: Cart, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Yamamoto, Robert T.
APPLICANT: W. H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFREENCE: ELTRA.011A
CURRENT APPLICATION NUMBER: 00/20/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/20/7,727
PRIOR APPLICATION NUMBER: 60/20/7,727
PRIOR APPLICATION NUMBER: 60/20/7,727
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52.3%; Pred. No. 0.38;
Live 0; Mismatches 73;
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Patent No. US20020061569Al
Sequence 3678, Application US/09880107
Patent No. US20020142981A1
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PRIOR APPLICATION NUMBER: 60/253,625
           Seque...

Patent No. USzvo...

GENERAL INFORMATION:

APPLICANT: Horne, Darci T.

APPLICANT: Vockley, Joseph G.

Andrew C. Control Control

Andrew C. Control

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APPLICANT: Ohlsen, Kari L.
APPLICANT: 2yskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3678
LENGTH: 2693
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Best Local Similarity 52.3°
Matches 80; Conservative
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TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
CURRENT APPLICATION NUMBER: US/09/864,761

PRIOR PEDICATION NUMBER: US/09/864,761

PRIOR APPLICATION NUMBER: US 60/180,312

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR APPLICATION NUMBER: US 60/207,466

PRIOR APPLICATION NUMBER: US 60/203,366

PRIOR FILING DATE: 2000-09-03

PRIOR FILING DATE: 2000-00-04

PRIOR FILING DATE: 2000-00-04

PRIOR FILING DATE: 2000-00-04

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: US 60/236,359

PRIOR PELING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00664

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00669

PRIOR APPLICATION NUMBER: PCT/US01/00669

PRIOR PELING DATE: 2001-01-30

PRIOR PELING DATE: 2001-01-30

PRIOR PELING DATE: 2001-01-30

PRIOR PELING DATE: 2001-01-30

PRIOR PELING DATE: 2001-01-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67 ACACCAATCATCCGATCACCACGACGACGTGACCGAAGAAGACGTCGTCGCCACCATCG 126
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OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.8
OTHER INFORMATION: SWISSPROT HIT: P49911, EVALUE 2.20e-02
OTHER INFORMATION: EST_HUMAN HIT: AA524458.1, EVALUE 0.00e+00
US-09-864-761-32324
   PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01.30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR PLING DATE: 2001-01.30
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers: 1.1
SEQ ID NO 32324
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Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Chen, Wensheng
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Best Local Similarity 52.87
Matches 75; Conservative
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ORGANISM: Homo sapiens
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APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17.1%; Score 35.6; DB
53.6%; Pred. No. 0.5;
Live 0; Mismatches
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PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR PPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 32324, Application US/09864761
Patent No. US20020048763A1
                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
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Best Local Similarity 53.69
Matches 74; Conservative
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: LOCATION: (1)...(1437)
US-09-815-242-7738
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CURRENT FILING DATE: 2001-08-06
NUMBER OF SEQ ID NOS: 155
SOFTWARE: FSSLSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67; Indels
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/0068
PRIOR PLICATION NUMBER: PCT/US01/00663
PRIOR PLICATION NUMBER: PCT/US01/00663
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PRIOR APPLICATION NUMBER: PCT/US01/00601
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-09-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
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OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL - 1.8
US-09-864-761-15816
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. Patent No. US20020076721A1
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LOCATION: 547, 552, 610, 621
OTHER INFORMATION: n = A,T,C or G
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51.3%;
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52.8%;
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Matches 75, Conservative
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Best Local Similarity
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US-09-923-779-43
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        Matches
        81; Conservative
        0; Mismatches
        77; Indels
        0; Gaps
        0;

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        48 AACAAGAAGCTGGGCTGAACACCCAATCATCCGATCACCACGACGACGAGAA
        107
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MEST156-D
MEST209-B
MEST67-H1
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MEST323-F
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MEST209-C
MEST181-G
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MEST209-H
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Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 1282)
Muruqasu-Oei,B., Tay,A. and Dick,T.
Upregulation of stress response genes and ABC transporters
anaerobic stationary-phase Mycobacterium smegmatis
Mol. Gen. Genet. 262 (4-5), 677-682 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mycobacterium Laboratory
Institute of Molecular and Cell Biology
30 Medial Drive, Singapore 117609, Republic of Singapore
Tel: 65 874 3011
Fax: 65 779 1117
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BM266851 M
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Insert Length: 1282 Std Error: 0.00
Seq primer: T3 Forward: T7 Backward.
Location/Qualifiers
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BG556957
BG322881
BH374681
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B1097733
B1096671
              BQ817943
BQ817941
BM501065
                                                         BF008145
BG321153
BG321153
AK104676
AY109418
B1960536
BG836253
BQ836253
BQ8719187
BQ57118
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AV628007
AV631761
AV631497
AL825144
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AL108909 Drosephil
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A1405617 GH25702.5
BF070792 1477141 A
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Compugen Ltd.
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            GenCore version
Copyright (c) 1993 - 2002
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Score

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Result

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Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
Plate: 259 row: E column: 5
High quality sequence stop: 481.
Location/Qualiflers
1. 630
/organism="brosophila melanogaster"
/db.xref="taxon:7227"
/clone="GH25953"
/c
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1 (bases 1 to 630)
1 (bases 1 to 630)
1 warvey, D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G., Lewis, S. and Rubin, G.M.
Buggp/HMI prosophila EST Project
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                                                                                                                                                                                                                                                                                                                    67 others
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Pred. No. 0.67;
2; Mismatches 92; Indels
                                                                            /organism="Drosophila melanogaster"
/db_xref="taxon:727"
/clone="BACN01F12"
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One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
                                                                                                                                                                                                                                                                                                                    305
                                                                                                                                                                                                /clone_lib="DrosBAC"
/plasmid="pBeloBAC11"
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1. .1019
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Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GSS 26-JUL-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster genome survey sequence T7 end of BAC abcNollF12 of DrosBAC library from Drosophila melanogaster (fruit AL108909
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                                                                                                                        /clone_lib # Mycobacterium anaerobic stationary phase
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila
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/organism="Mycobacterium smegmatis"
/strain="mc2155"
                                                                                                                                                                                                /lab_host~"E. coli XL1-Blue MRF''
                                                                                /db_xref-"taxon:1772"
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568 bp mRNA linear EST 25-OCT-2001 Lambda Zap II (normalized), Lambda Zap II Chlamydomonas reinhardtii cDNA, mRNA sequence. B1995346 B1995346.1 GI:16430136
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/db_xref="taxon:6943"
/clone_lib="Amblyomma americanum adult Lambda Zap Express"
/sex="Male, Female"
/dev_stage="Adult"
                                                                                                                                                                                                                                                                                                                                         397 bp mRNA linear EST 06.0CT-2000 americanum adult Lambda Zap Express Amblyomma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Amblyonna
tag
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(bases 1 to 397)
Hill, C.A and Gutierrez, J.A.
Analysis of the expressed genome of the lone star tick, Amblyon americanum (Acari:Ixodidae) using an expressed sequence tag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                283 GAAGACCGCCGAAGACCTCCAGGCCACCGAGGACAAGGTGAACCACCTGAACAAGGTCAA 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95 GCTGACCGAAGAGGCGTCGTCGCCACCATCGAGTATCTGGTCCGCCTGCACGAGGGCCA 154
35 CCGATACAAGGTCAACAAGAAGCTGGGCCTGAACACCCAATCATCCGATCACCACGACGAC 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Microb. Comp. Genomics 5 (2), 89-101 (2000) In press Contact: Hill CA Animal Science Discovery Research Elanco Animal Health, A Division of Eli Lilly and Company Po Bor 708, 2010 West Main St., Greenfield, IN 46140, USA Tel: 317 277 0826
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Pred. No. 4;
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Vector: pBK-CMV;
110 c 124 g 3
                                                                                                                                                                                                                                                                                                                                                                      1477141 Amblyomma americanum advamericanum cDNA, mRNA sequence.
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55.2%;
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Matches 79; Conserv
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BI995346
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A1405617

A140562.5prime GH Drosophila melanogaster head pOT2 brosophila melanogaster cDNA clone GH25702 5prime similar to AF001796: KrT955Prime GH25702, mkNA sequence.
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/db_xref="taxon:7227"
/clone="GH25702"
/clone="lb="culto"
/clone="lb="culto"
/clone="lb="culto"
/db_xref="and female"
/clone=lb="culto"
/dev_stage="adult"
/lab_host="nulto"
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Bukaryota; Mctazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Bukaryota; Endopterygota; Diptera; Brachycera; Muscomorpha;
Roptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
I (bases 1 to 662)
I (bases 1 to 662)
Harvey, D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G.,
BNGP/HHMI Drosophila EST Project
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                                                                                                                                                                                                                                                                                                                                                   Gaps
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Fax: 510 486 6798
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
Plate: 257 row: A column: 2
High quality sequence stop: 564.
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                                                                             Gaps
                                                                                                                           9 AAGCGCTACGACCTGGCCCGTGTCGGCCGATACAAGGTCAACAAGAAGCTGGGCCTGAAC 68
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                              Length 630;
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                                                                             Indels
                                                                        93;
                            Score 43.2; DB 9;
Pred. No. 0.99;
0; Mismatches 93;
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0; Mismatches
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1..662
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Contact: Stapleton, M.
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Best Local Similarity 51.6%;
Matches 99; Conservative
                              20.8%;
51.6%;
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Gaps

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/note="Vector: pBluescript 11 SK-; Site_1: EcoRI: Site_2:
XhOI: This library, constructed by John Davies and Jeffrey
McDermott, combines cDNAs from CC-1690 cells grown to
mid-log phase in TAP (acetate-containing) medium in
light, TAP medium in the dark, HS (minimal) medium in
ambient levels of CO2 and HS medium bubbled with 5% CO2.
PO17A mRNA was purified from each sample, pooled and cDNA
synthesized. The cDNA was directionally cloned into lambda
ZAP II (Stratagene) in the EcoRI (5') and XhOI (3') sites.
pBluescript II SK- plasmids were excised from the lambda
ZAP clones by superinfection with ExAssist (Stratagene)
phage. The library was normalized using method 4 described
in Bonaldo et al (1996) Genome Research 6: 791-806.
                                                                                                      E 1 (bases 1 Lo 516)
S Grossman.A. Davies, J., Federspiel, N., Harris, E., Lefebvre, P., Grossman, A., Davies, J., Federspiel, N., Harris, E., Lefebvre, P., Analyses of the Chiamydomonas reinhardtii Genome: A Model, Unicellular System for Analyzing Gene Function and Regulation In Vascular Plants; project phase 2
Confact: Elizabeth H. Harris
DCMB Box 91000
Duke University
Durham, WC 27708-1000, USA
Tel: 919 613 8164
Fax: 919 613 8177
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Stern, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BQ817943 666 bp mRNA linear EST 01-AUG-2002 1030067C06.yl C. reinhardtii CC-1690, Deflagellation (normalized), chanda Zap II Chlamydomonas reinhardtii CDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="C. reinhardtii CC-1690, normalized, Lambda Zap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chlamydomonas reinhardtii
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
Chlamydomonas reinhardtii.
Chlamydomonas reinhardtii
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 246 TACCGCATGTTCGAGCTGGGCAGCCGCATCCTGGTCGACGGCGTGGACATCCCACC 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               186 GAGAAGGTCGGCGCCGTGGGCCCCACCGGCTCCGGCAAGTCCACCACGCTGCTGGCGCTG 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66 AACACCAATCATCGATCACCACGACGCTGACCGAAGAAGACGTCGTCGCCACCATC 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 GAGAAGCGCTACGACCTGGCCCGTGTCGGCCGATACAAGGTCAACAAGAAGCTGGGCCTG 65
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,P., McDermott,J.P., Shrager,J., Silflow,C. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Chlamydomonas reinhardtii"
/strain="CC-1690 wild type mt+ 21gr"
/db_xref="taxon:3055"
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                                                                               Chlamydomonadaceae; Chlamydomonas.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /strain="Cc-1690 wild type mit-1914"
/strain="Cc-1690 wild type mit-1914"
/strain="Cc-1690 wild type mit-1914"
/db.xref-"taxon:3055"
/clone_lib="C. reinhardtil CC-1690, Stress II (normalized
), Lambda 2ap 1"
/note="Wector: pBluescript II SK-; Site_1: EcoRI; Site_2:
XhoI; Stress condition II library, constructed by John
Davies and Jeffrey McDermott, combines cDNAs from CC-1690
cells grown to mid-log phase in TAP (NH4+ - containing)
and shifted to TAP - NO3* (24Hrs); H2 production
conditions (0, 12hr, 24hr) see Melis et al.,(2000) plant
Phys. 122: 127-135; TAP + H202 (1, 12, 24 hr); TAP +
sorbitol (1, 2, 6, 24 hr); TAP + Cd (1, 2, 6, 24 hr).
PolyA mRNA was purified from each sample, pooled and cDNA
synthesized. The cDNA was directionally cloned into lambda
Zap II (Stratagene) in the EcoRT (5) and XhoR (3)
sites: pBluescript II SK- plasmids were excised from the
lambda ZAP clones by superinfection with ExAssist
(Stratagene) phage. The library was normalized using
method 4 described in Bonaldo et al., (1996) Genome
Research 6: 791-806."
                                                                                                                         Grossman, A., Chauge, C. W., Davics, J., Harris, E., Hauser, C., Lefebvre, P., McDermott, J.P., Shrager, J., Silflow, C. and Stern, D.
Analyses of the Chlamydomenas reinhardtii Genome: A Model,
Unicellular System for Analyzing Gene Function and Regulation in Vascular Plants. Project: 1031
Unpublished (2001)
Contact: Charles Hauser
Contact: Charles Hauser
Contact: Carles Hauser
Contact: Carles Hauser
Fars, 919 613 8159
Fax: 919 613 8177
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1. .568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: chauser@duke.edu.
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                                                                                                                                                                                                                                                                                                             /strain-"cc-1690 wild type mut 21gr."
/db.xref-"Laxon:3055"
/clone_lib-"C. reinhardtii CC-1690, Deflagellation
(normalized), Lambda Zap II"
/rote-"Vector: pBluescript II SK-; Site_I: ECORI; Site_2:
Xhoi: Deflagellation library, constructed by John Davies
and Jeffrey McDermott, combines cDNAs from CC-1690 cells
which had been re-synthesizing flagella for 15, 30 and 60
min after being deflagellated by pH shock. PolyA mRNA was
purlied from each sample, pooled and cDNA synthesized.
The CDNA was directionally cloned into lambda Zap II (Stratagene) in the EcoRI (5') and XhoRI (3') sites.
pBluescript II SK- plasmids were excised from the lambda
ZAP clones by superinfection with ExAssist (Stratagene)
phage. The library was normalized using method 4 described
in Bonaldo et al., (1996) Genome Research 6: 791-806."
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Grossman, A., Chonglo, C. W., Davies, J., Harris, E., Hauser, C., Lefebvre
P., McDermott, J.P., Shrager, J., Silflow, C. and Stern, D.
Analyses of the Chlamydomonas reinhardtii Genome: A Model,
Unicellular System for Analyzing Gene Function and Regulation in
Vascular Plants. Project: 1030
Gnpublished (2002)
Contact: Charles Hauser
DCMB Box 91000
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1030067C05.yl C. reinhardtii CC-1690, Deflagellation (normalized),
Lambda Zap II Chlamydomonas reinhardtii cDNA, mRNA sequence.
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Eukaryota, Viridiplantae, Chlorophyta, Chlorophyceae, Volvocales,
Chlamydomonadaceae, Chlamydomonas.
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Unpublished (2002)
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Duke University
Durham, NC 27708-1000
Tel: 919 613 8159
Fax: 919 613 8177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66 AACACCAATCATCCGATCACCACGACGACGCTGACCGAAGAAGAGGTCGTCGCCACCATC 125
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                                                                                                                                                                                                                                chauser@duke.edu.
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Durham, NC 27708-1000
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Hunter, B.G., Beatty, M., Singletary, G., Hamaker, B., Larkins, B.A. and
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; 2ea.
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Trait and Technology Development, Food and Feed Research
Pioneer Hi Bred International, Inc.
7300 NW 62nd Ave., P.O. Box 1004, Johnston, IA 50131-1004, USA
Tel: 515 270 5934
Fax: 515 254 2619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66 AACACCAATCCTATCCGATCACCACGACGCTGACCGAAGAAGACGTCGTCGCCCACCATC 125
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/clone_lib="Pioneer AF-1 array"
/note="Vector: pSport1; Site_1: Sal1; Site_2: Not1"
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                                                                                                                  /organism="Chlamydomonas reinhardtii"
                                                                                                                                        /strain="CC-1690 wild type mt+ 21gr"
/db_xref="taxon:3055"
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Location/Qualifiers
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Tel: 919 613 8159
Fax: 919 613 8177
Email: chauser@duke.edu.
Location/Qualitiers
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Unpublished (2002)
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/db_xref="taxon:6943"
/db_xref="taxon:6943"
/dclone_lib="Amblyomma americanum adult Lambda Zap Express"
/sex="Male, Female"
/dev_stage="Adult"
/note="Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI"
149 c 175 g 52 t
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tag
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1682830 Amblyomma americanum adult Lambda Zap Express Amblyomma
americanum cDNA, mRNA sequence.
BF008145
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                                                                                          47 CAACAAGAAGCTGGGCCTGAACACCAATCATCGATCACCACGACGACGCTGACCGAAGA 106
                                                                                                           Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari; Parasitiformes; Ixodida; Ixodidae; Amblyomma.
1 (bases I to 540)
1 (bases I to 540)
Analysis of the expressed genome of the lone star tick, Amblyon americanum (Acari:Ixodidae) using an expressed sequence tag
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Microb. Comp. Genomics 5 (2), 89-101 (2000) In press Contact: Hill CA Animal Science Discovery Research Elanco Animal Health, A Division of Eli Lilly and Company PO Box 708, 2001 West Main St., Greenfield, IN 46140, USA Fax: 317 277 6826
Fax: 317 277 4522
Email: HILL_CATHERINE_A@LILLY.COM.
                                                                       .;
0
                                          Length 464;
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Pred. No. 10;
0; Mismatches 65; Indels
     1 others
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Pred. No. 10;
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/cultivar="Co328"
/db_xref="muckan:4577"
/clone="lib="Zm04_AAFC_ECORC_cold_stressed_maize_scedlings"
/tissue_type="Leaf, crown"
/note="Vector: Bluescript SK-/Xhol-EcoRI; Site_1: Eco RI;
Site_2: Xho I: Lower temperature 50 C / hour from 22 to
120C; bring to 50 in 1 hour from 120C. Leave at 50C 2 days
/photoperiod 16 hours. Light intensity was 125 uE-1.
Library prepared by in vivo mass excision from amplified
library.
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BG321153
Zm04_05f06_R Zm04_AAFC_ECORC_cold_stressed_maize_seedlings Zea mays CDNA clone Zm04_05f06, mRNA sequence.
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(bases 1 to 762)
Harris, L.J., Balcerzak, M., Allard, S., Saparno, A., Couroux, P., De Moors, A., Hatlori, J.I., Ouellet, T., Robert, L.S., Singh, J.A, Sprott
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Singh.J.A.
Eastern Cereal and Oilseed Research Centre
Eastern Cereal and Oilseed Research Centre
Agriculture and Agri-food Canada
MW Neatby Bldg , Central Experimental Farm, Ottawa, Ontario, KIA
0C6, Canada
179: (613) 759-1662
Fax: (613) 759-1701
Email: singhja@em.agr.ca.
Location/Oualifiers
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Best Local Similarity 59.5%;
Matches 66; Conservative (
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/organism≈"2ea mays"

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1. 762
/cotanism="zea mays"
/cultivar="CO387"
/db_xref="taxon:4577"
/colone="zm06_o1a02"
/clone=_lip="zm06_AAFC_ECORC_Fusarium_graminearum_inoculate
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                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type=r.2.5 cm of top of unfertilized ear"
/dev_stage="6-7 days post-silk emergence"
/dev_stage="10-7 days post-silk emergence"
/note="vector: Bluescript Sk+/Xhol Ecork: Site_1: EcoRI:
Site_2: Xhol: Field-grown unpollinated maize ears wather
silk channel-inoculated in the morning (-10 am) with 1 ml
of a Fusarium graminearum macroconidial suspension (500
,000 spores/ml) and whole ears were collected and
immediately frozen in liquid nitrogen 48 hours later."

223 c 280 g 123 t 12 others
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoldeae; Andropogoneae; 2ea.
                          Silk
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Agriculture and Agri-food Canada
Bldg. 21, Central Experimental Farm, Ottawa, Ontario, KIA OC6,
Bldg. 21, Central Experimental Farm, Ottawa, Ontario, KIA OC6,
Cel: (613) 759-1314
Fax: (613) 759-6566
Email: harris19em.agr.ca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    47 CAACAAGAAGCTGGGCCTGAACACCAATCATCCGATCACCACGACGACGACGACGAAGA 106
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Hainey.C.F., Dolan,M., Miao,C.H., Vogel,J.M., Whitsitt,M.S.,
Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V.
Maize Mapping Project/DuPont Consensus Sequences for Design of
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Submitted (25-APR-2002) Maize Mapping Project, University of
Missouri, Columbia, MO 65211, USA
Location/Qualifiers
1. .996
,D. and Tinker,N.A.
Expressed Sequence Tags from Maize Ear Tips 48 Hours after
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Zea mays PC0085803 mRNA sequence.
AY104676
                                                              Unpublished (2001)
Contact: Harris, Linda J.
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2 (bases 1 to 996)
Coe, E.C.
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clade; Panicoideae; Andropogoneae; Zea.
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Library"
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Location/Qualifiers
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Pred. No. 11;
0; Mismatches 75
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/db_xref="MaizeDB:634819"
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                  /db_xref="taxon:4577"
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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ø the number of results predicted by chance to have is. Pred. No.

Mycobacterium tuberculosis partial rpoB gene for RNA polymerase beta subunit, isolate 1415-97.
AJ318818.1 GI:22208412
RNA polymerase

RESULT 1 MTU318818 LOCUS DEFINITION

ALIGNMENTS

1057 39207

7954 166753 1057 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium tuberculosis complex.

Herrera, L., Jimenez, M.S. and Saez, J.A.

AUTHORS REFERENCE

RNA polymerase beta subunit; rpoB gene. Mycobacterium tuberculosis. Mycobacterium tuberculosis

VERSION KEYWORDS SOURCE ORGANISM

ACCESSION

AF130448 Deinococc Y19223 Thermus aqu AP002866 Oryza sat AB085282 Unculture AB085282 Unculture AL391039 Streptomy

SBU72186 AF130448

E03373 128835

3306 149777

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AZ12043 Sequence AL646073 Raistonia AL646073 Raistonia AL65889 Sequence AE002027 Deinococc AF204401 Streptomy U70470 Pseudomonas AE00458 Pseudomona AL646072 Ralstonia E03373 DNA sequenc 128835 Sequence 71 AP003573 Oryza sat U72186 Streptomyce AJ318818 Mycobacte score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution. SUMMARIES MTU318818 MTU318819 MTU318815 MTU318817 MTU318814 18816 18821 AL646070 AC092779 AC097277 D90905 AL646073 MSGRPOB AE006964 MTCI376 MSU24494 AR067447 MLB1790G MLEPRTN7 AF242549 SCD82 AP005275 AX127144 AE004589 AL646072 AX058889 AX120631 PAU70470 DB 3534 3853 3853 19352 19370 19770 3752 37617 37617 37617 37617 37617 37617 37617 37617 37617 37617 37617 37617 37617 37617 37617 37617 37617 37617 37617 37617 37617 37617 37617 37617 37617 37617 37617 37617 37617 37617 37617 37617 37617 37617 37617 37617 37617 37617 37617 37617 37617 37617 37617 37617 37617 37617 37617 37617 37617 37617 37617 37617 37617 37617 37617 37617 37617 37617 37617 37617 37617 37617 37617 37617 37617 37617 37617 37617 37617 37617 37617 37617 37617 37617 37617 37617 37617 37617 37617 37617 37617 37617 37617 37617 37617 37617 37617 37617 37617 37617 37617 37617 37617 37617 37617 37617 37617 37617 37617 37617 37617 37617 37617 37617 37617 37617 37617 37617 37617 37617 37617 37617 37617 37617 37617 37617 37617 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0PSQFWGQNNQTNGTKRRSALGPGGLSRERAGLEVRDVHP"
Molecular analysis of ritampin-resistant Mycobacterium tuberculosis isolated in Spain (1996-2001). Description of new alleles into rpoB gene and review
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Molecular analysis of rifampin-resistant Mycobacterium tuberculosis
isolated in Spain (1996-2001). Description of new alleles into rpob
gene and review
                                                                                                    Direct Submission
Submitted (07-AUG-2001) Herrera L., Servicio Bacteriologia, Centro
Nacional Microbiologia., Ctra. Majadahonda-Pozuelo, Km 2.5,
Majadahonda. Madrid. 28220, SPAIN
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Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium
tuberculosis complex.
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Herrera, L.
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Herrera, L.
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Direct Submission
Submitted (07-AUG-2001) Herrera L., Servicio Bacteriologia, Centro
Nacional Microbiologia., Ctra. Majadahonda-Pozuelo, Km 2.5,
Majadahonda. Madrid. 28220, SPAIN
Location/Qualifiers
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Submitted (07-AUG-2001) Herrera L., Servicio Bacteriologia,
Nacional Microbiologia., Ctra. Majadahonda-Pozuelo, Km 2.5,
Majadahonda. Madrid. 28220, SPAIN
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AJ318813.1 GI:22208402
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Matches 171; Conservative
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us-09-697-123b-13.rge

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2 (bases 1 to 618)
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                                                                                                                                  /product."RNA polymorase beta subunit."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mycobacterium Luberculosis partial rpoB gene for RNA polymerase AJ318915
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Molecular analysis of rifampin-resistant Mycobacterium tuberculosis isolated in Spain (1996-2001). Description of new alleles into rpob gene and review
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Mycobacterium tuberculosis.
Mycobacterium tuberculosis
Mycobacterium tuberculosis
Bacteria: Actinobacteria; Actinobacteriae;
Corymebacterinee: Mycobacteriaceae; Mycobacterium: Mycobacterium tuberculosis complex.
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                                                                                                                                                                                                                                                                                                                                              1 TCAAGGAGAAGCGCTACGACCTGGCCGCGTCGGCCGCTACAAGATCAACAAGAAGCTGG
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Pred. No. 8.7e-14;
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                               /db_xref-"taxon:1773"
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                                                                           <i..>615
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                                                              /gene="rpoB"
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76.7%;
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<1. .>618
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Molecular analysis of rifampin-resistant Mycobacterium tuberculosis
isolated in Spain (1996-2001). Description of new alleles into rpob
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lahonda-Pozuelo, Km 2.5,
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Nacional Microbiologia., Ctra. Majadahonda-Pozuelo, Km
Majadahonda. Madrid. 28220, SPAIN
                                                                                                                                                                                                                                                                                                                   Length 618;
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Pred. No. 8.7e-14;
0; Mismatches 37;
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Mycobacterium tuberculosis.
Mycobacterium tuberculosis
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AJ318816.1 GI:22208408
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76.78;
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76.7%;
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Herrera, L.
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FFGTSQPSQPSGPGGONNPLSGLTHKRRLSALGPGGLSRERAGLEVRDV"
192 c 207 g 95 t
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Molecular analysis of rifampin-resistant Mycobacterium tuberculosis isolated in Spain (1996-2001). Description of new alleles into rpoB gene and review
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 circular BCT 09-AUG-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (07-AUG-2001) Herrera L., Servicio Bacteriologia, Centro
Nacional Microbiologia., Ctra. Majadahonda-Pozuelo, Km 2.5,
Majadahonda. Madrid. 28220, SPAIN
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Mycobacterium tuberculosis.
Mycbacterium tuberculosis
Hacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corymebacterinee: Mycobacteriaceae; Mycobacterium; Mycobacterium tuberculosis complex.
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                                                                                                                                       15;
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/db_xref="taxon:1773"
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                                                                                                         DB 1;
                                                                                                                                       37;
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Pred. No. 8.7e-14;
); Mismatches 37
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                                                                                                      55.5%;
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                                                                                                                                   171; Conservative
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gene for RNA polymerase
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Molecular analysis of rifampin-resistant Mycobacterium tuberculosis isolated in Spain (1996-2001). Description of new alleles into rpob gene and review
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="VGTDEALLD1YRKLRPGEPPTKESAQTLLENLFFKEKRYDLARV
GRYKYNKKLGLHVGEPITSSTLTEEDVVATIEYLVRLHEGGTTWTVPGGVEVPVETDD
IDHFGURRTYGELIONQIRVGMSRMERVVRRRWTYODVEAITPOTLINIRPVVAAI
KEFFGTSQLSGFMDONNPLSGLTHKRMFALGPGGLSRERAGLEVRDVHPSH"
198 c 101 g 101 t
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Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium
tuberculosis complex.
                                                                                                                GCCTGAACACCGATCATCCGATCACCACCACGACGCTGACCGAAGAGACGTCGTCGCCA 120
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                                                                                                                                                                                                                                                                                                          1 TCAAGGAGAAGCGCTACGACCTGGCCCGCGTCGGCCGCTACAAGAAGGTCAACAAGAAGCTGG
                                               15;
     Length 633;
                                               Indels
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/isolate="1255-98"
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                                               37;
DB 1;
                                                                                                                                                                                                                                                                                                                                                                             181 CTGTCCCCGGCGGGTCGAGGTGCCGGTGGAAACCGACGAT
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Pred. No. 8.7e-14;
); Mismatches 37;
                      Pred. No. 8.7e-14;
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beta subunit, isolate 1255-98.
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                                             0; Mismatches
Score 123.8;
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/product="RNA polymerase
/protein_id="CAC87033.1"
/db_xref="G1:22208409"
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Mycobacterium tuberculosis.
Mycobacterium tuberculosis
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Molecular analysis of rifampin-resistant Mycobacterium tuberculosis isolated in Spain (1996-2001). Description of new alleles into rpoB gene and review
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="RRTDEALLDIYRKLRPGEPPTKESAQTLLENLFFKEKRYDLARV
GRYKVNKKLGIHVGEPITSSTLTEEDVVATIEYLVRLHEGGTTMTVPGGVEVPVETDD
IDHFGNRRLRTVGELIQNOIRVGMSRMERVVRERMTTQDVEATPOTLINIRRAVAAI
KEFFGTSOGFWVQNNPLSGLTQRRRLSALGPGGLSRERAGLEVRDVHPSHS"

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                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium
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GCCTGAACACCGATCATCGATCACCACCACGACGCTGACCGAAGAAGACGTCGTCGCCA 120
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                                                                                                                  61 GCCTGAACACCGATCATCCGATCACCACGACGTGACGAAGAAGACGTCGTCGCCA
                                                                                                    121 CCATCGAGTACCTGGTTCGCCTGCACCACGCTCTCAGGGTGGCCAGGCCCCCGGTTATGA
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/protein_id="CAC87038.1"
/db_xref="G1:22208419"
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/isolate="1071-98"
                                                                                                                                                                         DB 1;
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Pred. No. 8.7e-14;
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RNA polymerase beta subunit; rpoB gene.
Mycobacterium tuberculosis.
Mycobacterium tuberculosis.
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/transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                          tuberculosis complex.
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Best Local Similarity 76.7%;
Matches 171; Conservative
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Herrera, L.
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PAT 07-UCT-1997
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Mycobacterium; Mycobacterineae; Mycobacteriacae;
Mycobacterium; Mycobacterineae; Mycobacteriacae;
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CCATCGAGTACCTGGTTCGCCTGCACCACGCCTCTCAGGGTGGCCAGGCCCCCGTTATGA
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Mycobacterium tuberculosis
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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Persing,D.H., Hunt,J.J., Young,K.K.Y., Felmlee,T.A., and Whelan, A.Christian.
Detection of a genetic locus encoding resistance to r mycobacterial cultures and in clinical specimens Patent: US 5643723-A 1 01-JUL-1997;
Location/Qualifiers
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                                                                                                                                                                                                                                                                      DNA
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Sequence 1 from patent US 5643723.
150706
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76.78;
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Best Local Similarity 76.7'
Matches 171; Conservative
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us-09-697-123b-13.rge

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3853 bp DNA linear BCT 02-MAR-2000 Mycobacterium tuberculosis H37Rv RNA-polymerase beta subunit (rpob) 012205
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REPLEVPGLLDVQTDSFEWLIGSPRWRESAAERGDVNPVGGLEEVLYELSPIEDFSGS
MSLSFSDPRFDDVKAPVDECKDKDMTYAAPLFVTAEFINNNTGEIKSQTVFMGDFPMM
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SDTVGVRIDBKRRQPVTVLLAALGWYSEQIVERFGFSEIMRSTLEKONTVGTDEALLD
IYRKLRFGEPPTKESAQTLLENLFREKRYDLARVGRYKNNKKLGLHVGEPITSSTLT
EEDVVATIEYLVRLHEGQTTMTVPGGVEVPVETDDIDHFGNRRLRTVGELIQNOIRVG
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                                                                                                                                                     Gaps
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1 (bases 1 to 3853)
Imboden,P., Troller,R., Marchesi,F., Telenti,A., Bodmer,T., Cole,S., Schopfer,K. and Burkart,T.

The robs gene of Mycobacterium tuberculosis
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (11-JUL-1994) Paul Imboden, Institute for Medical Microbiology, University of Berne, Friedbuehlstrasse 51, Be 3010, Switzerland, Qualifiers
                                                                                                                                                                                      1 TCAAGGAGAAGCGCTACGACCTGGCCCGCGTCGGCCTACAAGAAGAAGCTGG
                                                                                                                                                   15;
                                                                                                                Length 3534;
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                                                                                                       Score 123.8; DB 6; Length
Pred. No. 7.2e-14;
O: Mismatches 37; Indels
/organism="Mycobacterium tuberculosis"
/strain-"Rv"
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/protein_id="AAAA20242.2"
/db_xref="G1:7144499"
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/organism="Mycobacterium tuberculosis"
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                                    /db_xref*"taxon:1773"
1081 c 1188 g
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/db_xref="taxon:1773"
576. .>3853
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576. .>3853
                                                                                                              55.5%;
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/gene="rpoB"
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Imboden, P.
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TITLE
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MSRMERVVRERMTTQDVEA1TPQTLINIRPVVAAIKEFFGTSQLSQFMDQNNPLSGLT
HKRRLSALGPGGLSRERAGLEVRDVHPSHYGRMCPIETPEGPNIGLIGSLSVYARVNP
FGFIETPYRKVVDGVVSDGIVYLTADEEDRHVVAQANSPIDADGRFVEPRVLVRRKAG
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protein_id="AAA21416.1"
/db_xref="GI:46834"
/translation="MLEGCILADSRQSKTAASPSPSRPQSSSNNSVPGAPNRVSFAKL
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Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium
tuberculosis complex.
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Miller,L.P., Crawford,J.T. and Shinnick,T.M.
The rpoB gene of Mycobacterium tuberculosis
Antimicrob. Agents Chemother. 38 (4), 805-811 (1994)
94304130
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/strain="Rv"
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Mycobacterium tuberculosis (strain Rv) DNA.
Mycobacterium tuberculosis
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1065. 4598
/gene="rpob"
1065. 4598
/gene="rpob"
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Matches 171; Conservative
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TYRK LEGEPPPINE SOTTEMEN SOTTE
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GLFCEKIFGPTRDWECYCGKYKRVRFKGIICERCGVEVTRAKVRRERMGHIELAAPVT
HIWYFKGVPSRLGYLLDLAPKDLEKIIYFAAYVITSVDEEMRHNEL"
TEKCTFIINGTERVUVSQLVRSPGVYFDETIDKSTDKTLHSVKVIPSRGAWLEFDVDK
RDTVGVRIDRKRRQPVTVLLKALGWTSEQIVERFGFSEIMRSTLEKDNTVGTDEALLD
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Mycobacterium tuberculosis CDC1551, section 50 of 280 of the
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1 (bases 1 to 1935)
Fleischmann, R.D., Alland, D., Eisen, J.A., Carpenter, L., White, O., Peterson, J., DeBoy, R., Dodson, R., Gwinn, M., Haft, D., Hickey, E., Kolonay, J.F., Nelson, W.C., Umayam, L.A., Ermolaeva, M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="kNA polymerase beta'-subunit"
/protein_id="AAA21417.1"
/db_xref="G1:537608"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2131 CCGTTCCGGGCGGCGTCGAGGTGCCGGTGGAACCGACGACT 2173
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Mycobacterium tuberculosis CDC1551
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4641
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/gene="rpoC"
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Matches 171; Conservative
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AE006964 AE000516
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TEKGTFI INGTERTOYOUGURSPGOVFDET IOKSTDKTLHSVKVI PSKGAWLEPDYDK
RDTYGVRIDRKRROPYTULLKALGWTSEQI VERFGFSE IMRSTLEKDNTVGTDEALLD
I YRKLERGEPPFFKERKSYDLARVGRYKWINKLGLHVGEPITESTLI
EEDVVAT IET LYRLHEGGTLENLEFREKRYDLARVGRYKWINKLGLHVGEDITESTLT
EEDVVAT IET LYRLHEGGTTWTYPGGVEPVETDD DHFGNRRLRTVGELIQNOI NUG
MSRWERVYRERMTTODVEATTPOTLINI RPVYAAD IKEFGTSOLSOFNOONDLUGGLT
HKRRLSALGPGGLSRERAGLEVRDWHPSHVGRMCPTETPEGPNIGLIGSLSVYARVNP
FGFIETPRKVVDGVVSDEIVYLTADEEDRHVVAQANSPIDADGRFVEPREVLYRRKAG
EVEYVPSSEVDYMDVSPROWYSVATAMIPFLEHDDARRALMGANMORQAVPLYRSEAP
LVGTGMELRAAI DAGDVVVAEESGVI EEVSADY ITVMHDNGTRRTYRMRK FARSNHGT
CANQCPIVDAGDREVBAGOVI RAGPCTDDGEMALGKNILLVAI IMPWEGHNYEDAI ILSNR
LVEEDVLYSI INI EEHEI DARDYKAGAEET RAEFRAR REVRENE
GDILVGKVYPPRGETELTPERELLAR FGERKARREVROPTSLKVPHGESGKVI IGIRVFSKE
DEDELPAGVNELVRYYVAOKRKI SDGDKLAGRHGNKGVIGK ILLPVEDMPFLADGTPVD
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protein_id="AAK44921.1"
/db_xref="GI:11880218"
/translation="MLEGCILADSROSKTAASPSPSRPOSSSNNSVPGAPNRVSFAKL.
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MSLSFSDPRFDDVKAPVDECKDKDMTYAAPLFVTAEF I NNNTGEI KSQTVFMGDFPMM
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GFORNRPLKSLSDLLKGKGGRRRONLGKRVDYSGRSYIVVGPOLKLHOGGLPKLMALE
LEKPEYWKRLUDLWARONIKSARRWYERQRPOYWDVLEEVIAEHPVLLNRAPTLHRLG
IQAFEPMLVEGKAIQLHPLVCEAFNADFDGDOMAVHLPLSAEAQAEARILMLSSNNIL
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LTIKSDDTVGRVKVYEAIVKGENIPEPGIPESFKVLLKELQSLCLNVEVLSSDGAAIE
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/protein_id="AaK44922.1"
/db_xref="G1:13880219"
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HIWYFKGVPSRLGYLLDLAPKDLEKIIYFAAYVITSVDEEMRHNELSTLEAEMAVERK
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LRDVIRNGKGQKKLRALKRLKVVAAFQQSGNSPMGMVLDAVPVIPPELRPMVQLDGGR
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Salzberg,S.L., Delcher,A., Utterback,T., Weldman,J., Khourl,H.,
Gill,J., Mikula,A. and Bishai,W.
Whole genome comparison of Mycobacterium tuberculosis clinical and
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                                                                                                                                                                                                                                                              "The state of the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PID:149992; identified by sequence similarity; putative" /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:83331"
/note="clinical strain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /transl_table*11
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/gene="MT0696"
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/gene="MT0696"
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                                                                                                                                                                             laboratory strains
                                                                                                                                                                                                                                 Unpublished
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JOURNAL
                                                                                                                                                                                                                                                                                REFERENCE
AUTHORS
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                                                                                                                   TITLE
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/transl_table=11
/product-"AP endonuclease, family 2"
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/db_xref="G1:1380221"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALKAATLPIYVHAPYLINLASANNRVRIPSRKILOETCAAADIGAAAVIVHGGHVAD
DNDIOKGFQVRRKALDRLETRYVVYLENTAGGDHAMRRFDTIARLMDVIGDTGIGC
LDTCHTWAAGGEALTDAVDRIKALTGRIDLVHCNDSRDEAGSGRDRHANLGSGQIDPDL
LVAAVKAAGAPVICETADQGRKDDIAFLRFRTGS"
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/transl_table=11
/transl_table=11
/product="hydrolase/esterase, putative"
/protein_id="aAK44925.1"
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TETSAYARTLGTDAVDEAGNVIVERGODLGDPEIDALLAGAGTTQVKVRSVLTCATST
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VQELFEARVPRGKAPIADVTGKVRLEDGERFYKITIVPDDGGEBVVYDKISKRORLRV
                                                                                                                                                                                                                                                                                                  FKHEDGSERVLSDGDHVEVGQOLMEGSADPHEVLRVOGPREVQIHLVREVOEVYRAOG
VSIHDKHIEVIVRQMLRRVTIIDSGSTEFLPGSLIDRAEFEAENRRVVAEGGEPAAGR
PVLMGITKASLATDSWLSAASFQETTRVLTDAAINCRSDKLNGLKENVIIGKLIPAGT
SPASCRPLAMPRLUMVTGLYYLTTEVPEDTGEYQPASGDHPETGYYSSPAEAIMAADR
GVLSVRAKIKVRLTGLRPPVE1EAELFGHSGWQPGDAWMAETTLGRVMFNELLPLGYP
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1TIVDSGATGNFTQTRTLAGMKGLVTNPKGEFIPRPVKSSFREGLTVLEYFINTHGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="MFDSAAAITNPGHAWASAWERSGLLECVAGLDEOPFGEFTADKL
NPDKGSSRRVPRRQADGGIATHVERGGGQRQSGGAGVVPQRMHGFPALAMQDRLIHH
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SIFAAIGVVSGTQLDPCQSPRPVSVIHIHGTADPLVRYHGGPGAGFARIDGPPVPDLN
AFWREVNRCGALDTTTEGPVTTSGATCADNRRVVLLITVDDAGHRWPSFATQTLWRFFA
                                                                 FVNKQMHKKVQAAIINDLAERYPMIVVAQTVDKLKDAGFYWATRSGVTVSMADVLVPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="This region contains an authentic frame shift and is not the result of a sequencing artifact; identified by Glimmer2; putative; conserved hypothetical protein, authentic frameshift"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note-"similar to SP:P33224 GB:L20915 PID:457172
PID:457174 PID:537028; identified by sequence similarity;
putative"
                                                                                                                                                                                                                                                                                                                                                                                                      GINRYRNIAVQPTEEARAAAYTIPSYEDQYYSPDFGAATGAAVPLDDYGYSDYR"
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/note="similar to GB:U00012 PID:466863; identified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="identified by Glimmer2; putative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note-"identified by match to PFAM PF01261"
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                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(7691. .8065)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="MT0697"
complement(7691. .8065)
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/gene="MT0701"
11859. .13487
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WADDREGAHVVRAAKTSVWTVEPGHICPISMTYAVVPALRYNSELAAVYEPLLTSREY
DELKRATTAGITAGMSWTEKOGGSDVRAGTTOAPDNADGSYSLTGHKWETSAPMCD
IFLULAQAPDGLSCFLLPRVLPDGTRANMFLORLKOKIGNHANASSEVEYDGAVAMLV
GEBGRCYPTITEWNUTRLOCALGSATSMRTGLTRAVHAOHRRAFGAYL IDOPLMRN
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ELSALVERADLDPGVHVILVSGRGEGFCAGFDLSAYAEGSSSTGGGGAYQGTVLDGKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OAVNHLPNOPWDPMIDYOMMSRFVRGFÄSLMHADKPTVVKIHGYCVAGGTDIALHADO
VAAADAKIGYPPTRWGVPAAGLWARHGADGARRILETGOTITGAQAAEWGLAVEA
PEPALDERTERLUARIAALPVNOLIMVKLALNSALLQQGVATSRMVSTVFDGAARHT
PEGHAPVADAVEHGFRDAVRRREPFCDYGROASKV*
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                                                                /translation="mSDTHVVTNQVPPLENYNPASSPVLIEALIOEGGGWGLDEVNEV
GAISASCQAQRWGELADRNRPILHTHDAYGYRVDEVEYDPAYHELMRTAITHGMHAAP
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Mycobacterium tuberculosis H37Rv complete genome; segment 32/162.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 GCCTGAACACCGATCATCCGATCACCACCACGACGCTGACGAAGAGACGTCGTCGCA 120
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                                                                                                                                                                                                                                                                                                                                                                                   /note="similar to GP:3885480; identified by sequence similarity; putative" /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 TCAAGGAGAAGCGCTACGACCTGGCCCGCGTCGGCCGTACAAGGTCAACAAGAAGCTGG
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Mycobacterium tuberculosis H37Rv
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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Mycobacterium; Mycobacterium tuberculosis complex.
/product="acyl-CoA dehydrogenase, putative"
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0; Mismatches 37; Indels
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13498. .14436
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Conservative
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Z95972.1 GI:3261790
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Matches 171;
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KEYWORDS
SOURCE
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//note="RV0655, (MTC1376.21), len: 359, abc transporter, PASTA score: YRBF_ECOLI P5393 hypothetical abc transporter atp-binding (269 aa) opt: 644 zesore: 721.8 E(): 3.4e-33 (38.5% identity in 244 aa overlap); contains ps00017 ATP/GTP-binding site motif A, ps00211 ABC transporters family signature, highly similar to M. leprae MKL_MYCLE P30769 possible ribonucleotide transport atp- (347 aa) opt: 2021 z-score:2244.4 E(): 0, (92.2% identity in 315 aa overlap). Also similar to many otherM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="MRYSDSYHTTGRWQPRASTEGFPMGVSIEVNGLTKSFGSSRIWE
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RTLFGVLFQDGALFGSMNLYDNTAFPLREHTKKKESEIRDIVMEKLALVGLGGDEKKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PGEISGGMRKRAGLARALVLDPQIILCDEPDSGLDPVRTAYLSQLIMDINAQIDATIL
IVTHNINIARTVPDNMGMLFRKHLVMFGPREVLLTSDEPVVRGFLNGRRIGPIGMSEE
KDEATWAEEQALLDAGHHAGGVEEIEGVPPQISATPGMPERKAVARRQARVREMLHTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /traislation="maaattigthrolelraaqraygscepqraefcrsarnadepdo
msrmfgdyypdypyvpksywrwidsaqhrlaragaygalsyydllicdtaaarglyylh
Ddadyelaerhlpdiryrryysadd"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="MSVTQIDLDDEALADVMRIAAVHTKKEAVNLAMRDYVERFRRIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(3052. .3435)
/gene="Rv0656c"
/note="Rv0656c, (MTCI376.20, unknown), len: 127 aa"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="PS00017 ATP/GTP-binding site motif A" 2074 . 2118 /gene="Rv0655"
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/note="possible RBS upstream
complement(3761. .4477)
/gene="Rv0658c"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=1
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                                               CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  available on the World Wide Web.

(URL, http://www.sanger.ac.uk/Projects/M_tuberculosis/) CDS have been renumbered from the original cosmid submissions but the old gene designations are in brackets after the new gene numbers.

Gene prediction was based on a Hidden Markov Model of TB genes implemented in TBparse (Krogh) supplemented with visual inspection of positional base preference in codons, especially where there is an increase in the observed/expected third position G + C.

CAUTION: In some cases we may not have predicted the correct initiation codon. Where possible we choose an initiation codon (atg., gtg., or ttg) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most upstream
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (11-JUN-1998) Submitted on behalf of the Mycobacterium tuberculosis sequencing and mapping teams, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA Unite de Genetique Moleculaire Bacterienne, Institut Pasteur, 28 rue du Docteur Roux, 75724 Paris Cedex 15, France E-mail: parkhill@sanger.ac.uk On Jun 27, 1998 this sequence version replaced gi:2143285.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Rv0654, (MTC1376.22), len: 501. unknown, FASTA score: Q53353 LIGNOSTILBENE-ALPHA, BETA-DIOXYGENASE (485 and) opt:280 z-score: 330.1 E(): 2.39-11, (28.5% identity in 522 accoverapp). Also similar to M. tuberculosis protein MTCY21C12.07c (29.5% identity in 522 accoverlap).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="mttaqaaeSqupyLegFlapvstevtatDLpvtgRIPEHLDGRY
LRNGPNPVAEVDPATYHWFTGDAMVHGVALRDGKARWYRNRWVFTPAVCAALGEPISA
RPHPRTGIIEGGPNTNVLTHAGRTLALVEAGVVNYELTDELDTVGPCDFDGTLHGGYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AHPQRDPHTGELHAVSYSFARGHRVQYSVIGTDGHARRTVDIEVAGSPWMHSFSLTDN
YVVIYDLPVTFDPMQVVPASVPRWLQRPARLVIQSVLGRVRIPDPIAALGNRMQGHSD
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SYRWFDRRRGPGGDSRPSLDRWTINLATGAYTAECRDDAGGFPRINETLYGGPHR
PAYPWGIEGGFLVAGAAALSTPLYKQDCYTGSSTVASLDPDLIJGEWVFVPNPSARAE
DDGILMGYGWHRGRDEGQLLLLDAGTLESIATVHLPQRYPMGFHGNWAPFT"
                              Cole, S. T., Brosch, R., Parkhill, J., Garnier, T., Churcher, C., Harris, D., Gordon, S. W., Eiglmeier, K., Gas, S., Barry Ill, G. E., Tekais, F., Badcock, K., Basham, D., Brown, D., Chillingworth, T., Connor, R., Davies, K., Devlin, K., Feltwell, T., Gentles, S., Hamlin, N., Holroyd, S., Hornsby, T., Jagels, K., Krogh, A., McLean, J., Murphy, L., Gliver, S., Osborne, J., Quail, M.A., Rogers, J., Rutter, S., Seeger, K., Skelton, S., Squares, S., Sqares, R., Sulston, J.E., Taylor, K., Whitehead, S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Details of M. tuberculosis sequencing at the Sanger Centre are
                                                                                                                                                                                                                                                                                                                              Deciphering the biology of Mycobacterium tuberculosis from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="aqga, possible rbs upstream of Rv0654"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Mycobacterium tuberculosis H37Rv"
/strain="H37Rv"
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/db_xref="G1:2143307"
/db_xref="SPTREMBL:006785"
                                                                                                                                                                                                                                                                                                                                                         complete genome sequence
Nature 393 (6685), 537-544 (1998)
98295987
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/clone="1376"
57.
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68. .1573
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      (bases 1 to 19770)
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Parkhill, J.
Direct Submission
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TITLE
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MEDLINE
REFERENCE
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KGETELTPEERILRAIFGEKAREVROTSLKVPHGESGKVIGIRVFREDDDELVGVN
ELVRVVVAQKRKISDGDKLARRHGNKGVIGKILPVEDMPFLPDGTPVDIILNTHGCRV
VLNIGQILETHLGWGARAGWNIDVLAGVPDWARALPEELYSAADSTYVATPVFDGAOE
GELGGSTLPNRDGARAGWNIDVLAGVPDWARALPEPPPYPVATGVILLALLGSTLANDLOGGREGENECWAMOAYGAAYTLQELLIKSDDTV
KIHARSTGPYSMITQOPLGGRAQFGGORFGENECWAMOAYGAAYTLQELLTIKSDDTV
GRVKYYEAINKGENIPEPGIPESFKVLLKELOSLCLNVEVLSSDGRAIEMRDGDDEDL
                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Sübmission
Submitted (11-APR-1995) Seth V. Hetherington, Infectious Diseases,
St. Jude Children's Research Hospital, 332 N. Lauderdale, Memphls,
TN 38101, USA
                                                                                                                                 Mycobacterium.

1 (bases 1 to 3752)
Hetherington,S.V., Watson,A.S. and Patrick,C.C.
Sequence and analysis of the rpoB gene of Mycobacterium smcgmatis
Antimicrob. Agents Chemother. 39 (9), 2164-2166 (1995)
96050766
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                                                                        Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                   Actinomycetales; Corynebacterineae; Mycobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 122.8; DB 1; Length
Pred. No. 1.1e-13;
0; Mismatches 17; Indels

    .3752 // Appropries | Approprie
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1225 c 1210 q 61
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         Mycobacterium smegmatis. Mycobacterium smegmatis
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/gene="rpoB"
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/gene="rpoB"
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Best Local Similarity 88.7%;
Matches 133; Conservative
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2 (bases 1 to 3752)
Hetherington, S.V.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    to YW28_MYCTU 010867 hypothetical 12.3 kd protein cY39.28 (114 aa), fasta scores; opt: 144 z-score: 213.2 E(): 7.3e-05, 30.8% identity in 107 aa overlap. Also similar to MTCY09F9.22 (32.7% identity in 101 aa overlap)"
                                                                                                                                                                                                                                                                                                             /db_xref="SPTERBHL:006781"
//db_xref="SPTERBHL:006781"
//translation="MEAGRADTVAPSHRWGLGAFLVVELVFLVASTSLAVVLTGHGPV
SAGVIALAAPTVVAAGALILTREMSGNGLEFPUDLENEWSWRGLRLGLMEGFCGMLVT
IPASLVYTATVGPEANSAVVRIFGGVRASWPWALVVFLVVVVFVAPLCEEIIYRGLLMG
AVDRRWGRWAALLVTTVVFALAHLEFARAPLLVVVAIPIALARFYSGGLLASIVTHQV
TNLLFGIVLLGGLTGAISLP"
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LVSELELTAVENRVPSDCVVNFDNIHTLPRTAFRRRITRLSPARLHEACQTLRASTGC
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probablemembrane protein, similar to YPRB_ECOLI P33774 hypothetical24.3 kd protein (urf 1) (217 aa), fasta scores, opt: 174 z-scores: 215.8 E(): 5.3e-05, (25.6% identity in 223 aa overlap). Also similar to MTCY359.10 (28.7% identity in 178 aa overlap).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mycobacterium smegmatis DNA polymerase (rpoB) gene, complete cds U24494
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(4480. .4483)
/note="possible RBS upstream of Rv0658c"
complement(4753. .5061)
complement(4753. .5061)
/gene="Rv0659c"
                                                                                                                                                                                                                    /product-"hypothetical protein Rv0658c"
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/transl_table=11
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/protein_id="CAR0938.1"
/db_xref="GI:2143302"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="Rv0660c"
complement(5048..5293)
/gene="Rv0660c"
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Matches 171; Conservative
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DE	Myc	cobacter	ium g	astri rpoB		gene fragment.	
× ×	Non	-tuberc		mycobact	erië	: rpoB gene fragment; NTM; HIV	; PRA; RFLP;
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ine present sequence to mycourcerism qualit prob galler

fragments is 1 of 24 rpob gene fragments (AAS05201-AAS0524) from
various Mycobacterial species. These rpoB gene fragments can be used
in the diagnosis and identification of Mycobacterium species using a
novel pekr-restriction fragment length polymorphism analysis (PRA)
method. The method comprises obtaining a restriction fragment length
convel pekr-restriction fragment length polymorphism (RFLP) pattern of the 24 rpoB gene fragments. Isolating,
amplitying and digesting the DNA fragment from the microorganism to
concern that the unidentified fragment. The rpoB gene fragments are useful to identify a wide range of Mycobacterium species, e.g. for
diagnosis or to obtain epidemiological and pathogenesis information for
selection of appropriate theraphes, including M. tuberculosis, M. leprae
and non-tuberculous mycobacteria (NTM) encountered in subjects infected
with human immunodeficiency virus (HIV). Analysis of the rpoB gene
fragments is rapid, precise, simple and cost effective (only 1 PCR
required), and can differentiate between many species in a single
experiment, including those difficult to distinguish by usual biochemical
control of an order of the probes (AAS05227-AAS05242) for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Non-tuberculous mycobacteria; rpoB gene fragment; NTM; HIV; PRA; RFLP; PCR-restriction fragment length polymorphism analysis; ds.
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                                       The present sequence for Mycobacterium gastri rpoB gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kim Y,
                                                                                                                                                                                                                                                                                                             Sequence 223 BP; 49 A; 77 C; 65 G; 32 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mycobacterium scrofulaceum rpoB gene fragment.
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               Claim 1; Page 44; 50pp; English
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                                                                                                                                                                                                                                                                                                                                                     al Similarity 100.
223; Conservative
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Matches 22
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The present sequence for Mycobacterium scrofulaceum rpoB gene fragment is 1 of 24 rpoB gene fragments (AAS05201-AAS05224) from fragment is 1 of 24 rpoB gene fragments can be used various Mycobacterial species. These rpoB gene fragments can be used in the diagnosis and identification of Mycobacterium species using a novel pCR-restriction fragment length polymorphism analysis (PRA) novel PCR-restriction fragment length are polymorphism analysis (PRA) method comprises obtaining a restriction fragment length polymorphism analysis (PRA) amplifying and digesting the DNA fragment from the microorganism to be identified and comparing the RFLP patterns from the known rpoB gene fragments with the unidentified fragment. The rpoB gene fragments fragment to appropriate theraples including M. tuberculosis, e.g. for diagnosis or to obtain epidemiological and pathogenesis information for selection of appropriate theraples, including M. tuberculosis, M. leprae and non-tuberculous mycobacteria (NTM) encountered in subjects infected with human immunodeficiency virus (HTV). Analysis of the rpoB gene required), and can differentiate between many species in a single experiment, including those difficult to distinguish by usual biochemical defection of described are oligonucleotide probes (AAS05227-AAS05242) for detecting aspecies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HIV; PRA; RFLP;
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                                                       New DNA fragments from the rpoB gene of mycobacteria, useful for diagnosis and identification of many mycobacterial species by
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 223;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 3.56
0; Mismatches
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Pred, No. 3.5
                                                                                                                            restriction fragment length polymorphism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       detecting specific Mycobacterial species
                                                                                                                                                                                              Claim 1; Page 42-43; 50pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mycobacterium kansasii.
WPI; 2001-300520/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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WO200131061-A1
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                                                                                                                                                                                          The present sequence for Mycobacterium kansasii rpoB gene
Tragment is 1 of 24 rpoB gene tragments (AAS05201-AAS05224) from
Tragment is 1 of 24 rpoB gene tragments (AAS05201-AAS05224) from
Tragment is 1 of 24 rpoB gene tragments can be used
The diagnosis and identification of Mycobacterium species using a
The diagnosis and identification of Mycobacterium species using a
Tragment of the method comprises obtaining a restriction fragment length
Tragment in the method comprises obtaining a restriction fragment length
Tragments with the unidentified fragment from the microorganism to
Tragments with the unidentified fragment. The rpoB gene fragments
Tragments with the unidentified fragment. The rpoB gene fragments
Tragments of to obtain epidemiological and pathogenesis information for
Selection of appropriate theraples, including M. tuberculosis, M. leprae
and non-tuberculous mycobacteria (NTM) encountered in subjects infected
with human immunodeficiency virus (HTV). Analysis of the rpoB gene
Tragments is rapid, precise, simple and cost effective (only 1 PCR
Tragment, including those difficult to distinguish by usual biochemical
cester. Also described are oligonucleotide probes (AAS05227-AAS05242) for
Very
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 GCCTGAACAATCATCCGATCACCACGACGACGACGAAGAAGAAGACGTCGTCGCA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 152.6; DB 22; Length 208; Pred. No. 3.8e-27;
                                                                                                                    New DNA fragments from the rpoB gene of mycobacteria, useful diagnosis and identification of many mycobacterial species by restriction fragment length polymorphism
                                                                    Park HJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 CTGTCCCCGGCGGGGTCGAGGTGCCGGTGGAAACCGACGACAT 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 208 BP; 51 A; 65 C; 65 G; 27 T; 0 other;
                                                                    Kim Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                    cho s,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mycobacterium avium rpoB gene fragment.
                                                                    Kim S,
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                                                                                                                                                                          Cluim 1; Page 42; 50pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              / Match 68.4%;
Local Similarity 84.8%;
es 189; Conservative (
                                         (ERUM-) ERUME BIOTECH CO LTD.
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               99KR-0046795
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                                                                     Bai G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mycobacterium avium
                                                                                            WPI; 2001-300520/31.
                                                                    Park YK,
               27 - OCT - 1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAS05215;
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                                                                     Lee H,
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Matches
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The present sequence for Mycobacterium avium rpoB gene
fragment is 1 of 24 rpoB gene fragments (AASO5201-AASO5224) from
fragment is 1 of 24 rpoB gene fragments can be used
various Mycobacterial species. These rpoB gene fragments can be used
on the diagnosis and identification of Mycobacterium species using a
novel PCR-restriction fragment length polymorphism analysis (PRA)
method comparises obtaining a restriction fragment length
polymorphism (RPLP) pattern of the 24 rpoB gene fragments; 1solating,
amplifying and digesting the DNA fragment from the microorganism to
be identified and comparing the RPLP patterns from the known rpoB gene
fragments with the unidentified fragment. The rpoB gene fragments
are useful to identify a wide range of Mycobacterium species, e.g. for
diagnosis or to obtain epidemiological and pathogenesis information for
selection of appropriate therapies, including M. tuberculosis, M. leprac
and non-tuberculous mycobacteria (NTM) encountered in subjects infected
with human immunodeficiency virus (HTW). Analysis of the rpoB gene
fragments is rapid, precise, simple and cost effective (only 1 PCR
fragments in including those difficult to distinguish by usual biochemical
experiment, including those difficult to distinguish by usual biochemical
cests. Also described are oligonoucleotide probes (AASO5227-AASO5242) for
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                                                                                                                                                                                                                                                                                                                                                                                                                                New DNA fragments from the rpoB gene of mycobacteria, useful for diagnosis and identification of many mycobacterial species by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 208;
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0; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                    Park HJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 CTGTCCCCGGCGGGGTCGAGGTGCCGGTGGAAACCGACGACAT 223
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                                                                                                                                                                                                                                                                                    Kim Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 63.4%; Score 141.4; Best Local Similarity 81.6%; Pred. No. 1.7 Matches 182; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                    Cho S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  restriction fragment length polymorphism
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                                                                  27-OCT-2000; 2000WO-KR01223.
                                                                                                                                        99KR-0046795
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                                                                                                                                                                                                                                                                                            Park YK,
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03-MAY-2001
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Non-tuberculous mycobacteria; rpoB gene fragment; NTM; HIV; PRA; RFLP; PCR-restriction fragment length polymorphism analysis; ds.

Mycobacterium gordonae type I.

WO200131061-A1.

03-MAY-2001

4ycobacterium gordonae type I rpoB gene fragment.

(first entry)

07-SEP-2001

BP.

AAS05201 standard; DNA; 208

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The present sequence for Mycobacterium celatum rpoB gene
Iragment is 1 of 24 rpoB gene fragments (AASO5201-AASO5224) from
various Mycobacterial species. These rpoB gene fragments can be used
in the diagnosis and identification of Mycobacterium species using a
novel PCR-restriction fragment length polymorphism analysis (PRA)

method. The method comprises obtaining a restriction fragment length
polymorphism (RFLP) pattern of the 24 rpoB gene fragment length
polymorphism (RFLP) pattern of the 24 rpoB gene fragment Log
polymorphism (RFLP) pattern of the 24 rpoB gene fragment Log
be identified and comparing the RFLP patterns from the Mnown rpoB gene
fragments with the unidentified fragment. The rpoB gene fragments
fragments with the unidentified fragment. The rpoB gene fragments
are useful to identify a wider range of Mycobacterium species, e.g. for
diagnosis or to obtain epidemiological and pathogenesis information for
selection of appropriate therapies, including M. tuberculosis, M. leprae
and non-tuberculous mycobacteria (NTM) encountered in subjects infected
with human immunodeficiency virus (HIV). Analysis of the rpoB gene
fragments is rapid, precise, simple and cost effective (only 1 PCR
required), and can differentiate between many species in a single
tragment, including those difficult to distinguish by usual biochemical
cests. Also described are oligonucleotide probes (AASO5227-AASO5242) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1;
                                       HIV; PRA; RFLP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 GCCTGAACACCGCGTCCCCGATCACGACGACCACTCTGACGAAGAGGACGTCGTCGCA 120
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Pred. No. 9.5e-24;
0; Mismatches 28; Indels 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                        New DNA fragments from the rpoB gene of mycobacteria, useful diagnosis and identification of many mycobacterial species by restriction fragment length polymorphism
                                                                                                                                                                                                                                                                                                                                                             Park HJ;
                                       Non-Luberculous mycobacteria; rpoB gene tragment; NTM; PCR-restriction fragment length polymorphism analysis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTGTCCCCGGCGGGGTCCAGGTGCCGGTGGAAACCGACGACAT 223
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                                                                                                                                                                                                                                                                                                                                                             Kim Y,
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                                                                                                                                                                                                                                                                                                                                                           Cho S,
Mycobacterium celatum rpoB gene fragment
                                                                                                                                                                                                                                                                                                                                                             Park YK, Bai G, Kim S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 45; 50pp; English.
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80.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              180; Conservative
                                                                                                       Mycobacterium celatum
                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-300520/31.
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Best Local Similarity
Matches 180; Conserv
                                                                                                                                             WO200131061-A1
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                                                                                                                                                                                                                                                                                                                                                           Lee H,
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New DNA fragments from the rpoB gene of mycobacteria, useful for diagnosis and identification of many mycobacterial species by restriction fragment length polymorphism

Claim 1; Page 40; 50pp; English

Kim Y,

s, Cho

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Kin

Bai G,

Lee H,

WPI; 2001-300520/31. Park YK,

(ERUM-) ERUME BIOTECH CO LTD.

27-OCT-2000; 2000WO-KR01223.

99KR-0046795

27-0CT-1999;

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The present sequence for Mycobacterium gordonae type I rpoB gene fragment is 1 of 24 rpoB gene fragments (AAS05201-AAS05224) from various Mycobacterial species. These rpoB gene fragments can be used in the diagnosis and identification of Mycobacterium species using a convel PCR-restriction fragment length polymorphism malysis (PRA) and polymorphism (RFLP) pattern of the 24 rpoB gene fragments isolating, applymorphism (RFLP) pattern of the 24 rpoB gene fragments; isolating, and identified and comparing the RFLP patterns from the Mrown rpoB gene fragments with the unidentified fragment. The rpoB gene fragments is information for can exeful to identify a wide range of Mycobacterium species, e.g. for diagnosis or to obtain epidemiological and pathogenesis information for selection of appropriate therapies, including M. tuberculosis, M. leprae and non-tuberculous mycobacteria (NTM) encountered in subjects infected with human immunodeficiency virus (HIV). Analysis of the rpoB gene fragments is rapid, precise, simple and cost effective (only 1 PCR required), and can differentiate between many species in a single experiment, including those difficult to distinguish by usual biochemical experiment, including those difficult to distinguish by usual biochemical and cost fragments.
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79.8%; Pred. No. ....
79.8%; O; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               detecting specific Mycobacterial species.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 60.5'
Best Local Similarity 79.8'
Matches 178; Conservative
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<u>:</u>

DB 22; Length 208; 30; Indels --CACGATGA 165

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RESULT 6 AAS05201

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HIV; PRA; RFLP;

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CCATCGAGTACCTGGTTCGCCTGCACCACGCCTCTAGGGTGGCCAGGCCCCCGTTATGA 180
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                                                                                                                                                                                                                                                                                                                                                                                                        Non-tuberculous mycobacteria; rpoB gene fragment; NTM; PCR-restriction fragment length polymorphism analysis;
                                                                                                                    CTGTCCCCGGGGGGTCGAGGTGCCGGTGGAAACCGACGACAT 223
                                                                                                                                                                                                                                                                                                                                                                  Mycobacterium xenopi rpoB gene fragment.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 G, Kim
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                                                                                                                                                                                                                                         AAS05224 standard; DNA; 208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mycobacterium xenopi.
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tes 178; Conserv
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Matches
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                                                                                                                                                                                                     RESULT 8
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                                                                                                                                                                                                                                                                                   Non-tuberculous mycobacteria; rpoB gene fragment; NTM; HIV; PRA; RFLP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Park HJ;
                                                                                                                                                                                                                                                                                                       PCR-restriction fragment length polymorphism analysis;
Sequence 208 BP; 43 A; 69 C; 69 G; 27 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kim Y,
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Pred. No. 5.4e-23;
                                                                                                                                                                                                                                           Mycobacterium fortuitum rpoB gene fragment.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cho S,
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                                                                                                                    AAS05219 standard; DNA; 208
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Bost Local Similarity 79.8
Matches 178; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bai G,
                                                                                                                                                                                                                                                                                                                                                 Mycobacterium fortuitum.
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                                                                                RESULT 7
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Park HJ;

Kim Y,

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The present sequence for Mycobacterium xenopi rpoB gene
fragment is 1 of 24 rpoB gene fragments (AASO5201-AASO5224) from
craines Mycobacterial species. These rpoB gene fragments can be used
in the diagnosis and identification of Mycobacterium species using a
cnovel PCR-restriction fragment length polymorphism ranalysis (PRA)
method. The method comprises obtaining a restriction fragment length
cc polymorphism (FRLP) pattern of the 24 rpoB gene fragments; isolating,
amplifying and digesting the DRA fragment from the microorganism to
be identified and comparing the RFLP patterns from the known rpoB gene
cc amplifying and digesting the PRA FRLP patterns from the known rpoB gene
cc and infinity a wide range of Mycobacterium species, e.g. for
diagnosis or to obtain epidemiological and pathogenesis information for
selection of appropriate therapies, including M. tuberculosis, M. leprae
cc and non-tuberculous mycobacteria (NTM) encountered in subjects infected
with human immunodeficiency virus (NTM) encountered in subjects infected
cwith human immunodeficiency virus (NTM) analysis of the rpoB gene
fragments is rapid, precise, simple and cost effective (only 1 PCR
crequired), and can differentiate between many species in a single
credited, and can differentiate between many species in a single
experiment, including those difficult to distinguish by usual blochemical
cesperiment, including those difficult to distinguish by usual blochemical
cesperiment, and considered are oligonucleotide probes (AASO5227-AASO5242) for
detecting specific Mycobacterial species.
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DB 22;

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and non-tuberculous mycobacteria (NTM) encountered in subjects infected with human immunodeficiency virus (HIV). Analysis of the rpoB gene fragments is rapid, precise, simple and cost effective (only 1 PCR required), and can differentiate between many species in a single experiment, including those difficult to distinguish by usual biochemical tests. Also described are oligonucleotide probes (AASO5277-AASO5242) for
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                                                              120
                                                                                 61 GCCTGAACACCGAGAATGCGCCAACCACCACGACCTGACCGAAGAGGACGTCGTCGCCA 120
                                                                                                                                           121 CCATCGAGTACCTGGTTCGCCTGCACCACGCCTCTCAGGGTGGCCAGGCCCCCGTTATGA 180
                                                                                                                                                                                 121 CCATCGAATACCTGGTGCGCTTGCACGAGG-------GGCACGCCACGATGA 165
GCCTGAACACCGATCATCCGATCACCACCACGCTGACCGAAGAAGACGTCGTCGCCA
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                                                                                                                                                                                                                          181 CTGTCCCCGGCGGGGTCGAGGTGCCGGTGGAAACCGACGACAT 223
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                                                                                                                                                                                                                                                                                                                                                                     AAS05203 standard; DNA; 208 BP
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The present sequence for Mycobacterium marinum rpoB gene fragment is 1 of 24 rpoB gene fragments (AASO5201-AASO5224) from various Mycobacterial species. These rpoB gene fragments can be used in the diagnosis and identification of Mycobacterium species using a novel PCR-restriction fragment length polymorphism analysis (PRA) method comprises obtaining a restriction fragment length polymorphism (RFLP) pattern of the 24 rpoB gene fragments; isolating, amplifying and digesting the DNA fragment from the microorganism to be identified and comparing the RFLP patterns from the known rpoB gene fragments with the unidentified fragment. The rpoB gene fragments are useful to identify a wide range of Mycobacterium species, e.g. for diagnosis or to obtain epidemiological and pathogenes1s information for selection of appropriate therapies, including M. tuberculosis, M. leprae and non-tuberculous mycobacteria (NTM) encountered in subjects infected with human immunodeficiency virus (HIV). Analysis of the rpoB gene fragments is rapid, precise, simple and cost effective (only 1 PCR
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                                                                                                                                      61 GCCTGAACACCGATCATCCGATCACCACCACGACGACGAAGAAGACGTCGTCGCCA 120
                                                                                                                                                                                                           121 CCATCGAGTACCTGGTTCGCCTGCACCACGCCTCTCAGGGTGGCCAGGCCCCCGTTATGA 180
                                                                                                                                                                                                                               121 CCATCGAGTACCTGGTCCGTCTGCACGAGGTCAGCA--------CACGATGA 165
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                                   Gaps
                                                                                     1 TCAAGGAGAAGCGCTACGACCTGGCCCGTGTGCGCCGCTACAAGGTCAACAAGAAGCTCG
                                                                   1 TCAAGGAGAAGCGCTACGACCTGGCCCGCGCTCGGCCGCTACAAGAAGCTGG
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                                                                                                                                                                                                                                                                                    181 CTGTCCCCGGGGGTCGAGGTGCCGGTGGAACCGACGACAT
Score 133.4; DB 2
Pred. No. 1.3e-22;
                                   Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 43; 50pp; English.
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                                   Conservative
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                Similarity
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Query Match
Best Local Sim.
Matches 177;
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required), and can differentiate between many species in a single experiment, including those difficult to distinguish by usual biochemical tests. Also described are oligonucleotide probes (AASO5227-AASO5242) for detecting specific Mycobacterial species.
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                                                                                                                                                                                                                                                            61 GCCTGAACGCGGCCAGCCCATCACCAGCTCGACGTGACGAGAAGACGTCGTCGCCA 120
                                                                                                                                                                                                                                                                                                         CCATCGAGTACCTGGTTCGCCTGCACCACGCCTCTCAGGGTGGCCAGGCCCCCGTTATGA 180
                                                                                                                                                                                                                                                                                                                         GCCTGAACACCGATCATCCGATCACCACCACGACGCTGACCGAAGAAGACGTCGTCGCCA 120
                                                                                                                                                                              ] TCAAGGAGAAGCGCTACGACCTGGCCCGCGTCGGCCGCTACAAGGTCAACAAGAAGCTGG 60
                                                                                                                                                                                               Now DNA fragments from the rpoB gene of mycobacteria, useful for diagnosis and identification of many mycobacterial species by
                                                                                                                59.8%; Score 133.4; DB 22; Length 208;
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                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                        181 CTGTCCCCGGGGGGGCTCGAGGTGCGGTGGAAACCGACGACAT 223
                                                                                                                                                                                                                                                                                                                                                                                       Mycobacterium gordonae type II rpoB gene fragment.
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                                                                                                                                              31;
                                                                                   Sequence 208 BP; 45 A; 69 C; 68 G; 26 T; 0 other;
                                                                                                                                 3e-22;
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                                                                                                                                                0; Mismatches
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                                                                                                                                   Pred. No.
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                                                                                                                                   79.48;
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                                                                                                                                                  Matches 177; Conservative
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                                                                                                                                   Best Local Similarity
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                                                                                                                    Query Match
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diagnosis or to obtain epidemiological and pathogenesis information for diagnosis or to obtain epidemiological and pathogenesis information for selection of appropriate therapies, including W. tuberculosis, M. leprae and non-tuberculous mycobacteria (NTM) encountered in subjects infected with human immunodeficiency virus (HIV). Analysis of the rpoB gene fragments is rapid, precise, simple and cost effective (only I PCR required), and can differentiate between many species in a single experiment, including those difficult to distinguish by usual blochemical tests. Also described are oligonuclectide probes (AASO5227-AASO5242) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HIV; PRA; RFLP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTCTGAACGTCGGCAAGCCGATCACCACGCTCACCACGAGGAAGACGTCGTAGCCA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCATCGAGTACCTGGTTCGCCTGCACCACGCCTCTCAGGGTGGCCAGGCCCCCGTTATGA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 GCCTGAACACCGATCATCCGATCACCACCACGACGTGACCGAAGAAGAGACGTCGTCGCCA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 TCAAGGAGAAGCGCTACGACCTGGCCCGGGTGGCCCCTACAAGGTCAACAAGAAGACTCG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 TCAAGGAGAAGCGCTACGACCTGGCCCGCGTCGGCCGCTACAAGAAGAAGATGG
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                                                                                                                                                                                                                                                                                                                                                                                                                    Length 208;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Park HJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  3.1e-22;
ches 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Non-tuberculous mycobacteria; rpoB gene fragment; NTM; PCR-restriction fragment length polymorphism analysis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTGTCCCCGGCGGGGTCGAGGTGCCGGTGGAAACCGACGACAT 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    166 CGGTTCCCGGCGCGCGGCGAGGTGCGGTGGAGACCGACGACAT 208
                                                                                                                                                                                                                                                                                                                                                                                                                    DB 22;
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                                                                                                                                                                                                                                                                                                                                                        Sequence 208 BP; 45 A; 62 C; 73 G; 28 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 3.16
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                    59.1%; Score 131.8; 78.9%; Pred. No. 3.1
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                                                                                                                                                                                                                                                                                         detecting specific Mycobacterial species.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mycobacterium ulcerans.
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Claim 1; Page 41; 50pp; English.

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method. The method comprises obtaining a restriction fragment length polymorphism (RFLP) pattern of the 24 rpob gene fragments; length polymorphism (RFLP) pattern of the 24 rpob gene fragments; lasolating, amplifying and digesting the DNA fragment from the microorganism to be identified and comparing the RFLP patterns from the known rpob gene fragments with the unidentified fragment. The rpob gene fragments fragments with the unidentified fragment. The rpob gene fragments fragments with the unidentified fragment. The rpob gene fragments fragments of the obtain epidemiological and pathogenesis information for selection of appropriate therapies, including M. tuberculosis, M. leprac selection of appropriate therapies, including M. tuberculosis, M. leprac with human immunodeficiency virus (HIV). Analysis of the rpob gene fragments is rapid, precise, simple and cost effective (only 1 PCR required), and can differentiate between many species in a single experiment, including those difficult to distinguish by usual biochemical tests. Also described are oligonucleoclide probes (AASO5227-AASO5242) for certain specific Mycobacterial species.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HIV; PRA; RFLP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCATCGAGTACCTGGTTCGCCTGCACCACGCCTCTCAGGGTGGCCAGGCCCCGTTATGA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 GCCTGAACACCGATCATCCGATCACCACCACGACGCTGACCGAAGAAGACGTCGTCGCCA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New DNA fragments from the rpoB gene of mycobacteria, useful for diagnosis and identification of many mycobacterial species by restriction fragment length polymorphism
                                                                                                                                                                                                                                                                                                                                                                        Score 131.8; DB 22; Length 208; Pred. No. 3.1e-22; O; Mismatches 32; Indels 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Non-tuberculous mycobacteria; rpoB gene fragment; NTM; PCR-restriction fragment length polymorphism analysis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mycobacterium gordonae type IV rpoB gene fragment.
                                                                                                                                                                                                                                                                                                                                     Sequence 208 BP; 45 A; 68 C; 67 G; 28 T; 0 other;
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Best Local Similarity 78.9%;
Matches 176; Conservative (
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The present sequence for Mycobacterium gordonae type IV rpob gene fragment is 1 of 24 rpoB gene fragments (AAS05201-AAS05224) from toward Mycobacterial species. These rpoB gene fragments can be used in the diagnosis and identification of Mycobacterium species using a novel pCR-restriction fragment length polymorphism analysis (PRA) and polymorphism (RPLP) pattern of the 24 rpoB gene fragment length polymorphism (RPLP) pattern of the 24 rpoB gene fragments; isolating, amplifying and digesting the DNA fragment from the microorganism to be identified and comparing the RPLP patterns from the known rpoB gene fragments with the unidentified fragment. The rpoB gene fragments fragments with the unidentified range of Mycobacterium species, e.g. for diagnosis or to obtain epidemiological and pathogenesis information for selection of appropriate therapies, including M. tuberculosis, M. leprae and non-tuberculous mycobacteria (NTM) encountered in subjects infected with human immunodeficiency virus (HIV). Analysis of the rpoB gene fragments is rapid, precise, simple and cost effective (Only 1 pCR required), and can differentiate between many species in a single experiment, including those difficult to distinguish by usual biochemical cests. Also described are oligonucleotide probes (AAS05227-AAS05242) for cests.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 GCCTGAACACCGATCATCGGATCACCACCACGACGACGAAGAAGAAGACGTCGTCGCCA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 126.6; DB 22; Length 207; Pred. No. 5.2e-21;
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                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 207 BP; 45 A; 66 C; 66 G; 30 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mycobacterium tuberculosis rpoB gene fragment.
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27-OCT-1999;
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                                                                                                             New DNA fragments from the rpoB gene of mycobacteria, useful adiagnosis and identification of many mycobacterial species by restriction fragment length polymorphism
                                                                                                                                                                                                                                                                                                                                                                                                                                                            present sequence for Mycobacterium tuberculosis rpoB gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 CTGTCCCCGGCGGGGTCGAGGTGCCGGTGGAAACCGACGACAT 223
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Pred. No. 2.4e-20;
0; Mismatches 37;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mycobacterium terrae rpoB gene fragment.
                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 41; 50pp; English.
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Best Local Similarity 76.7%;
Matches 171; Conservative (
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The present sequence for Mycobacterium terrae rpoB gene fragment is 1 of 24 rpoB gene fragments (AASO5201-AASO5224) from various Mycobacterial species. These rpoB gene fragments can be used in the diagnosis and identification of Mycobacterium species using a novel PCR-restriction fragment length polymorphism analysis (PRA) anoyel PCR-restriction fragment length polymorphism (RFLP) pattern of the 24 rpoB gene fragments; isolating, amplifying and digesting the DNA fragment from the microorganism to be identified and comparing the RFLP patterns from the known rpoB gene fragments with the unidentified fragment. The rpoB gene fragments are useful to identify a wide range of Mycobacterium species, e.g. for diagnosis or to obtain epidemiological and pathogenesis information for selection of appropriate theraptes, including M. tuberculosis, M. leprae and non-tuberculous mycobacteria (NTM) encountered in subjects infected with human immunodeficiency virus (HTV). Analysis of the rpoB gene fragments is rapid, precise, simple and cost effective (only 1 PCR required), and can differentiate between many species in a single experiment, including those difficult to distinguish by usual blochemical contents. Also described are oligonuclectide probes (AASO5227-AASO5242) for easts.
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0; Mismatches 37; Indels
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                                                                                                                                                                                                                                                                 Claim 1; Page 42; 50pp; English
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Best Local Similarity 76.7%;
Matches 171; Conservative
WPI; 2001-300520/31.
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us-09-697-123b-13.rni

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Sequence 57, Appl
Sequence 57, Appl
Sequence 71, Appl
Sequence 4, Appl 1
Sequence 4, Appl 1
Sequence 1070, Appl 2
Sequence 1070, Appl 3
Sequence 1, Appl 1
Sequence 1, Appl 1
Sequence 6, Appl 1
Sequence 6, Appl 1
Sequence 6, Appl 1
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Sequence 19, Appl 1
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Sequence 1, Ap
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Sequence 2, A
Sequence 4, Ap
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(c) 1993 - 2002 Compugen Ltd.
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US-09-105-537-38
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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length: 2000000000
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Resistance to Rifampin in Mycobacterial Cultures and
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                                                                                                                                              Sequence 3, A Sequence 9, A Sequence 9, A Sequence 9, A Sequence 9, A Sequence 1, A Sequence 29, A Sequence 20, A Sequence 20,
                                                                                       Sequence 9,
Sequence 9,
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Sequence 1
Sequence 1
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DAFA:

APPLICATION NUMBER: US/08/250,030

FILING DATE: 26-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    55.5%; Score 123.8; DB 1; 76.7%; Pred. No. 1.4e-22;
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0; Mismatches 37;
                         US-08-439-009A-3
US-08-620-694A-9
US-08-620-696-9
US-09-022-696-9
US-09-022-259-9
US-09-022-259-9
US-09-022-259-9
US-09-022-259-9
US-09-022-259-9
US-09-248-335-27
US-09-248-335-27
US-09-248-335-27
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US-08-363-255-13
US-08-471-112A-2
US-09-012-515A-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Schwegman, Lundberg & Woessner
STREET: 3500 IDS Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Methor, Mon M.
REGISTRATION NUMBER: 33,977
REPERENCE/DOCKET NUMBER: 150.105US1
TELEPHONE: 612-339-0331
TELEPHONE: 612-339-3061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-250-030-1
Sequence 1, Application US/08250030
Patent No. 5643723
GENERAL INFORMATION:
APPLICANT: Persing, David H.
TITLE OF INVENTION: Detection of a TITLE OF INVENTION: Clinical Specil NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schwegman, Lundberg &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 612-339-3061
INFORMATION FOR SEQ 1D NO:
SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 76.7
Matches 171; Conservative
Minneapolis
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61 GCCTGAACACCGATCATCCGATCACCACCACGACGTGACCGAAGAAGACGTCGTCGCCA 120

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TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance TITLE OF INVENTION: in Mycobacterium Tuberculosis NUMBER OF SEQUENCES: 66 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                        Finnegan, Henderson, Farabow, Garrett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25.146
REFERENCE/DOCKET NUMBER: 02356.0068-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4400
TELEPHONE: (202) 408-4400
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 3447 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/313,185
FILING DATE: 12-OCT-1994
CLASSIFICATION: 435
                                        Sequence 57, Application US/08313185 Patent No. 5851763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Finnegan, Hender
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: DNA (genomic) US-08-313-185-57
                                                                                                                                                                              Honore, Nadine
Telenti, Amalio
Bodmer, Thomas
                                                                                                                     cole, Stewart
Young, Douglas
Zhang, Ying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 73.1'
Matches 163; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
                                                                                               APPLICANT: Heym, Beate
APPLICANT: Cole, Stewar
APPLICANT: Young, Dougl
APPLICANT: Zhang, Ying
                                                                                                                                                                                                                                                                                                                                                                                      Washington
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20005-3315
                                                                                GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 4
US-09-082-614A-57
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                                                                                                                                                                                APPLICANT:
APPLICANT:
APPLICANT:
                     US-08-313-185-57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 CCATCGAGTACCTGGTTCGCCTGCACCACCCTCTCAGGGTGGCCAGGCCCCGGTTATGA 180
  86 GGCTGCATGTCGGCGAGCCCATCACGTCGTCGAGGCGTGAAGAAGAGGTCGTGGCCA 145
                                          121 CCATCGAGTACCTGGTTCGCCTGCACCACGCCTCTCAGGGTGGCCAGGCCCCCGTTATGA 180
                                                               26 TCAAGGAGAAGCGCTACGACCTGCCCCCGCTCGTCGTCGTTAAAGGTCAAGAAGAAGCTCG 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 TCAAGGAGAAGCGCTACGACCTGGCCCGCGTCGGCCGCTACAAGGTCAACAAGAAGCTGG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15;
                                                                                                                                                                                                                                                                                                 APPLICANT: Mayo Foundation for Medical Education and Research
APPLICANT: and Hoffmann-La Roche Inc.
TITLE OF INVENTION: Detection of a Genetic Locus Encoding
TITLE OF INVENTION: Resistance to Rifampin
NUMBER OF SECUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schwegman, Lundberg & Woessner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 123.8; DB 5; Length 970; Pred. No. 1.4e-22; 0; Mismatches 37; Indels 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTGTCCCCGGCGGGGTGCGGGTGCGGTGGAAACCGACGACAT 223
                                                                                                                                                191 CCGTTCCGGCCGCCGCCTCGAGGTGCCGGTGGAAACCGACGACAT 233
                                                                                                                         181 CTGTCCCCGGCGGGGTCGAGGTGCCGGTGGAAACCGACGACAT 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC Compatible
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06790
FILING DATE: 26-MAY-1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Schwegman, Lundberg & Woessner
STREET: 3500 IDS Center
CITY: Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
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                                                                                                                                                                                                                                                                 Sequence 1, Application PC/TUS9506790 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY AGENT INFORMATION:
NAME: RASCD, Kevin W.
REGISTATION NUMBER: 35,651
REFERENCE/DOCKET NUMBER: 150.1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612.339-0331
TELEFAX: 612.339-1061
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 970 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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1; 61 GCCTGAACACCGATCATCACCACCACGACGCTGACCGAAGAAGACGTCGTCGCCA 120 121 CCATCGAGTACCTGGTTCGCCTGCACCACGCCTCTCAGGGTGGCCAGGCCCCCCGTTATGA 180 9 Gaps 1 TCAAGGAGAAGCGCTACGACCTGGCCGCGCTCGGCCGCTACAAGGTCAACAAGAAGCTGG 15; Length 3447; 45; Indels 181 CTGTCCCCGGGGGGTCGAGGTGCCGGTGGAAACCGACAT 223 49.8%; Score III; DB 2; 73.1%; Pred. No. 2.5e-19; Live 0; Mismatches 45

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GENERAL INFORMATION:
         Patent No. 5574007
                                             APPLICANT:
                                                                APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 CCATCGAGTACCTGGTTCGCCTGCACGCCTCTCAGGGTGGCCAGGCCCCCGGTATGA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15;
                                                                                                 APPLICANT: Young, Douglas
APPLICANT: Zhang, Ying
APPLICANT: Telonit, Amalio
APPLICANT: Honder, Thomas
ITILE OF INVENTION: Rapid Detection of Antibiotic Resistance
NUMBER OF SEQUENCES: 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 3447;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS: ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/082,614A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match 49.8%; Score 111; DB 3; Best Local Similarity 73.1%; Pred. No. 2.5e-19; Matches 163; Conservative 0; Mismatches 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02356.0068-00000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/313,185
FILLING DATE: 12-OCT-1994
ATTOKNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
Sequence 57, Application US/09082614A
Patent No. 6124098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY AMEN: INFORMATION:
NAME: MAYERS, KENNECH J.
REGISTRATION NUMBER: 25,146
REFRENCE/DOCKET NUMBER: 02356
TELECOMMUNICATION:
TELECHONE: (202) 408-4400
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 3447 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                    STREET: 1300 I Street, N.W. CITY: Washington
                                                                  Heym, Beate
Cole, Stewart
                                                                                                                                                                                                                                                                                       Dunner
                                                                                                                                                                                                                                                                                                                                                                       20005-3315
                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                            USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-082-614A-57
                                                                                                                                                                                                                                                                                       ADDRESSEE:
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                                                                  APPLICANT:
                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                          STATE:
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; Sequence 71, Application US/08261206A

US-08-261-206A-71

RESULT 5

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/note= "Nuclectide sequence of region A in Figure
59. The sequence is presented as Figure 61."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18.5%; Score 41.2; DB 1; Length 3306;
49.1%; Pred. No. 0.062;
tive 0; Mismatches 113; Indels 0.
                                  APPLICANT: Yamamoto, Shuji
APPLICANT: Suzuki, Koji
APPLICANT: Buzuki, Koji
APPLICANT: Matsuda, Akio
TITLE OF INVENTION: A Polypeptide Capable of Interacting
TITLE OF INVENTION: with Thrombin
NUMBER OF SEQUENCES: 80
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             join(1252..1317, 1463..1883, 1948..2714)
                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/261,206A
                                                                                                                                                           ADDRESSEE: Birch, Stewart, Kolasch & Birch
STREET: 301 N. Washington St.
CITY: Falls Church
                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/740,492
FILING DATE: 03-AUG-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: CDNA
ORIGINAL SOURCE:
ORGANISM: Acremonium chrysogenum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 30330
REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-241-1300
Zushi, Mitichitaka
Gomi, Komakazu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LECUPACE: 703-241-2848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              double
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1948..2715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: doub
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LOCATION: 1..3306
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM:
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                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 22046-0747
                                                                                                                                                                                                                      STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; LOCATION:
US-08-261-206A-71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION:
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121 CCATCGAGTACCTGGTTCGCCTGCACCACGCCTCTAGGGTGGCCAGGCCCCCGTTATGA 180
                     220 TCGACGAGGGGTTCGGGTCCTTCGACATTCGTGCCCAATTCCACGCCGCCGCCACA 279
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FILING DATE: 08-JUN-1993
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PC-DOS/MS-DOS
                                                                                                                                                                                                           ; Sequence 4, Application US/08074121
; Patent No. 5767362
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATOCNEY AGENT INFORMATION:
NAME: Rac-Venter, Barbara
REGISTRATION NUMBER: 32.750
REFERENCE/DOCKET NUMBER: 059:
TELECHMONICATION INFORMATION:
TELEPHONE: (415) 854-0875
TELEFAX: (415) 854-0875
TELEFAX: 200154
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32,750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: DNA (qenomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 3231 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94025
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                           US-08-074-121-4
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                                           61 GCCTGAACACCGATCATCCGATCACCACCACGACGTGACCGAAGAGGACGTCGTCGTCT 120
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                     61 GCCTGAACACCGATCATCCGATCACCACCACGACGCTGACCGAAGAGACGTCGTCGCCA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                               CCATCGAGTACCTGGTTCGCCTGCACCACGCCTTCTCAGGGTGGCCAGGCCCCGTTATGA
                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Methods and reagents for detection of TITLE OF INVENTION: pathogens using superoxide dismutase gene TITLE OF INVENTION: Largeting NUMBER OF SUCCESS: 44 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17.4%; Score 38.8; DB 1; Length 491; 48.6%; Pred. No. 0.19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
CLASSIFICATION NUMBER: US/08/133,711
FILING DATE:
CLASSIFICATION ATE:
PHIOR APPLICATION DATE:
PHIOR APPLICATION DATE:
APPLICATION NUMBER: EP 92810780.4
FILING DATE:
ATFORMET INFORMATION:
NAME: PALLICIA S. ROCHA
REGISTRATION NUMBER: 31,054
REFERENCE/DOCKET NUMBER: 4095/95
TELECOMMUNICATION NUMBER: 32,050
TELEPHONE: (201) 235 3500
                                                                                                                                                                                             181 CTGTCCCGGGGGGGGGTCGAGGTGCCGGTGGAAACCGACGACA 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches 112;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hoffmann-La Roche Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC COmpatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                      Sequence 36, Application US/08133711
Patent No. 525463
GENERAL INFORMATION:
APPLICANT: Zolg, Werner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 340 Kingsland Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Floppy disk
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TYPE: nucleic acid
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21P: 07110-1199
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
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Matches 106; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nutley
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                                                                                                                                                                                                                                                                                      US-08-133-711-36
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                                                                                               121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CACGACGCTGACCGAAGAAGACGTCGTCGCCACCATCGAGTACCTGGTTCGCCTGCACCA 148
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                                                                                                                                                                                                                             APPLICANT: Best, Elaine
APPLICANT: Knauf, Vic C.
TITLE OF INVENTION: Methods and Compositions for Modulating
TITLE OF INVENTION: Lipid Content of Plant Tissues
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2116 CTTGGCCGGCGCGCGCCTGCATCGAGATCGGCTACCGCGGCGCCG 2165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1;
181 CTGTCCCCGGCGGGGTCGAGGTGCCGGTGGAAACCGAC 218
                        Pred. No. 0.61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Fish & Richardson
STREET: 2200 Sand Hill Road, Suite 100
CITY: Menlo Park
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16.7%; Score 37.2;
Best Local Similarity 51.2%; Pred. No. 0 6
Matches 87; Conservation
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NUMBER OF SEQUENCES: 1120
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: Palo Alto
                                                                                                                                              94304-1018
                                                                                                                                                                                             MEDIUM TYPE:
                                                                                                                               USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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Sequence 1070, Application US/09221017B

Patent No. 6444799

GENERAL INFORMATION:
APPLICANT: ROSS, Bruce C.

TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
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                                                                                                                                            Methods and Compositions for Modulating
Lipid Content of Plant Tissues
15
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                                                                                                                                                                                                                                                                                                                                                                                                                                            PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                           ADDPSSEE: Weil, Gotshal & Manges
STREET: 2882 Sand Hill Road, Suite 280
CITY: Menlo Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AFTOKNEY/AGENT INFORMATION:
NAME: Rae-Venler, Barbara
REGISTRATION NUMBER: 32,750
REFERENCE/DOCKET NUMBER: CGNF-097/WO
                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/06447
FILLING DATE: 06-JUN-1994
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                  COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                               Sequence 4, Application PC/TUS9406447 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (415) 926-6200
TELEFAX: (415) 854-3713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 3231 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                  APPLICANT Calgene, Inc.
TITLE OF INVENTION: Methor TITLE OF INVENTION: Lipid MUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                             California
: US
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SOFFWARE: PatentI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
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PCT-US94-06447-4
                                                             PCT-US94-06447-4
                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                             SIATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
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61 GCCTGAACACCGATCATCCGATCACCACGACGCTGACCGAAGAAGACGTCGTCGCCA 120
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59.9%; Pred. No. 0.71;
tive 0; Mismatches 49;
                                 SOFTHARE: Fastson for Windows
SOFTHARE: Fastson for Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/221,017B
FILING DATE: 23-DEC-1998
CLASSIFICATION:
                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP1182
FILING DATE: 31-DEC-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP1546
FILING DATE: 30-JAN 1998
FILING DATE: 09-APR-1998
PRIOR APPLICATION NUMBER: PP2911
FILING DATE: 09-APR-1998
PRIOR APPLICATION NUMBER: PCI/AU98/01023
FILING DATE: 10-DEC-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: PORYPHYROMONAS GINGIVALIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 10
US-08-718-904-79
; Sequence 79, Application US/08718904
                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: MONIOY, Gladys H
REGISTRATION NUMBER: 32,430
REFERENCE/DOCKET NUMBER: 27
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32,430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              circular
E: DNA (genomic)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; NAME/KEY: misc_feature
; LOCATION: 1...734
US-09-221-017B-1070
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|118 TCATCAAGTATCTTATT 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 734 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 650-494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO:
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Matches 82; Conservative
                         Diskette
COMPUTER READABLE FORM:
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ANTI-SENSE: UNKNOWN
ORIGINAL SOURCE:
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600 CAAGTCCTTCAAGCTCGTGCAGAACAAGTACCTCGGCGTGATCATCCAGTGCCTCGTGAC 659
No. 5929301el Nucleic Acid Sequence Enroding FLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: No. 6175058el Nucleic Acid Sequence Encoding FLP
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                                       Recombinase and Method of Using Same
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                                                                                                                                                                                                                                                                                                  Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Synthetic sequence (optimized)
                                                                                                                     Suite 310
                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/972,258
                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gordon-Kamm, William J.
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; Patent No. 6175058
                                                                                                3605 Glenwood Ave. S
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APPLICANT: Sandahl, Gary A.
APPLICANT: Tagliani, Laura A.
APPLICANT: Zhao, Zuo-Yu
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Drummond, Bruce J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 57
TELECOMMUNICATION INFORMATION
TELEPHONE: 919 420 2202
TELEPHONE: 919 881 3175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA (genomic)
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48.8%;
                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 1272 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 16.2
Best Local Similarity 48.8
Matches 98; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleic acid
EDNESS: double
                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                      COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: DNA (ORIGINAL SOURCE: ORGANITY
                                       TITLE OF INVENTION:
NUMBER OF SEQUENCES:
  TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: BASZCZY
APPLICANT: Bowen, E
APPLICANT: Grummonc
APPLICANT: Gordon-P
APPLICANT: Gordon-P
APPLICANT: Sandahl,
                                                                                                                                                                                                                                                                                                                                                          FILING DATE: CLASSIFICATION:
                                                                                                                                      Raleigh
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                                                                                                   ADDRESSEE:
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US-09-263-128-1
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                                 APPLICANT: Baird, J. Andrew
APPLICANT: Chandler, Lois Ann
APPLICANT: Sosnowski, Barbara A.
TITLE OF INVENTION: COMPOSITIONS CONTAINING NUCLEIC ACIDS AND LIGANDS FOR THERAPE
NUMBER OF SEQUENCES: 128
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/718,904
FILING DATE: 24-SEP-1996
CLASSIFICATION: 424
ATTORNEY/AGENT INNORMATION:
NAME: NO: 6037329tenburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 760100.415C1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                        5: SEED and BERRY LLP
6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                :69
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Peterson, David J.
Sandahl, Gary A.
Tagliani, Laura A.
Zhao, Zuo-Yu
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                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 5929301
GENERAL INFORMATION:
APPLICANT: Baszczynski, Chris
APPLICANT: Bowen, Benjamin A.
APPLICANT: Drummond, Bruce J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bowen, Benjamin A.
Drummond, Bruce J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 79:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 765 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
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COTHER INFORMATION:
COTHER INFORMATION:
US-08-718-904-79
                                                                                                                                                                           STREET: 6300 Colum
CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match
Best Local Similarity
Matches 78; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 98104-7092
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                                                                                                                                                            ADDRESSEE:
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT: Baszczynski, Christopher L.
APPLICANT: Lyznik, Leszek A.
APPLICANT: Cordon-Kamm, William J.
APPLICANT: Guon, Xueni
APPLICANT: Rao, Guru
APPLICANT: Ray, Guru
APPLICANT: Ray, Guru
APPLICANT: Ray, Guru
APPLICANT: Bukaryotic Genomes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1674 CAAGTCCTTCAAGCTCGTGCAGAACAAGTACCTCGGCGTGATCATCCAGTGCCTCGTGAC 1733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1734 CGAGACCAAGACCTCCGTGTCCAGGCACATCTACTTCTTCTCCGCTCGCGGGGGGATCGA 1793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80 GATCACCACCACGACGCTGACCGAAGAGGCGTCGTCGCCACCATCGAGTACCTGGTTCG 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Description of Artificial Sequence:Nucleotide COTHER INFORMATION: Sequence encoding a Cre:FLDm polypeptide, Cre COTHER INFORMATION: from Bacteriophage Pl and FLP (Maize preferred US-09-193-503B-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16.2%; Score 36.2; DB 4; Length 2346;
48.8%; Pred. No. 1;
tive 0; Mismatches 103; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: EURATOLIC GENIOMES FILE REFERENCE: 5718-66 (amended listing) CURRENT APPLICATION NUMBER: US/09/193,503B CURRENT FILING DATE: 1998-11-17 PRIOR PRIOR FILING DATE: 1998-09-08 PRIOR FILING DATE: 1998-09-08 PRIOR FILING DATE: 1997-11-18 PRIOR PLING DATE: 1997-11-18 NUMBER OF SEQ ID NOS: 11 
                                         FILE REFERENCE: 3.740 SO (Amended IISLING)
CURRENT PELLOATION NUMBER: US/09/193,503B
CURRENT FILING DATE: 1998-11.17
PRIOR PELLOR DATE: 1998-09-08
PRIOR FILING DATE: 1998-09-08
PRIOR FILING DATE: 1998-09-08
PRIOR FILING DATE: 1997-11-18
PRIOR FILING DATE: 1997-11-18
SEQ ID NOS: 11
SEQ ID NO 4
                 5718-66 (amended listing)
Eukaryotic Genomes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 5, Application US/09193503B Patent No. 6262341
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Matches 98; Conservative
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TITLE OF INVENTION:
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US-09-193-503B-5
                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 2346
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APPLICANT: Rao, Guru
APPLICANT: Tagliani, Laura A.
TITLE OF INVENTION: A NO. 6262341el Method For The Integration Of Foreign DNA Into
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                       TITLE OF INVENTION: Recombinase and Mathod of Using Same NUMBER OF SEQUENCES: 4 CURRESPONDENCE ADDRESS: ADDRESSE: W. Murray Spruill STREET: 3605 Glenwood Ave. Suite 310
                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-00S/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,128
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Patent No. 6262341
GENERAL INFORMATION:
APPLICANT: Baszczynski, Christopher
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/972,258
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Gordon-Kamm, William J.
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RECISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: 5718-
TELECOMMUNICATION INFORMATION:
TELEFAX: 919 420 2202
INFORMATION FOR SEQ 1D NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1272 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      720 CCCCTCGTGTACCTCGACGA 740
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STRANDEDNESS: double
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
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Matches 98; Conserv
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MOLECULE TYPE: D
ORIGINAL SOURCE:
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Patent No. 6175058
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US-09-193-503B-4
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Description of Artiticial Sequence: sequence encoding moCre:FLPm, Cre from Bacteriophage Pl and FLP from Saccharomyces, both maize preferred
                                                                                                                                                                                                                                20 CCTGGCCCGCGTCGGCCGCTACAAGGTCAACAAGAAGCTGGGCCTGAACACCGATCATCC 79
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                                                                                                                                                   16.2%; Score 36.2; DB 4; Length 2346; 48.8%; Pred. No. 1;
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Gordon-Kamm, William J.
Guan, Xueni
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CTHER INFORMATION: Descripti
O'THER INFORMATION: encoding
O'THER INFORMATION: FLP from
O'THER INFORMATION: CODONS
NAMMYKEY: CDS
: LOCATION: (1)..(2346)
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Matches 98; Conservative
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Best Local Similarity
Matches 98; Conserv
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US-09-193-503B-8
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APPLICANT:
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Sequence 109, App
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Sequence 132, App
Sequence 7717, App
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Sequence 7707, App
Sequence 7065, App
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3487.380 Million cell updates/sec
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                                                          November 12, 2002, 16:05:40; Search time 22.6867 Seconds
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US-09-923-876-5702

US-10-062-254-115

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US-09-815-242-7005

US-10-062-254-107
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compug
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Maximum Match 100%
Listing first 45 summaries
                                        - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Match Length DB
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Perfect score:
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Sequence 38, Appl
Sequence 7742, Ap
Sequence 37, Appl
Sequence 216, Appl
Sequence 4009, Ap
Sequence 4009, Ap
Sequence 7740, Ap
Sequence 7771, Appl
Sequence 7771, Appl
Sequence 1271, Appl
Sequence 17, Appl
Sequence 1, Appl 1
Sequence 1, Appl 1
Sequence 1, Appl 1
Sequence 7, Appl 1
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APPLICANT: MATHE, Brigitte
APPLICANT: STEPHAN, Hans
APPLICANT: STEPHAN, Hans
APPLICANT: REUTZER, Caroline
APPLICANT: REEFFERE, Walter
APPLICANT: HERMANN, Thomas
APPLICANT: HERFERIE, Walter
APPLICANT: BINDER, Michael
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE rpsL GENE
FILE REFERENCE: 204209403
CURRENT APPLICATION NUMBER: US/09/984,711
PRIOR FILING DATE: 2001-10-31
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 6
SEQ ID NOS: 6
LENGTH: 5096
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                                       US-10-108-605-216
US-09-815-242-4009
US-09-815-242-74009
US-09-815-242-7740
US-09-815-242-7971
US-09-815-242-7971
US-09-815-242-7871
US-09-864-761-15816
US-09-864-761-15816
US-09-913-814-1
US-09-913-814-1
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US-09-913-814-1
US-09-888-615-3
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Pred. No. 6.1e-08;
0; Mismatches 37;
  US-09-861-289-38
US-09-815-242-7742
US-09-815-242-3999
US-09-888-615-37
                                                                                                                                                                                                                                                                                             ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Corynebacterium glutamicum
                                                                                                                                                                                                                                                                                                                                    US-09-984-711-5; Sequence 5, Application US/09984711; Patent No. US20020119549A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28.2%;
llarity 71.0%;
Conservative
    , LUCATION: (702)..(4196); OTHER INFORMATION:
US-09-984-711-5
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Matches 98; Conserv
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1638 GGCGACCACGATGGTTTGAT - - GACTCTTACTGAAGAGGACATCGCAACCACCATCGAG 1694 69 ACCGATCATCCGATCACCACCACGACGCTGACCGAAGAAGACGTCGTCGCCACCATCGAG 128

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LENGTH: 5099
TYPE: DNA
ORGANISM: Corynebacterium glutamicum
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LENGTH: 5099
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                                                          FEATURE:
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APPLICANT: BATHE, Brightte
APPLICANT: HERMANN, Thomas
APPLICANT: HERMANN, Thomas
APPLICANT: HERMANN, Thomas
TITLE OF INVENTION: NUCLECTIDE SEEQUENCES WHICH CODE FOR THE rpoB GENE
TITLE OF INVENTION NUMBER: US/09/887,052
CURRENT APPLICATION NUMBER: US/09/887,052
CURRENT FILING DATE: 2001-06-25
PRIOR APPLICATION NUMBER: DEI0107229.5
PRIOR APPLICATION NUMBER: DEI0107229.5
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEO ID NOS: 8
SOFTWARE: Patentin version 3.0
SEO ID NO 1
                                                                                                                                                                                  APPLICANT: MATHE, BRIGITE
APPLICANT: MATHE, BRIGITE
APPLICANT: HANS, STEFAN
APPLICANT: HANS, STEFAN
APPLICANT: HANS, STEFAN
APPLICANT: HERMANN, THOMAS
APPLICANT: PEPEFFRELE, WALTER
APPLICANT: PEFFFRELE, WALTER
APPLICANT: BRIDER, MICHAEL
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE FPSL GENE
FILE REFERENCE: 2184720SX
CURRENT APPLICATION NUMBER: DS 10107230.9
PRIOR FILING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: DE 10162386.0
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-12-19
NUMBER OF SEQ ID NOS: 14
SOFTWANE: PALCALIN VERSION 3.1
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Pred. No. 6.1e-08;
0; Mismatches 37;
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Patent No. US20020119537A1
GENERAL INFORMATION:
                                                                                                                                  Sequence 5, Application US/10075460
; Patcnt No. US20020155557A1
; GENERAL INFORMATION:
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Best Local Similarity 71.09
Matches 98; Conservative
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LOCATION: (702)..(4196)
OTHER INFORMATION:
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LENGTH: 5099
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Sequence 3, Application US/09887052;
Patent No. US20020119337A1
GENERAL INFORMATION:
APPLICANT: MOCKELL Bettina
APPLICANT: HERMANN, Thomas
APPLICANT: HERMANN, Thomas
APPLICANT: HERMANN, Thomas
TITLE OF INVENTION: NUCLEOTIDE SEEQUENCES WHICH CODE FOR THE rPOB GENE
FILE REFERENCE: 204212USOX
CURRENT FILING DATE: 2001-06-25
CURRENT FILING DATE: 2001-06-25
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEO ID NOS: 8
SOFTWARE: PATENTIN VERSION 3.0
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                                                                                                                                Indels
                                                                                    Score 62.8; UB 10;
Pred. No. 6.1e-08;
0; Mismatches 37;
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; Patent No. US20020119537A1
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71.0%;
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Matches 98; Conservative
                                                                                       Query Match
Best Local Similarity 71.03
Matches 98; Conservative
; NAME/KEY: CDS
; LOCATION: (702)..(4196)
US-09-887-052-1
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; LOCATION: (702)...(4196)
US-09-887-052-3
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LOCATION: (640)
NAME/KEY: unsure
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LOCATION: (696)
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395 TCGA 398
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LENGTH: 704
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APPLICANT:
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APPLICANT:
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APPLICANT:
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APPLICANT: Morgante, Michele
APPLICANT: Nou, Xiping
APPLICANT: Odell, Joan
APPLICANT: Rafalski, Antoni
APPLICANT: Sakal, Hajime
APPLICANT: Zheng, Peizhong
APPLICANT: Zheng, Peizhong
APPLICANT: Zhu, Qun
TITLE OF INVENTION: Polynucleotides Encoding Proteins Involved In Plant Metabolism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
GENEKAL INFORMATION:
APPLICANT: MOSCKEL, Bettina
APPLICANT: BATHE, BrigitLe
APPLICANT: BATHE, BrigitLe
APPLICANT: BTEFFERLE, Walter
APPLICANT: HIGHER MICHARA
TITLE OF INVENTION: NUCLECTIDE SEEGUENCES WHICH CODE FOR THE FPOB GENE
FILE REFERENCE: 2042120SOX
CURRENT FILING NUMBER: DE10107229.5
PRIOR PLICATION NUMBER: DE10107229.5
PRIOR PLICATION NUMBER: 2001-06-16
NUMBER OF SEQ ID NOS: 8
SUFTWARE: PALCHIN VETSION 3.0
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CURRENT FILING DATE: 2002-02-01
PRIOR APPLICATION NUMBER: 09/630,346
PRIOR FILING DATE: 2000-07-28
PRIOR FILING DATE: 1999-07-30
PRIOR FILING DATE: 1999-07-30
PRIOR FILING DATE: 1999-09-20
PRIOR FILING DATE: 1999-09-20
PRIOR FILING DATE: 1999-09-30
PRIOR PLING DATE: 1999-09-30
PRIOR APPLICATION NUMBER: 60/156899
PRIOR FILING DATE: 1999-09-30
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Patent No. US/20020138882A1
GENERAL INFORMATION:
APPLICANT: Cahoon, Edgar B
APPLICANT: Cahoon, Rebecca E
APPLICANT: Falco Saverio Carl
APPLICANT: Fang, Yiwen
APPLICANT: Hantke, Sabine S.
APPLICANT: Lee, Jian-Ming
APPLICANT: Lee, Jian-Ming
                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Corynebacterium glutamicum
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US-09-887-052-5
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LENGTH: 5099
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APPLICANT:
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APPLICANT: Zhu, Qun
TITLE OF INVENTION: Polynucleotides Encoding Proteins Involved In Plant Metabolism
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/062,254
CURRENT FILING DATE: 2002-02-01
PRIOR APPLICATION NUMBER: 09/630,346
PRIOR FILING DATE: 2000-07-28
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PRIOR FILING DATE: 1999-10-01
PRIOR APPLICATION NUMBER: 60/169767
PRIOR FILING DATE: 1999-12-09
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-17
PRIOR FILING DATE: 1999-12-21
PRIOR APPLICATION NUMBER: 60/171515
PRIOR APPLICATION NUMBER: 60/171515
PRIOR APPLICATION NUMBER: 60/171515
PRIOR FILING DATE: 1999-12-22
PRIOR FILING DATE: 1999-12-29
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Falco, Saverio Carl
Fang, Viwen
Hantke, Sabine S.
Lee, Jian-Ming
Li, Zhongsen
Miao, Guo-Hua
Morgante, Michele
Niu, Xiping
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SOFTWARE: Microsoft Office 97
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Sakai, Hajime
Zheng, Peizhong
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Best Local Similarity 58.3.
The T3: Conservative
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                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Zea mays
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61 GCCTGAACACCGATCATCCGATCACCACCACGACGAAGAAGAAGACGTCGTCGCCA 120
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                                                4 AGGAGAAGCGCTACGACCTGGCCCGCGTCGGCCCTACAAGCTCAACAAGAGCTGGGCC 63
  0; Caps
                                                                                                                                                 Length 471;
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APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Yamamoto, Robert T.
CURRENT PILICANTION: PROMARYOUS
FILE REFERENCE: ELITRA.011A
CURRENT PLILOG DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/206, 848
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,931
PRIOR APPLICATION NUMBER: 60/253,931
PRIOR PLICATION NUMBER: 60/269,308
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR PLILOR DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR PLILOR DATE: 2000-11-27
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0; Mismatches 45; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                             Sequence 7717, Application US/09815242 Patent No. US20020061569A1 GENERAL INFORMATION:
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Zyskind, Judith W.
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        68; Conservative
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US-09-815-242-7717
          Matches
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CURRENT FILING DATE: 1999-04-16
PRIOR FILING DATE: APPLI 1999
PRIOR FILING DATE: APPLI 1998
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Pred. No. 0.0095;
0; Mismatches 51; Indels 0
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OTHER INFORMATION: Incyte ID No. US20010051335A1 700344235H1
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; Patent No. US20010051335A1
; GENERAL INFORMATION:
     PRIOR APPLICATION NUMBER: 60/146511
PRIOR FILING DATE: 1999-07-30
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: 60/15606
PRIOR APPLICATION NUMBER: 60/15699
PRIOR FILING DATE: 1999-09-30
PRIOR FILING DATE: 1999-09-30
PRIOR FILING DATE: 1999-10-01
PRIOR FILING DATE: 1999-12-09
PRIOR FILING DATE: 1999-12-09
PRIOR FILING DATE: 1999-12-09
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-21
PRIOR FILING DATE: 1999-12-29
PRIOR FILING DATE: 1999-12-29
PRIOR FILING DATE: 1999-12-29
NUMBER OF SEQ ID NOS: 375
SOFTWARE: MICROSOFT Office 97
LENGTH: 752
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Best Local Similarity 58.9%;
Matches 73; Conservative
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SOFTWARE: PERL P.
SEQ ID NO 1392
LENGTH: 278
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ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Zea mays
US-10-062-254-111
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LOCATION: 158
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61 GCCTGAACACCGATCATCCGATCACCACCACGACGACGAAGAAGACGTCGTCGCCA 120
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APPLICANT: Zyskind, Judith W.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Yu.H. Howard
TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes
FILE REPERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
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55.9%; Pred. No. 0.18;
11ve 0; Mismatches 56;
PRIOR FILING DATE: 1999-09-30
PRIOR APPLICATION NUMBER: 60/157287
PRIOR FILING DATE: 1999-10-01
PRIOR APPLICATION NUMBER: 60/169767
PRIOR PRIOR DATE: 1999-12-09
PRIOR PRILING DATE: 1999-12-09
PRIOR PRILING DATE: 1999-12-16
PRIOR PRILING DATE: 1999-12-21
PRIOR PRILING DATE: 1999-12-21
PRIOR PRILING DATE: 1999-12-22
PRIOR FILING DATE: 1999-12-22
PRIOR PRILING DATE: 1999-12-29
PRIOR FILING DATE: 1999-12-29
PRIOR FILING DATE: 1999-12-29
PRIOR FILING DATE: 1999-12-29
NUMBER OF SEQ ID NOS: 375
SOFTWARE: MICROSOFT OFFICE 97
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Patent No. US20020061569A1
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APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Ohlsen, Kari L.
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Best Local Similarity 55.9°
Matches 71; Conservative
                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: (602)..(603)
NAME/KEY: unsure
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(619)
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NAME/KEY: unsure
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NAME/KEY: U
LOCATION:
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TITLE OF INVENTION: Polynucleotides Encoding Proteins Involved In Plant Metabolism
                                                                                                                                                                   APPLICANT: Sherman, Bradley K.

APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: POLYNOLEDTIDES DERIVED FROM CORN SEEDLING
FILE REFERENCE: PL-0012-1 CON
CURRENT APPLICATION NUMBER: US/09/923,876
CURRENT FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: 09/298,329
PRIOR PILING DATE: 1999-04-21
PRIOR APPLICATION NUMBER: 60/085,331
PRIOR FILING DATE: 1999-05
NUMBER OF SEQ ID NOS: 6332
SOFTWARE: PERL PROGram
SEQ ID NOS: 6332
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; OTHER INFORMATION: Incyte ID No. US20020013958A1 700457525H1
US-09-921-876-5702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 17.0%; Score 38; DB 10; Length 175; Best Local Similarity 59.1%; Pred. No. 0.11; Matches 65; Conservative 0; Mismatches 45; Indels
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CURRENT APPLICATION NUMBER: US/10/062,254
CURRENT FILING DATE: 2002-02-01
PRIOR PPLICATION NUMBER: 09/630,346
PRIOR PLILNG DATE: 2000-07-28
PRIOR PPLICATION NUMBER: 60/146511
PRIOR PLICATION NUMBER: 60/146511
PRIOR PLICATION NUMBER: 60/156006
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: 60/15699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 115, Application US/10062254
Patent No. US20020138882A1
GENERAL INFORMATION:
APPLICANT: Cahoon, Edgar B
APPLICANT: Cahoon, Rebecca E
APPLICANT: Falco, Saverio Carl
APPLICANT: Falco, Saverio Carl
APPLICANT: Hantke, Sabine S.
APPLICANT: Lee, Jian-Ming
APPLICANT: Li, Zhongsen
                                                                                    Sequence 5702, Application US/09923876
Patent No. US20020013958A1
                                                                                                                               GENERAL INFORMATION:
APPLICANT: Lalgudi, Raghunath V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Miao, Guo-Hua
Morgante, Michele
Niu, Xiping
Odell, Joan
Rafalski, Antoni
Sakai, Hajime
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OKGANISM: Zea mays
                                                           US-09-521-876-5702
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APPLICANT: Zheng, Peizhong
APPLICANT: Zhu, Qun
TITLE OF INVENTION: Polynucleotides Encoding Proteins Involved in Plant Metabolism
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             107 AGACGTCGTCGCCACCATCGAGTACCTGGTTCGCCTGCACCACGCCTCTCAGGGTGGCCA 166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    167 GGCCCCCGTTATGACTGTCCCCGGCGGGGTCGAGGTGCCGGTGGGAAACCGACGA 220
                                                                                                                                                                                                                                                   Length 1806;
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                                                                                                                                                                                                                                              Score 36.4; DB 10;
Pred. No. 0.39;
0; Mismatches 86;
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CURRENT APPLICATION NUMBER: US/10/062,254

CURRENT APPLICATION NUMBER: US/10/062,254

CURRENT APPLICATION NUMBER: 09/630,346

PRIOR PLING DATE: 2000-07-28

PRIOR FILING DATE: 1999-07-30

PRIOR FILING DATE: 1999-07-30

PRIOR FILING DATE: 1999-09-30

PRIOR FILING DATE: 1999-09-30

PRIOR FILING DATE: 1999-09-30

PRIOR FILING DATE: 1999-09-30

PRIOR FILING DATE: 1999-12-09

PRIOR FILING DATE: 1999-12-09

PRIOR FILING DATE: 1999-12-09

PRIOR FILING DATE: 1999-12-16

PRIOR FILING DATE: 1999-12-16

PRIOR FILING DATE: 1999-12-16

PRIOR FILING DATE: 1999-12-16

PRIOR APPLICATION NUMBER: 60/172958

PRIOR FILING DATE: 1999-12-16

PRIOR APPLICATION NUMBER: 60/171954

PRIOR FILING DATE: 1999-12-16

PRIOR APPLICATION NUMBER: 60/171958

PRIOR FILING DATE: 1999-12-16

PRIOR FILING DATE: 1999-12-16
                                    NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4015
LENGTH: 1806
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PRIOR FILING DATE: 1999-12-29
NUMBER OF SEQ ID NOS: 375
SOFTWARE: Microsoft Office 97
SEQ ID NO 123
                                                                                                                                          TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
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Falco, Saverio Carl
Fang, Yiwen
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Morgante, Michele
Niu, Xiping
Odell, Joan
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16.3%;
Best Local Similarity 50.6%;
Matches 88; Conservative
           PRIOR FILING DATE: 2001-02-16
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Lee, Jian-Ming
Li, Zhongsen
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Sakai, Hajime
Zheng, Peizhong
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                                                                                                                                                                                            US-09-815-242-4015
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29 CCTCGGCCGCTACAAGGTCAACAAGAAGCTGGGCCTGAACACCGATCATCCGATCACCAC 88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   149 CCCCTCTCAGGGTGGCCCAGGCCCCGTTATGACTGTCCCCGGCGGGGTCG 198
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APPLICANT: Yangmoto, Robert T.
APPLICANT: Yangmoto, Robert T.
TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT FALLING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PLILNG DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       83; Indels
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51.2%; Pred. No. 0.23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                            PRIOR PELICATION NUMBER: 60/206, 848
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR PELICATION NUMBER: 60/207, 727
PRIOR PELING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR PELING DATE: 2000-11-27
PRIOR PELING DATE: 2000-11-27
PRIOR PELING DATE: 2000-11-27
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2000-16-22
PRIOR PILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SEQ ID NO 7965
LENGTH: 1350
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APPLICATION NUMBER: 60/191,078
FILING DATE: 2000-03-21
APPLICATION NUMBER: 60/206,848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 2000-12-22
APPLICATION NUMBER: 60/269,308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
OKGANISM: Pseudomonas aeruginosa
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APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
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Matches 87; Conservative
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; LOCATION: (1)...(1350)
US-09-815-242-7965
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296 TCGTCTACCACCTCAACATCTCGCCCAAGAAGATGGGCGTGGACGAGGAGGATCTTCGTCG 355
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16.1%; Score 36; DB 10; Length 918;
Best Local Similarity 47.7%; Pred. No. 0.45;
Matches 105; Conservative 0; Mismatches 115; Indels
                                                                                                                                                                                                                      DB 12; Length 642;
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APPLICANT: Oblean, Kari L.
APPLICANT: Oblean, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Tyskind, Judith W.
APPLICANT: Truck, John D.
APPLICANT: Tammorco, Robert T.
APPLICANT: Yammorco, Robert T.
APPLICANT: Yammorco, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
TITLE OF INVENTION: Prokaryotes
TITLE OF INVENTION: Prokaryotes
TITLE OF INVENTION: DATE: 2001-03-21
CURRENT FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/253,930
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ. ID NOS: 14110
SSOFTWARE: FRASEEC FOR WINDOWS VERSION 4.0
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                                                                                                                                                                                                                 16.1%; Score 36; DB : 55.6%; Pred. No. 0.43.
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Patent No. US2002006156941
APPLICANT: Haselbeck, Robert
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ORGANISM: Pseudomonas aeruginosa
                  TYPE: DNA
ORGANISM: Triticum aestivum
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Host Local Similarity 55.69
Matches 69; Conservative
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US-09-815-242-7705
                                                                                NAME/KEY: unsure
: LOCATION: (34)
: NAME/KEY: unsure
: LOCATION: (624)
US-10-062-254-123
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2 CAAGGAGAAGCGCTACGACCTGGCCCGCGTCGGCCGCTACAAGAGGTCAACAAGAAGCTGGG
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Page

Mycobacterium xeno Mycobacterium gord Mycobacterium gord Mycobacterium gast Mycobacterium gast Mycobacterium absc Mycobacterium absc Mycobacterium absc Mycobacterium absc Mycobacterium absc

Mycobacterium tube Mycobacterium tube Mycobacterium tube Mycobacterium tube M. tuberculosis rp Mycobacterium afri

Mycobacterium flav Mycobacterium chel Mycobacterium acro G glutamicum codin C glutamicum codin Propionibacterium

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Non-tuberculous mycobacteria; rpoB gene fragment; NTM; PCR-restriction fragment length polymorphism analysis;
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ABL09357
ABL09356
AAZ43922
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AAT78176
ABQ90502
ABQ90984
AAT66542
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AAN91083
AAQ12000
AAF61045
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 (first entry)
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WO200131061-A1.
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1. SIDS2/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*

2. SIDS2/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*

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11. SIDS2/gcgdata/geneseqn-embl/NA1992.DAT:*

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17. SIDS2/gcgdata/geneseqn-embl/NA1993.DAT:*

18. SIDS2/gcgdata/geneseqn-embl/NA1993.DAT:*

19. SIDS2/gcgdata/geneseqn-embl/NA1999.DAT:*

20. SIDS2/gcgdata/geneseqn-embl/NA1999.DAT:*

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22. SIDS2/gcgdata/geneseqn-embl/NA1999.DAT:*

23. SIDS2/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:*

24. SIDS2/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:*

25. SIDS2/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:*

26. SIDS2/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:*

27. SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*

28. SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*

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28. SIDS2/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*
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                                                                      November 12, 2002, 15:44:35; Search time 136.222 Seconds
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208
1 tcaaggagaaaccgacgacat 208
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          GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd
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Match Length
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M. capsulatus gene M. capsulatus gene 50K-cellulase gene Malze glutathione-DNA sequence encod Malze nitrite redu P. putida KT2440-a

HIV; PRA; RFLP;

New DNA fragments from the rpoB gene of mycobacteria, useful for diagnosis and identification of many mycobacterial species by restriction fragment length polymorphism -

Ξ,

Kim Y,

ŝ cho

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Lee H, Park YK, Bai WPI; 2001-300520/31.

Score

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174.4 171.2 169.6 169.6 168 168 168 166.4

S. tendae nikkomyc Streptomyces tende Recombinant squirr Drosophila melanog Drosophila melanog

us-09-697-123b-8.rng

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The present sequence for Mycobacterium celatum rpoB gene fragment is 1 of 24 rpoB gene fragments (AASO5201-AASO5224) from fragment is 1 of 24 rpoB gene fragments (CASO5201-AASO5224) from various Mycobacterial species. These rpoB gene fragments can be used in the diagnosis and identification of Mycobacterium species using a novel PCR-restriction fragment length polymorphism analysis (PRA) method. The method comprises obtaining a restriction fragment length polymorphism (RFLP) pattern of the 24 rpoB gene fragment length polymorphism (RFLP) pattern of the 24 rpoB gene fragment length polymorphism (RFLP) pattern of the 24 rpoB gene fragments amplifying and digesting the DNA fragment from the microorganism to be identified and comparing the RFLP patterns from the known rpoB gene fragments with the unidentified fragment. The rpoB gene fragments are seful to identify a wide range of Mycobacterium species, e.g. for selection of appropriate therapies, including M. tuberculosis, M. leprace and non-tuberculous mycobacteria (NTW) encountered in subjects infected with human immunodeficiency virus (HIV). Analysis of the rpoB gene fragments is rapid, precise, simple and cost effective (only 1 pCR required), and can differentiate between many species in a single captering those difficult to distinguish by usual biochemical ests. Also described are oligonucleotide probes (AASO5227-AASO5242) for detecting specific Mycobacterial species.
                                                     New DNA fragments from the rpoB gene of mycobacteria, useful for diagnosis and identification of many mycobacterial species by restriction fragment length polymorphism -
                                                                                                                             Claim 1; Page 45; 50pp; English.
                   WPI; 2001-300520/31.
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                                             fragment is 1 of 24 rpoB gene fragments (AAS05201-AAS05224) from
fragment is 1 of 24 rpoB gene fragments can be used
various Mycobacterial species. These rpoB gene fragments can be used
to the diagnosis and identification of Mycobacterium species using a
novel PCR-restriction fragment length polymorphism analysis (PRA)
method comprises obtaining a restriction fragment length
polymorphism (RFLP) pattern of the 24 rpoB gene fragment length
camplifying and digesting the DNA fragment from the microorganism to
be identified and comparing the RFLP patterns from the Known rpoB gene
fragments with the unidentified fragment. The rpoB gene fragments
are useful to identify a wide range of Mycobacterium species, e.g. for
diagnosis or to obtain epidemiological and pathogenesis information for
selection of appropriate therapies, including M. tuberculosis, M. leprae
and non-tuberculous mycobacteria (MTM) encountered in subjects infected
with human immunodeficiency virus (HTV). Analysis of the rpoB gene
fragments is rapid, precise, simple and cost effective (only 1 PCR
required), and can differentiate between many species in a single
experiment, including those difficult to distinguish by usual biochemical
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 208; DB 22;
100.0%; Pred. No. 6.6e-41;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 208 BP; 51 A; 65 C; 65 G; 27 T; 0 other;
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                 Claim 1; Page 42; 50pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 208;
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Non-tuberculous mycobacteria; rpoB gene fragment; NTM; HIV; PRA; RFLP; PCR-restriction fragment length polymorphism analysis; ds.
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                                                                                                                                                                                                                                                                                         61 GCCTGAACACCGCGTCCCCGATCACGACGACCACTCTGACCGAAGAGGACGTCGTCGCCA 120
                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                               1 TCAAGGAGAAGCGCTACGACCTGGCCCGTGTCGGCCGATACAAGGTCAACAAGAAGCTGG 60
                                                                                                                                                                        ;
                                              83.8%; Score 174.4; DB 22; Length 208;
89.9%; Pred. No. 7.2e-33;
11ve 0; Mismatches 21; Indels 0;
Sequence 208 BP; 48 A; 71 C; 64 G; 25 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mycobacterium avium rpoB gene fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 TCGAGGTGCCGGTGGAAACCGACGACAT 208
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                                                                       Best Local Similarity os.s.
Matches 187; Conservative
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                                                   Query Match
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fragment is 1 of 24 rpoB gene fragments (AAS05201-AAS05224) from
fragment is 1 of 24 rpoB gene fragments (AAS05201-AAS05224) from
various Mycobacterial species. These rpoB gene fragments can be used
to the diagnosis and identification of Mycobacterium species using a
novel PCR-restriction fragment length polymorphism manlysis (PRA)
method. The method comprises obtaining a restriction fragment length
method. The method comprises obtaining a restriction fragment length
caplifying and digesting the DNA fragment from the microorganism to
be identified and comparing the RFLP patterns from the Known rpoB gene
fragments with the unidentified fragment. The rpoB gene fragments
are useful to identify a wide range of Mycobacterium species, e.g. for
diagnosis or to obtain epidemiological and pathogenesis information for
selection of appropriate theraphes, including W. tuberculosis, M. leprae
and non-tuberculous mycobacteria (MTM) encountered in subjects infected
with human immunodeficiency virus (HTV). Analysis of the rpoB gene
fragments is rapid, precise, simple and cost effective (only 1 PCR
cequired), and can differentiate between many species in a single
experiment, including those difficult to distinguish by usual blochemical
distinctions and described are oligonucleotide probes (AAS05227-AAS05242) for
                                                                                                                                                                                                                                                                                                                   New DNA fragments from the rpoB gene of mycobacteria, useful for diagnosis and identification of many mycobacterial species by restriction fragment length polymorphism
                                                                                                                                                                                                                                   Park HJ;
                                                                                                                                                                                                                                   Cho S, Kim Y,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      detecting specific Mycobacterial species.
                                                                                                                                                                                                                                   Kim S,
Wed Nov 13 13:45:57 2002
                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 44; 50pp; English
                                                                                                                                                                                         (ERUM-) ERUME BIOTECH CO LTD.
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Best Local Similarity 88.9%;
Matches 185; Conservative (
                                                                                                                                               99KR-0046795
                                                                                                                                                                                                                                   Bai G,
                                                                                                                                                                                                                                                                         WPI; 2001-300520/31.
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                                                                                                                                               27-0CT-1999;
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ds.
                                                                                                                         GCCTGAACACCAATCATCGATCACCACGACGACGCTGACCGAAGAAGACGTCGTCGCCA 120
                                                                                                                                                                             Gaps
                                                                    1 TCAAGGAGAAGGCTACGACCTGGCCCGGTGGGCCCCTACAAGGTCAACAAGAAGCTCG 60
                                                      1 TCAAGGAGAAGCGCTACGACCTGGCCCGTGTCGGCCGATACAAGGTCAACAAGAAGCTGG 60
                             .;
0
Score 171.2; DB 22; Length 208; Pred. No. 4.2e-32; 0; Mismatches 23; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                      Non-tuberculous mycobacteria; rpoB gene fragment; NTM; PCR-restriction fragment length polymorphism analysis;
                                                                                                                                                                                                                                                                                                                                                                                             Mycobacterium gordonae type III rpoB gene fragment.
                                                                                                                                                                                                                                 TCGAGGTGCCGGTGGAAACCGACGT 208
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Mycobacterium gordonae type III.

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The present sequence for Mycobacterium gordonae type III rpoB gene fragment is 1 of 24 rpoB gene fragments (AAS05201-AAS05224) from various Mycobacterial species. These rpoB gene fragments can be used to the diagnosis and identification of Mycobacterium species using a novel PCR-restriction fragment length polymorphism analysis (PRA) method. The method comprises obtaining a restriction fragment length polymorphism (RFLP) pattern of the 24 rpoB gene fragment length, amplifying and digesting the DNA fragment from the microorganism to be identified and comparing the RFLP patterns from the known rpoB gene fragments with the unidentified fragment. The rpoB gene fragments fragments are useful to identify a wide range of Mycobacterium species, e.g. for diagnosis or to obtain epidemiological and pathogenesis information for selection of appropriate therapies, including M. tuberculosis, M. leprace and non-tuberculous mycobacteria (NTM) encountered in subjects infected with human immunodeficiency virus (HIV). Analysis of the rpoB gene fragments is rapid, precise, simple and cost effective (only 1 PCR required), and Can differentiate between many species in a single experiment, including those difficult to distinguish by usual blochemical tests. Also described are oligonucleotide probes (AAS05227-AAS05242) for detecting specific Mycobacterial species.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 GCCTGCACGTCGGCGATCCGATCACCAGCTCCACGCTGACCGAAGAAGAAGACGTCGTCGCCA 120
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                                                                                                                                                                                                                                                                            New DNA fragments from the rpoB gene of mycobacteria, useful diagnosis and identification of many mycobacterial species by restriction fragment length polymorphism
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                                                                                                                                                                                                           Park
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 208 BP; 46 A; 69 C; 63 G; 30 T; 0 other;
                                                                                                                                                                                                           Kim Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 41; 50pp; English
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                                                                                                                                                                 (ERUM-) ERUME BIOTECH CO LTD
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                                                                                        27-OCT-2000; 2000WO-KR01223
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Matches 184; Conservative
                                                                                                                                                                                                                                            WPI; 2001-300520/31.
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               WO200131061-A1.
                                                                                                                            27-OCT-1999;
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                                                     03-MAY-2001.
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AAS05201 standard; DNA; 208 BP.

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inc present suguence ou mycobacterium indivining Typob gene

rangement is 1 of 24 rpob gene fragments (AASO5224) from

various Mycobacterial species. These rpob gene fragments can be used
in the diagnosis and identification of Mycobacterium species using a
convel PCR-restriction fragment length polymorphism analysis (PRA)
method. The method comprises obtaining a restriction fragment length
polymorphism (RELP) pattern of the 24 rpob gene fragment is isolating,
amplifying and digesting the DNA fragment from the microorganism to
comparing the DNA fragment. The microorganism to
be identified and comparing the RELP patterns from the known rpob gene
fragments with the unidentified fragment. The rpob gene fragments
care useful to identify a wide range of Mycobacterium species, e.g. for
diagnosis or to obtain epidemiological and pathogenesis information for
selection of appropriate therapies, including M. tuberculosis, M. leprae
and non-tuberculous mycobacteria (MTW). Analysis of the rpob gene
fragments is rapid, precise, simple and cost effective (only 1 PCR
required), and can differentiate between many species in a single
captiment, including those difficult to distinguish by usual biochemical
cests. Also described are oligonucleotide probes (AASO5227-AASO5242) for
detecting specific Mycobacterial species.
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                                      Non-tuberculous mycobacteria; rpoB gene fragment; NTM; HIV; PRA; RFLP; PCR-restriction fragment length polymorphism analysis; ds.
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Pred. No. 1e-31;
0; Mismatches 24; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                             New DNA fragments from the rpoB gene of mycobacteria, useful diagnosis and identification of many mycobacterial species by restriction fragment length polymorphism
                                                                                                                                                                                                                                                                                                                                                  Park HJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     present sequence for Mycobacterium marinum rpoB gene
                                                                                                                                                                                                                                                                                                                                                Cho S, Kim Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 208 BP; 45 A; 69 C; 68 G; 26 T; 0 other;
Mycobacterium marinum rpoB gene fragment.
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88.5%;
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Best Local Similarity 88.55
Matches 184; Conservative
                                                                                                  Aycobacterium marinum
                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-300520/31.
                                                                                                                                         WO200131061-A1.
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The present sequence for Mycobacterium gordonae type I rpoB gene fragment is 1 of 24 rpoB gene fragments can be used various Mycobacterial species. These rpoB gene fragments can be used in the diagnosis and identification of Mycobacterium species using a novel PCR-restriction fragment length polymorphism analysis (PRA) method. The method comprises obtaining a restriction fragment length polymorphism (RFLP) pattern of the 24 rpoB gene fragment length polymorphism (RFLP) pattern of the 24 rpoB gene fragment is isolating, amplifying and digesting the DNA fragment from the microorganism to be identified and comparing the RFLP patterns from the known rpoB gene fragments with the unidentified fragment. The rpoB gene fragments are useful to identify a wide range of Mycobacterium species, e.g. for diagnosis or to obtain epidemiological and pathogenesis information for selection of appropriate therapies, including M. tuberculosis, M. leprae and non-tuberculous mycobacteria (NTM) encountered in subjects infected with human immunodeficiency virus (HIV). Analysis of the rpoB gene fragments is rapid, precise, simple and cost effective (only 1 PCR required), and can differentiate between many species in a single experiment, including those difficult to distinguish by usual blochemical tests. Also described are oligonuclectide probes (AASOS227-AASOS242) for detecting specific Mycobacterial species.
                                                                                                                                                  HIV; PRA; RFLP;
ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New DNA fragments from the rpoB gene of mycobacteria, useful diagnosis and identification of many mycobacterial species by restriction fragment length polymorphism
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Pred. No. 2.5e-31;
0; Mismatches 25; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                          Park
                                                                                                                                                  mycobacteria; rpoB gene fragment; NTM; fragment length polymorphism analysis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 208 BP; 46 A; 71 C; 65 G; 26 T; 0 other;
                                                                                                             Mycobacterium gordonae type I rpoB gene fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Kim Y,
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Cho
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Kim
                                                                                                                                                  Non-tuberculous mycobacteria;
PCR-restriction fragment lengt
                                                                                                                                                                                                          Mycobacterium gordonae type I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80.8%;
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                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-300520/31.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Park YK,
                                                                                                                                                                                                                                              WO200131061-A1.
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181 TCGAGGTGCCGGTGGAAACCGACGACAT 208

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RESULT 6 AAS05201

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The present sequence for Mycobacterium tuberculosis rpoB gene fragment is 1 of 24 rpoB gene fragments (AASO5201-AASO5214) from various Mycobacterial species. These rpoB gene fragments can be used in the diagnosis and identification of Mycobacterium species using a novel PCR-restriction fragment length polymorphism analysis (PRA) a novel PCR-restriction fragment length polymorphism (RFLP) pattern of the 24 rpoB gene fragment; isolating, amplifying and digesting the DNA fragment from the microorganism to be identified and comparing the RFLP patterns from the microorganism to be identified and comparing the RFLP patterns from the known rpoB gene fragments with the unidentified fragment. The rpoB gene fragments is rapid to identify a wide range of Mycobacterium species, e.g. for diagnosis or to obtain epidemiological and pathogenesis information for selection of appropriate therapies, including M. tuberculosis, M. leprace and non-tuberculous mycobacteria (NTM) encountered in subjects infected with human immunodeficiency virus (HIV). Analysis of the rpoB gene fragments is rapid, precise, simple and cost effective (only 1 PCR required), and can differentiate between many species in a single experiment, including those difficult to distinguish by usual biochemical tests. Also described are oligonucleotide probes (AASO5227-AASO5242) for detecting specific Mycobacterial species.
                                                       1 TCAAGGAGAAGCGCTACGACCTGGCCCGTGTCGGCCGATACAAGGTCAACAAGAAGCTGG 60
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diagnosis and identification of many mycobacterial species by
restriction fragment length polymorphism
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87.5%; Pred. No. 5.9e-31;
Live 0; Mismatches 26;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mycobacterium tuberculosis rpoB gene fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cho S,
                                                                                                                               TCGAGGTGCCGGTGGAAACCGACGACAT 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 41; 50pp; English.
                                                                                                                                                              Kim S,
                                                                                                                                                                                                                                                                                                                    BP.
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                                                                                                                                                                                                                                                                                                                 AAS05205 standard; DNA; 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mycobacterium tuberculosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Non-tuberculous
PCR-restriction
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fragment is 1 of 24 rpoB gene fragments (AAS05201-AAS05224) from
various Mycobacterial species. These rpoB gene fragments can be used
in the diagnosis and identification of Mycobacterium species using a
novel PCR-restriction fragment length polymorphism analysis (PRA)
method The method comprises obtaining a restriction fragment length
polymorphism (RFLP) pattern of the 24 rpoB gene fragments; isolating,
amplifying and digesting the DNA fragment from the microorganism to
be identified and comparing the RFLP patterns from the Known rpoB gene
fragments with the unidentified fragment. The rpoB gene fragments
are useful to identify a wide range of Mycobacterium species, e.g. for
diagnosis or to obtain epidemiological and pathogenesis information for
selection of appropriate theraphes, including M. tuberculosis, M. laprae
and non-tuberculous mycobacteria (MTW) analysis of the rpoB gene
fragments is rapid, precise, simple and cost effective (only 1 PCR
required), and can differentiate between many species in a single
experiment, including those difficult to distinguish by usual blochemical
tests. Also described are oligonucleotide probes (AAS05227-AAS05242) for
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                                                                                                                                                                                                                                                                                                                                                                      Non-tuberculous mycobacteria; rpoB gene fragment; NTM; HIV; PRA; RFLP; PCR-restriction fragment length polymorphism analysis; ds.
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Pred. No. 2.5e-31;
0; Mismatches 25; Indels
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                                                                                                                                                                                                                                                                                                                    Mycobacterium fortuitum rpoB gene fragment.
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                        181 CCGAGGTGCCGGTTGAGACCGACGACAT 208
Kim S,
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                                                                                                                                                           BP
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88.0%;
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                                                                                                                                                           AAS05219 standard; DNA; 208
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Best Local S
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various Mycobacterial species. These rpoB gene fragments can be used
in the diagnosis and identification of Mycobacterium species using a
novel PCR-restriction fragment length polymorphism analysis (PRA)
method. The method comprises obtaining a restriction fragment length
complifying and digesting the DNA fragment from the microorganism to
be identified and comparing the RFLP patterns from the known rpoB gene
fragments with the unidentified fragment. The rpoB gene fragments
are useful to identify a wide range of Mycobacterium species, e.g. for
diagnosis or to obtain epidemiological and pathogenesis information for
selection of appropriate theraphes, including M. tuberculosis, M. leprae
and non-tuberculous mycobacteria (NTM) encountered in subjects infected
with human immunodeficiency virus (HIV). Analysis of the rpoB gene
fragments is rapid, precises, simple and cost effective (only 1 PCR
required), and can differentiate between many species in a single
experiment, including those difficult to distinguish by usual blochemical
control of a parcoprise of procies
control of a parcoprise of procies
control of the procies of the process (AAS05242) for
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                                      GCCTGAACACCAATCATCGATCACCACGACGACGCTGACCGAAGAGACGTCGTCGCCA 120
                                                     61 GCCTCCATGTCGGCGAGCCCATCACGTCGACGCTGACGCAAGAAGAAGACGTCGTGGCCA 120
                                                                                           121 CCATCGAGTATCTGGTCCGCCTGCACGAGGCCAGGCCACGATGACCGTGCCGGGGGGG 180
                                                                                                        121 CCATCGAATATCTGGTCCGCTTGCACGAGGGTCAGACCACGATGACCGTTCCGGGCGCG 180
TCAAGGAGAAGCGCTACGACCTGGCCCGCGTCGGTCGCTATAAGGTCAACAAGAAGCTCG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New DNA fragments from the rpoB gene of mycobacteria, useful for diagnosis and identification of many mycobacterial species by restriction fragment length polymorphism
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kim Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   specific Mycobacterial species.
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                                                                                                                                                                                                                                                                                                                              Mycobacterium terrae rpoB gene fragment
                                                                                                                                                             181 TCGAGGTGCCGGTGGAAACCGACGACAT 208
                                                                                                                                                 TCGAGGTGCCGGTGGAAACCGACGACAT 208
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                                                                                                                                                                                                                                            AAS05206 standard; DNA; 208 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HIV; PRA; RFLP;
ds.
                                                                                                                                                                                                                                                                                                                                                                          61 GCCTGAACACCAATCATCCGATCACCACGACGACGACGAAGAAGAAGACGTCGTCGCCA 120
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                                                                     Gaps
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                                                                                                                         1 TCAAGGAGAAGCGCTACGACCTGGCCCGTGTCGGCCGATACAAGGTCAACAAGAAGCTGG
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           Length 208;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Park HJ;
                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Non-tuberculous mycobacteria; rpoB gene fragment; NTM:
PCR-restriction fragment length polymorphism analysis;
Score 166.4; DB 22;
Pred. No. 5.9e-31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kim Y,
                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mycobacterium ulcerans rpoB gene fragment.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 43; 50pp; English.
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              Query Match 80.0%;
Best Local Similarity 87.5%;
Matches 182; Conservative
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required), and can differentiate between many species in a single experiment, including those difficult to distinguish by usual biochemical tests. Also described are oligonucleotide probes (AASO5227-AASO5242) for detecting specific Mycobacterial species.
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                                                                                                                                                                                                                                    121 CCATCGAATACCTGGTCCGCTTGCACGAGGGCCAGACCGCGATGACCGCTCCGGGCGGTG 180
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                                                                                                                Length 208;
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nes 26; Indels
                                                                                                             80.0%; Score 166.4; DB 22;
87.5%; Pred. No. 5.9e-31;
Live 0; Mismatches 26; I
                                                                                   Sequence 208 BP; 45 A; 68 C; 67 G; 28 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mycobacterium bovis rpoB gene fragment.
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Matches 182; Conservative
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                                                                                                                  Query Match
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are useful to identify a wide range of Mycobacterium species, e.g. for diagnosis or to obtain repidemiological and pathogenesis information for selection of appropriate therapies, including M. tuberculosis, M. leprae and non-tuberculous mycobacteria (NTM) encountered in subjects infected with human immunodeficiency virus (HTV). Analysis of the rpoB gene fragments is rapid, precise, simple and cost effective (only 1 PCR required), and can differentiate between many species in a single experiment, including those difficult to distinguish by usual biochemical tests. Also described are oligonucleotide probes (AASO5227-AASO5242) for detecting specific Mycobacterial species.
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                                                                                                                                                                                                                                                                                  Length 208;
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/note= "M. tuberculosis signature nucleotide"
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                                                                                                                                                                                                                                                                                     DB 22;
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                                                                                                                                                                                                                                                                                  80.0%; Score 166.4; DB 22;
87.5%; Pred. No. 5.9e-31;
iive 0; Mismatches 26;
                                                                                                                                                                                                                                           Sequence 208 BP; 46 A; 62 C; 67 G; 33 T; 0 other;
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/note= "primer DDIDHL"
226..240
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'note= "primer FENLFF"
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/note= "primer rpol05"
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/note= "primer DDIDH"
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/note= "primer rpo95"
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/note= "primer KY290"
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/*tag= h
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Matches 182; Conservative
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This oligonucleotide DNA primer is specific for Mycobacterium tuberculosis, and may be used to amplify a sample DNA by targeting a portion of the gene encoding rpoB. The 1st several bases comprise a nonhybridizing tail consisting of filler bases followed by a restriction site incorporated to facilitate cloning using the amplicon at a later date, if desired. The remaining bases hybridize to bacterial rpoB DNA. The method provides for the detection of M. tuberculosis and the concurrent determination of its drug susceptibility, particularly to rifamycin. The method can provide often greater than 95% sensitivity and 100% specificity. The biological sample is a fluid or tissue sample from a human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Detection of Mycobacterium tuberculosis - by amplifying sample DNA with a primer set that targets portions of the gene encoding rpoB.
/note= "M. tuberculosis signature nucleotide"
138
                                                        /*tag= j
/note= "M. tuberchlosis signature nucleotide"
486
                                          "M. tuberculosis signature nucleotide"
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note= "M. tuberculosis signature nucleotide"
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/note= "M. tuberculosis signature nucleotide"
516
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/note= "M. tuberculosis signature nucleotide"
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'note= "primer NMQRQ-1"
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/note= "primer NMQRQ-2"
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note= "primer rpo293"
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/note= "primer rpo397"
952..966
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'note= "primer KY292"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        polypeptide sequence that may be a drug target, or essential for growth or vlability of an organism. Polynucleotide sequences AAH51947 - AAH52092 represent DNA encoding proteins AAG81096 - AAG81241 Mycobacterium tuberculosis proteins which are potential drug targets. The DNA and protein sequences are used to illustrate the method of the invention. The method involves providing an unknown nucleotide or polypeptide sequences, and comparing it to a number of sequences along with at least one algorithm capable of analysing a functional relationship between nucleotide and polypeptide sequences. The method is useful for characterising the function of nucleic acids and polypeptides that may be useful as a target for a drug or essential for the growth or viability of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Identifying nucleotide or polypeptide sequence for use as drug target, involves providing algorithm that analyzes a functional relationship between nucleotide or polypeptide sequences, and comparing the
                                                                                                                                                  146 CCATCGAATATCTGGTCCGCTTGCACGAGGGTCAGCACCACGATGACCGTTCCGGGCGGCG
                                                                                                                               GCCTGAACACCAATCATCCGATCACCACGACGACGCTGACCGAAGAAGACGTCGTCGCCA 120
                                  Gaps
                                                                                              85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This invention relates to a method for identifying a nucleotide or
                                                                                26 TCAAGGAGAAGCGCTACGACCTGGCCCGCGTCGGTCGCTATAAGGTCAACAAGAAGCTCG
                                                                 1 TCAAGGAGAAGCGCTACGACCTGGCCCGTGTCGGCCGATACAAGGTCAACAAGAAGCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mycobacterium tuberculosis potential drug target gene SEQ ID 30
Length 970;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drug target; growth; organism viability; characterisation; ds.
                                26; Indels
 DB 17;
 Score 166.4; DB 1
Pred. No. 6.7e-31;
0; Mismatches 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Marcotte EM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 68-69; 207pp; English.
                                                                                                                                                                                                                                                                 181 TCGAGGTGCCGGTGGAAACCGACGACAT 208
                                                                                                                                                                                                                                                                                   AAH51976 standard; DNA; 3519 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99US-0165086.
99US-0165124.
2000US-0179531.
80.0%;
llarity 87.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-NOV-2000; 2000WO-US31152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rotstein SH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (REGC ) UNIV CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-329193/34.
P-PSDB; AAG81125.
                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200135317-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eisenberg D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-NOV-1999;
12-NOV-1999;
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                                  182;
                                                                                                                                                                                                                                                                                                                                                                                                                  AAH51976;
     Query Match
Best Local S
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AAH51976
                                Matches
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AAA74651;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes a method for generating a repertory of nucleic acids of tuf, fus, atpD and/or recA genes from which probes and/or primers are derived. The method comprises amplifying the nucleic acids of determined algal, archaeal, bacterial, fungal and parasitical species with a combination of defined primer pairs. The method can be used for producing probes and/or primers for detecting one or more related microorganisms e.g. algae, archaea, bacteria, fungi and parasites, for universal detection and for specific and ubiquitous detection and identification of an algal, archaeal, bacterial, fungal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      primers which can be used to identify and detect the presence of algal, archaeal, bacterial, fungal and parasitical species in a test sample {}^{\circ}
                                                                                                                                                                                            1004 CCATCGAATATCTGGTCCGCTTGCACGAGGTCAGACCACCAGATGACCGTTCCGGCGCGC 1063
                                                                                                                                                                         61 GCCTGAACACCAATCATCCGATCACCACGACGCTGACCGAAGAAGACGTCGTCGCCA 120
                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Species specific; genus specific; family specific; probe; detection; identification; algal; archaeal; bacterial; fungal; parasitical; microorganism; diagnosis; translation elongation factor Tu; toxin; translation elongation factor G; RecA recombinase; resistance; catalytic subunit of proton-translocating ATPase; antimicrobial;
                                                                                                       1 TCAAGGAGAAGCGCTACGACCTGGCCCGTGTCGGCCGATACAAGGTCAACAAGAAGCTGG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acid sequences are used to generate universal probes and
                                 Length 3519;
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                                                 .4e-31;
les 26; Indels
Sequence 3519 BP; 675 A; 1081 C; 1183 G; 580 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Menard C,
                               DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 1478-1479; 1580pp; English.
                                 Score 166.4; D
Pred. No. 7.4e-
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                     TCGAGGTGCCGGTGGAAACCGACGACAT 1091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (INFE-) INFECTIO DIAGNOSTIC (IDI) INC.
                                                                                                                                                                                                                                                                                                                    TCGAGGTGCCGGTGGAAACCGACGACAT
                                                                                                                                                                                                                                                                                                                                                                                                                                             BP
                                                                                                                                                                                                                                                                                                                                                                                                                                           AAH02079 standard; DNA; 3534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-SEP-2000; 2000WO-CA01150.
                                 Query Match 80.0%;
Best Local Similarity 87.5%;
Matches 182; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-SEP-1999; 99CA-2283458.
19-MAY-2000; 2000CA-2307010.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mycobacterium tuberculosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       I MG, bo_
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             vaccine; primer; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200123604-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAH02079;
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                                                                                                                                                                                                                                             121
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                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 14
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and parasitical species, genus, family and group. A nucleic acid (I) obtained using the method of the invention can be used for the universal detection of any bacterium, fungus or parasite in a sample and for the detection of at least one antimicrobial agent resistance gene or at least one toxin gene. hexA nucleic acids are used for the specific and ubjuditous detection and for identification of Streptococcus pneumoniae. (I) can be used to design a therapeutic agent which is effective against microorganisms. Microbial species or genus or family or phylum or group which can be detected include Abiotrophia adiacens, Bordetella sp., Corynebacterium sp., Enterobacteriaceae group, Escherichia coli, Mycobacteriaceae family, Pseudomonads group, Streptococcus sp., Whosecteriaceae family, Pseudomonads group, Streptococcus sp., Weisseria gonorrhoeae and Staphylococcus sp., Using DNA based tests provides faster results than substrate specificity tests as results can be determined in an hour and improved accuracy is also achieved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAH00010 to AAH002304 represent nucleotide sequences and primers/probes which are given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         962 GGCTGCATGTCGGCGGAGCCCATCACGTCGTCGACGCTGACCGGAAGAAGACGTCGTGGCCA 1021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 GCCTGAACACCAATCATCCGATCACCACGACGACGCTGACCGAAGAGACGTCGTCGCCA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 TCAAGGAGAAGCGCTACGACCTGGCCCGTGTCGGCCGATACAAGGTCAACAAGAAGCTGG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Method for detecting drug resistance in a strain of an organism, particularly for detecting rifampin resistance in Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 80.0%; Score 166.4; DB 22; Length 3534; Best Local Similarity 87.5%; Pred. No. 7.4e-31; Matches 182; Conservative 0; Mismatches 26; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3534 BP; 679 A; 1081 C; 1188 G; 586 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1082 TCGAGGTGCCGTGGAAACCGACGACAT 1109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 TCGAGGTGCCGGTGGAACCGACGACAT 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mycobacterium tuberculosis rpoB gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200043546-A2.
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The present sequence is the rpoB gene from Mycobacterium tuberculosis. Rifamphin resistance is largely associated with point mutations localised in a small core region of 81 base pairs in the rpoB gene, which encodes the RNA polymerase beta subunit. To detect a mutation, a complex is formed comprising a first sequence representing the predetermined region of the gene of the organism and a second sequence representing the corresponding region of the gene of the wild type organism in double stranded form. Each member of at least one pair of non-complementary stranded form. Each persence of the mutation of the labels in the complex has a label. The association of the labels in the complex is related to the presence of the mutation. The presence of the mutation is related to the drug resistance of the strain.
Example 1; Fig 4; 86pp; English.
\overset{\circ}{\times}\overset{\circ}{\times}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\ci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Sequence 3853 BP; 723 A; 1173 C; 1293 G; 664 T; 0 other;

ö 0; Gaps Ouery Match 80.0%; Score 166.4; DB 21; Length 3853; Best Local Similarity 87.5%; Pred. No. 7.5e-31; Matches 182; Conservative 0; Mismatches 26; Indels 0;

1 TCAAGGAGAAGCGCTACGACCTGGCCCGTGTCGGCCGATACAAGGTCAACAAGAAGCTGG g õ ò

61 GCCTGAACACCAATCATCCGATCACCACGACGCTGACCGAAGAAGACGTCGTCGCCA 120 QQ

1597 CCATCGAATATCTGGTCCGCTTGCACGAGGGTCAGACCACGATGACCGTTCCGGCGCGC 1656 ò op

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Search completed: November 12, 2002, 16:50:09 Job time : 141.222 secs